ISSN 2096-7071
CN 10-1629/R1

CHINA CDC WEEKLY

Vol. 2 No. 27 Jul. 3, 2020

CCDC weekly

中国疾病预防控制中心周报

Preplanned Studies

Notes from the Field

Outbreak Reports

Insights

ISSN 2096-7071
9 772096 707200 27

China CDC Weekly

Editorial Board

Editor-in-Chief George F. Gao

Deputy Editor-in-Chief Liming Li Gabriel M Leung Zijian Feng

Executive Editor Feng Tan

Members of the Editorial Board

Xiangsheng Chen
Xiaoyou Chen
Zhuo Chen (USA)
Xianbin Cong
Gangqiang Ding
Xiaoping Dong
Mengjie Han
Guangxue He
Xi Jin
Biao Kan
Haidong Kan
Qun Li
Tao Li
Zhongjie Li
Min Liu
Qiyong Liu
Jinxing Lu
Huiming Luo
Huilai Ma
Jiaqi Ma
Jun Ma
Ron Moolenaar (USA)
Daxin Ni
Lance Rodewald (USA)
RJ Simonds (USA)
Ruitai Shao
Yiming Shao
Xiaoming Shi
Yuelong Shu
Xu Su
Chengye Sun
Dianjun Sun
Hongqiang Sun
Quanfu Sun
Xin Sun
Jinling Tang
Kanglin Wan
Huaqing Wang
Linhong Wang
Guizhen Wu
Jing Wu
Weiping Wu
Xifeng Wu (USA)
Zunyou Wu
Fujie Xu (USA)
Wenbo Xu
Hong Yan
Hongyan Yao
Zundong Yin
Hongjie Yu
Shicheng Yu
Xuejie Yu (USA)
Jianzhong Zhan
Liubo Zhang
Rong Zhang
Tiemei Zhang
Wenhua Zhao
Yanlin Zhao
Zhijie Zheng (USA)
Maigeng Zhou
Xiaonong Zhou
Baoping Zhu (USA)

Advisory Board

Director of the Advisory Board Xinhua Li

Vice-Director of the Advisory Board Yu Wang Jianjun Liu

Members of the Advisory Board

Chen Fu
Gauden Galea (Malta)
Dongfeng Gu
Qing Gu
Yan Guo
Ailan Li
Jiafa Liu
Peilong Liu
Yuanli Liu (USA)
Roberta Ness (USA)
Guang Ning
Minghui Ren
Chen Wang
Hua Wang
Kean Wang
Xiaoqi Wang
Zijun Wang
Fan Wu
Xianping Wu
Jingjing Xi
Jianguo Xu
Gonghuan Yang
Tilahun Yilma (USA)
Guang Zeng
Xiaopeng Zeng
Yonghui Zhang

Editorial Office

Directing Editor Feng Tan

Managing Editors Lijie Zhang Qian Zhu

Scientific Editors Ning Wang Ruotao Wang

Editors Weihong Chen Yu Chen Peter Hao (USA) Xudong Li Jingxin Li Xi Xu Qing Yue Ying Zhang

---

Cover Photo: In response to COVID-19, the China CDC Mobile P3 Laboratory Truck was deployed to Wuhan, Hubei Province (February 5 to March 29), Mudanjiang, Heilongjiang Province (April 22 to May 13), Jinlin, Jilin Province (from May 14 to June 5), and Fengtai District, Beijing Municipality (June 17 to present) to assist with nucleic acid testing, viral genome sequencing, and setting up local viral labs by training local lab staff.

Preplanned Studies

Serial Interval and Reproductive Number of COVID-19 Among 116 Infector-infectee Pairs — Jingzhou City, Hubei Province, China, 2020

Tian Liu[1,2,&]; Li Qi[3,4,&]; Menglei Yao[1]; Keqing Tian[1]; Maowen Lin[1]; Hong Jiang[1]; Minmin Zeng[1]; Jigui Huang[1,#]

Summary

What is already known about this topic?

The key epidemiological parameters including serial interval, basic reproductive number (R_0), and effective reproductive number (R_t) are crucial for coronavirus disease 2019 (COVID-19) control and prevention. Previous studies provided different estimations but were often flawed by some limitations such as insufficient sample size and selection bias.

What is added by this report?

In this study, a total of 116 infector-infectee pairs meeting strict inclusion criteria were selected for analysis. The mean serial interval of COVID-19 was 5.81 days (standard deviation: 3.24). The estimated mean with 95% confidence interval of R_0 was 3.39 (3.07–3.75) and 2.98 (2.62–3.38) using exponential growth (EG) and maximum likelihood (ML) methods, respectively. The R_t in the early phase of the epidemic was above 1 with the peak of 4.43 occurring on January 8, and then showing subsequent declines and approaching 1 on January 24.

What are the implications for public health practices?

This study supports previous findings that COVID-19 has high transmissibility and that implementing comprehensive measures is effective in controlling the COVID-19 outbreak.

Coronavirus disease 2019 (COVID-19) is a respiratory infectious disease caused by COVID-19 virus, also know as SARS-CoV-2 and 2019-nCoV, that was first identified in Wuhan City, Hubei Province, China in December 2019. By April 24, 2020, COVID-19 has affected more than 2 million individuals and caused 15,000 deaths worldwide (*1*). Rapid and robust responses by the global scientific community described many key aspects of the transmission and natural history of COVID-19 (*2*), but the full spectrum of the epidemiological characteristics of the disease still require illustration; in particular, several key epidemiological parameters remain to be clarified.

In this study, we aimed to estimate serial interval, basic reproductive number (R_0) of COVID-19, and the time-dependent reproductive number (R_t) using epidemiolocal data from 1,365 confirmed cases and 116 infector-infectee pairs in Jingzhou City, Hubei Province. Jingzhou City was the fourth largest city with confirmed cases in Hubei Province, which was the epicenter of the COVID-19 epidemic in China.

We obtained data of laboratory-confirmed COVID-19 cases and clusters from Jingzhou City CDC in Hubei Province, China, from January 1, 2020 to March 12, 2020. A laboratory-confirmed case was defined as a case with a positive test of COVID-19 virus using the real-time reverse transcription polymerase chain reaction (real-time RT-PCR) assay.

The serial interval was defined as the time between symptom onset in a primary case (infector) and a second case (infectee) in a transmission chain (*3*). The serial interval distribution was estimated from the time lag between all infector-infectee pairs (*3*). In this study, we selected infector-infectee pairs by the following criteria: 1) the infectee had a clear history of contact with the infector; 2) the infectee had no history of contact with other confirmed or suspected COVID-19 cases; and 3) the infectee had no history of travel or residence in an area affected by COVID-19 within 14 days before symptom onset. Criteria 2 and 3 were used to exclude those infector-infectee pairs in which the infector and infectee shared a common source of exposure to a COVID-19 case or a place where cases were identified. We fit the probability distribution of the serial interval with three methods named "gamma", "Weibull", and "lognormal", and calculated the mean and standard deviation of serial interval using the best-fit method.

We assessed two types of different reproductive numbers: the basic reproductive number (R_0) and the effective reproductive number (R_t). R_0 was defined as the expected number of secondary infectious cases that one primary case will generate in a susceptible population (*4*). R_0 is a key indicator of the transmissibility of disease. R_t is an indicator of real-time transmissibility of disease, which is frequently used to evaluate the effectiveness of disease control measures. In this study, we estimated R_0 for COVID-19 using the maximum likelihood (ML) method (*5*) and exponential growth (EG) method (*5*) and evaluated the goodness of fit by coefficient of determination (R^2). A higher R^2 represents smaller differences between the observed data and the fitted values. We estimated R_t using a time-dependent method (*5*).

All statistical analyses and visualization were conducted using "R0" and "ggplot2" packages in R software 3.6.2 (R Development Core Team, Vienna, Austria). Two tailed $p<0.05$ was considered statistically significant for all statistical tests. To quantify the effect of parameters on R_0, a series of sensitivity analyses were conducted by varying the mean serial interval and transmission start date. The R^2 statistic was calculated to evaluate the goodness of fit of the model.

The first confirmed COVID-19 case in Jingzhou City was identified on January 1, 2020 with an average daily increase of 1–2 cases for the next 9 days. After that, the number of confirmed cases of COVID-19 started to increase rapidly to a total of 1,365 confirmed cases and 51 deaths reported as of March 12, 2020. The epidemic curve according to the illness onset date and key interventions date are shown in Figure 1.

A total of 116 infector-infectee pairs that met with the inclusion criteria were included in our analysis. Gamma distribution performed better than the other two methods. The serial interval distribution of COVID-19 is shown in Figure 2. The mean serial interval of COVID-19 was estimated as 5.81 days (standard deviation: 3.24).

Using the serial interval distribution described above, we estimated that R_0 was 2.98 (95% CI: 2.62–3.38) and 3.39 (95% CI: 3.07–3.75) by the ML and EG methods, respectively. The coefficient of determination (R^2) of the EG model (0.97) was higher than that of ML (0.75), which represents smaller differences between the observed data and the fitted values (Figure 3A).

The time-dependent reproductive number (Rt) in the early phase of the epidemic was above 1, with the peak of 4.43 (95% CI: 1.00–9.00) on January 8, then showed declines and approached 1 on January 24 (Figure 3B).

The results of sensitivity analyses indicated the robustness of R_0 estimation. The R_0 estimated by EG method ranged between 2.12 (95% CI: 2.00–2.26) to 4.51 (95% CI: 3.97–5.13) when the mean serial interval increased from 1.5 and 5 days, all of which are significantly higher than 1. Moreover, R_0 was

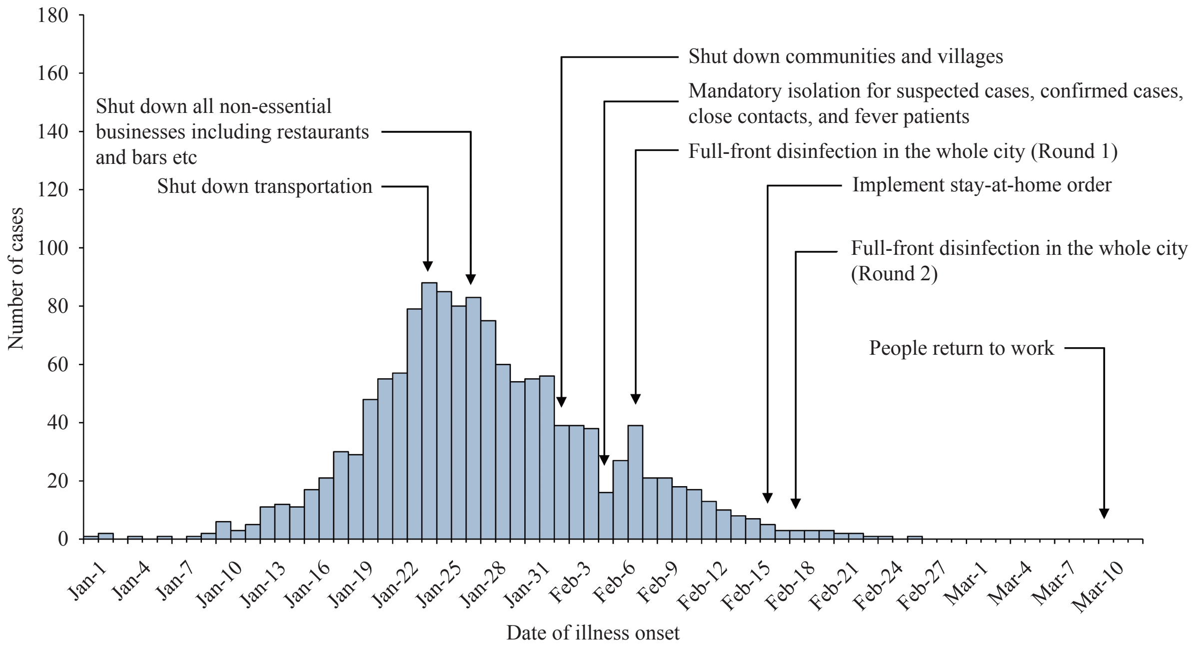


FIGURE 1. Onset of illness among 1,365 confirmed cases of COVID-19 in Jingzhou City, Hubei Province, China.

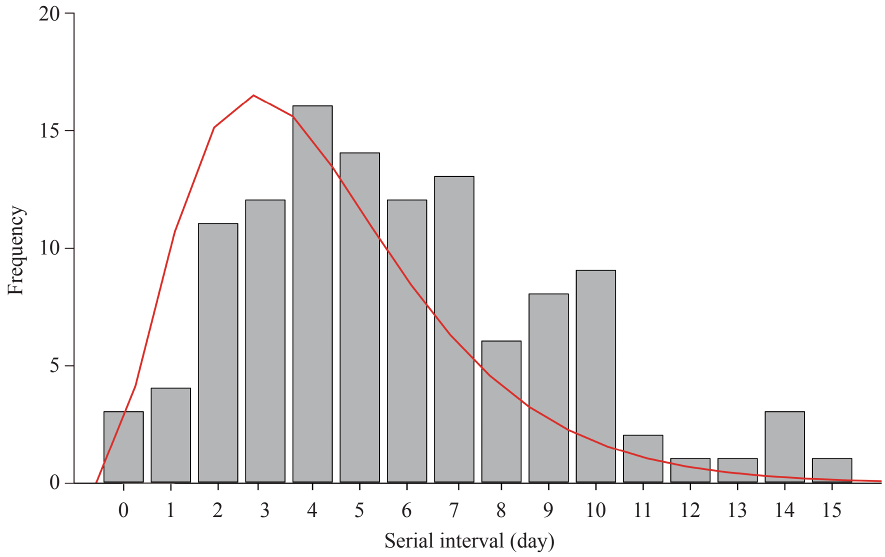


FIGURE 2. The distribution of serial interval of COVID-19 based on 116 infector-infectee transmission pairs in Jingzhou City, Hubei Province, January 1–March 12, 2020. The gray bars indicate the number of infector-infectee pairs with specified serial intervals, and the red line indicates the estimated serial interval distribution of COVID-19 infection.

estimated as 3.23 (95% CI: 2.88–3.64) by the EG method and R^2 reached its peak when we simulated the transmission start date on January 9, 2020.

DISCUSSION

In this study, we estimated two important parameters of COVID-19 including serial interval and R_0 using epidemiology data from Jingzhou City, Hubei Province. In order to estimate the serial interval more accurately, we set strict inclusion and exclusion criteria of infector-infectee pairs for analysis. The mean serial interval was estimated as 5.81 days (SD=3.24), which was higher than the estimate by Nishiura et al (4.6 days) (*6*) but lower than the early estimation in Wuhan City (7.5 days) (*4*). The difference in estimated serial intervals might be associated with different phases of the pandemic. The shorter serial interval of COVID-19 compared to SARS implies that contact tracing must be rapidly carried out to stop rapid replacement of case generation. Otherwise the number of cases is expected to quickly exceed capability of existing health and emergency response systems.

We estimated the R_0 value of approximately 3.4 and 3.0 by using the EG and ML methods, meaning that on average, each patient had been spreading infection to more than three other people. Our estimation is comparable to several recent studies (*4,7–9*); the R_0 value is also significantly larger than 1 and also much higher than that of SARS (*10*), which indicated a higher level of transmission. This discrepancy of R_0 between COVID-19 and SARS may be partially explained by transmission patterns. Clinical evidence showed that asymptomatic cases or mild cases could effectively transmit COVID-19, which was different from SARS because most SARS cases were transmitted by "super spreaders", and cases in incubation period and mild cases could not infected susceptible persons (*7,11*).

Furthermore, we found that the effective reproductive number was less than 1 after implementation of interventions, which indicated that tremendous joint efforts from the local government, healthcare workers, and the people in Jingzhou City had effectively reduced community spread of the disease. Therefore, containment measures should be implemented including rapid identification and isolation of cases, active contact tracing and quarantining, strict social distancing, community education, and precautions such as frequent hand sanitizing and the use of personal protection equipment (e.g. face masks), which were helpful for suppressing expansion of COVID-19 outbreak worldwide.

This was the first study to assess the serial interval of COVID-19 using more than 100 infector-infectee pairs that met strict inclusion criteria. The sample size was much greater than that of recent studies (*4,6,8–9*), which have less than 50 infector-infectee pairs.

This study was subject to some limitations. First, asymptomatic contacts may have been missed because

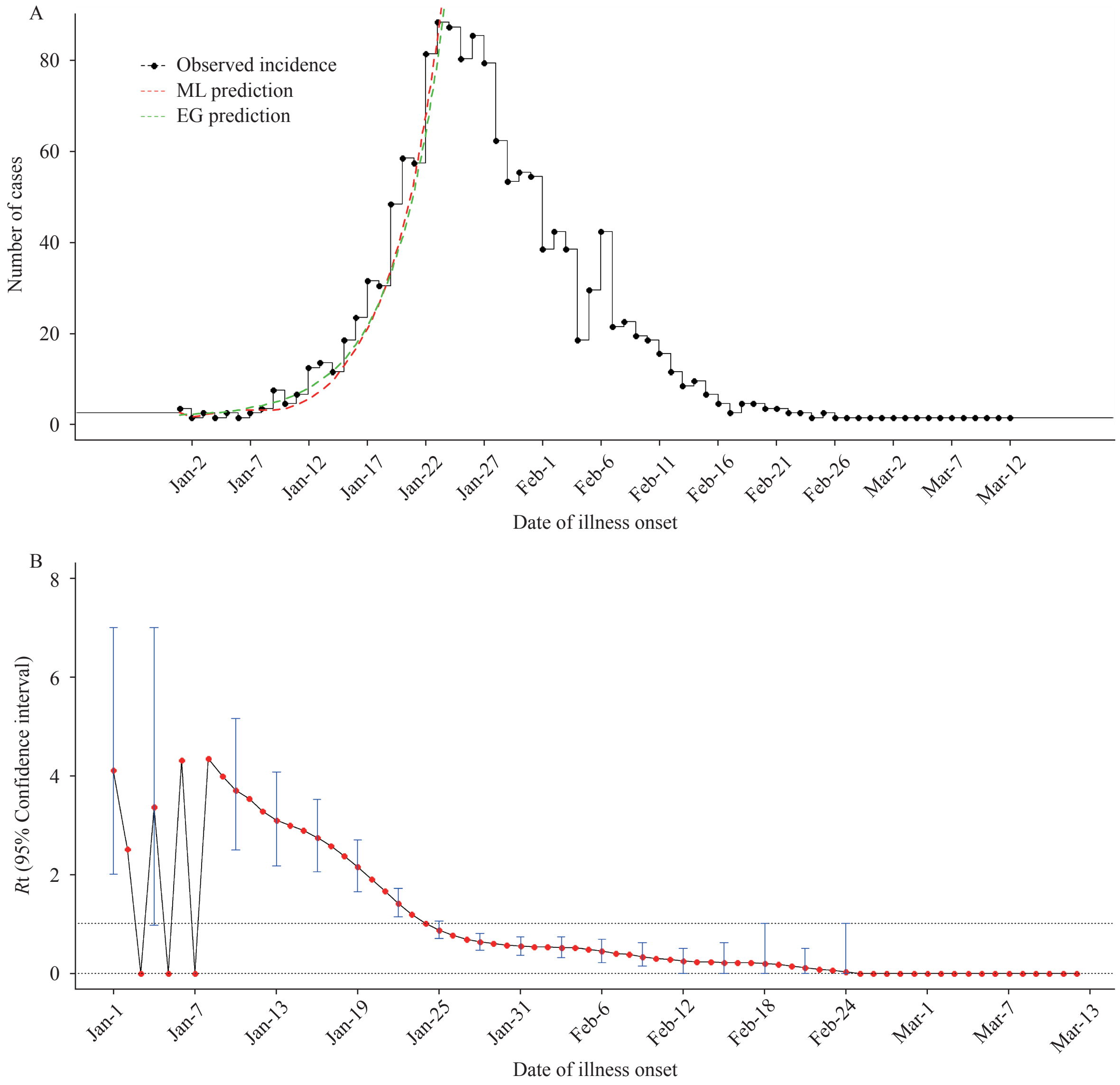


FIGURE 3. The fitted results in this study. (A) The observed incidence and fitted daily incidence by using the exponential growth model (EG) and maximum likelihood estimation (ML) methods. (B) The temporal distribution of time-dependent reproductive number (R_t) values of COVID-19 in Jingzhou City, Hubei Province. The red points represent mean R_t and the blue vertical bars represent 95% confidence intervals.

RT-PCR tests were mainly provided for patients with fever in the hospital early on in the epidemic and due to the imperfect sensitivity of the RT-PCR test (*12*). Second, as in any active outbreak response, the data were collected by multiple teams under protocols that, by necessity, changed as the situation developed. Hence, there may be inconsistencies in the definitions. Finally, strict inclusion and exclusion criteria of the study may have affected the representativeness of the study sample.

Acknowledgments: We thank all patients, close contacts and their families involved in the study; as well as the frontline medical staff and public health workers who collected this critical data.

Conflict of interest: The authors declare that they have no conflict of interest.

Fundings: This work was supported by Chongqing Health Commission (grant number 2019GDRC014) and China Postdoctoral Science Foundation (grant number 2019M660754).

doi: 10.46234/ccdcw2020.118

[#] Corresponding author: Jigui Huang, jzcrbs@163.com.

---

[1] Department of Infectious Diseases Prevention and Control, Jingzhou Center for Disease Control and Prevention, Jingzhou city, Hubei Province, China; [2] Chinese Field Epidemiology Training Program, Chinese Center for Disease Control and Prevention, Beijing, China; [3] Department of Infectious Diseases Prevention and Control,

Chongqing Municipal Center for Disease Control and Prevention, Chongqing, China; [4] State Key Laboratory of Infectious Disease Prevention and Control, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China.
[&] Joint first authors.

Submitted: June 16, 2020; Accepted: June 30, 2020

REFERENCES

1. World Health Organization. WHO coronavirus disease (COVID-19) dashboard. https://covid19.who.int/. [2020-06-04].
2. Du ZW, Xu XK, Wu Y, Wang L, Cowling BJ, Meyers LA. Serial interval of COVID-19 among publicly reported confirmed cases. Emerg Infect Dis 2020;26(6):1341 – 43. http://dx.doi.org/10.3201/eid2606.200357.
3. Svensson Å. A note on generation times in epidemic models. Math Biosci 2007;208(1):300 – 11. http://dx.doi.org/10.1016/j.mbs.2006.10.010.
4. Li Q, Guan XH, Wu P, Wang XY, Zhou L, Tong YQ, et al. Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia. N Engl J Med 2020;382(13):1199 – 207. http://dx.doi.org/10.1056/NEJMoa2001316.
5. Obadia T, Haneef R, Boëlle PY. The R0 package: a toolbox to estimate reproduction numbers for epidemic outbreaks. BMC Med Inform Decis Mak 2012;12:147. http://dx.doi.org/10.1186/1472-6947-12-147.
6. Nishiura H, Linton NM, Akhmetzhanov AR. Serial interval of novel coronavirus (COVID-19) infections. Int J Infect Dis 2020;93:284 – 6. http://dx.doi.org/10.1016/j.ijid.2020.02.060.
7. Zhao S, Lin QY, Ran JJ, Musa SS, Yang GP, Wang WM, et al. Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: a data-driven analysis in the early phase of the outbreak. Int J Infect Dis 2020;92:214 – 7. http://dx.doi.org/10.1016/j.ijid.2020.01.050.
8. Bi QF, Wu YS, Mei SJ, Ye CF, Zou X, Zhang Z, et al. Epidemiology and transmission of COVID-19 in 391 cases and 1286 of their close contacts in Shenzhen, China: a retrospective cohort study. Lancet Infect Dis 2020. http://dx.doi.org/10.1016/S1473-3099(20)30287-5.
9. Zhang JJ, Litvinova M, Wang W, Wang Y, Deng XW, Chen XH, et al. Evolving epidemiology and transmission dynamics of coronavirus disease 2019 outside Hubei province, China: a descriptive and modelling study. Lancet Infect Dis 2020;20(7):793 – 802. http://dx.doi.org/10.1016/S1473-3099(20)30230-9.
10. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and control of severe acute respiratory syndrome. Science 2003;300(5627):1966 – 70. http://dx.doi.org/10.1126/science.1086616.
11. Ling ZK, Xu X, Gan QX, Zhang LG, Luo LP, Tang XP, et al. Asymptomatic SARS-CoV-2 infected patients with persistent negative CT findings. Eur J Radiol 2020;126:108956. http://dx.doi.org/10.1016/j.ejrad.2020.108956.
12. Tang A, Tong ZD, Wang HL, Dai YX, Li KF, Liu JN, et al. Detection of novel coronavirus by RT-PCR in stool specimen from asymptomatic child, China. Emerg Infect Dis 2020;26(6):1337 – 9. http://dx.doi.org/10.3201/eid2606.200301.

Preplanned Studies

Health Status and Food Intake Frequency of Elderly Residents During COVID-19 Community Closure — Jiangxia District, Wuhan City, China, 2020

Pengkun Song[1]; Cheng Li[1]; Ganyu Feng[1]; Jian Zhang[1]; Li Li[1]; Titi Yang[1]; Mingna Dong[2]; Ailing Liu[1];
Qi Zhang[3]; Yujing Liu[3]; Jinglei Wang[3]; Tanxi Ge[3]; Qing Yu[4,#]; Gangqiang Ding[1,#]

Summary

What is already known about this topic?

Elderly persons are vulnerable to infectious diseases, and nutritional status and health conditions were important to evaluate for disease prevention and ability to recover for the elderly during the coronavirus disease 2019 (COVID-19) pandemic.

What is added by this report?

In our study, a rapid assessment questionnaire was used to investigate the change of household life and dietary intake of the elderly (aged 60 years or more) during community closure. Food consumption frequency of aquatic food products, soybeans, and fresh fruits declined dramatically with reductions of 70.9%, 70.9%, and 53.0%, respectively, and 49.6% of the elderly lived with chronic non-communicable diseases but had little knowledge of nutrition and health.

What are the implications for public health practice?

Community closure measures in Wuhan City have played a key role in cutting off the transmission route of COVID-19 and protecting vulnerable groups. As a high-risk population, the elderly should be advised to maintain and strengthen a balanced diet with proper nutrition through increasing intake of aquatic food products, soybeans, fruits, and vegetables, reducing total caloric intake, and decreasing oil and salt consumption. These measures will be significant for the elderly to reduce the risk of chronic disease complications and COVID-19 infection and to decrease the chance of critical illness.

The coronavirus disease 2019 (COVID-19) pandemic presented great physical and mental challenges for the residents of Wuhan (*1*). Elderly individuals aged 60 years or more were more susceptible and vulnerable to infectious diseases due to comparatively weaker immune functions and were a high-risk group in the pandemic. Except for effective personal protection, balanced diets and proper nutrition were effective means to maintain the immune function of the elderly. To assess the change of diet and health status of the elderly after community closure measures, we conducted a survey in Jiangxia District of Wuhan City, Hubei Province.

Considering the feasibility of field investigations, we selected two communities (A and B) in the Zhifang Sub-District, which had relatively strict management due to higher numbers of diagnosed cases compared to other sub-districts in Jiangxia District. The residents of the two communities were relatively concentrated; 11.6% of Community A were elderly individuals under social community management (where the community was managed by its own members) and 48.5% of Community B were elderly under factory group management (where residents had family members working in the factory, and this factory managed the community). Anonymous online surveys were conducted in Community A, and because some elderly individuals could not use smart phones, family members helped complete the online survey. Questionnaires in Community B were completed in person by trained team members.

A total of 117 questionnaires were completed from March 16 to 23, 2020 after 3 participants were excluded for being aged under 60 years. Overall, 35.9% of the questionnaires were completed independently, and 64.1% were completed by family members or community workers. SAS 9.4 software (SAS Institute Inc., Cary, NC, USA) was applied for statistical analysis. T-tests, analysis of variance, and chi-square tests were used to compare the differences among subgroups. Bilateral $p<0.05$ was considered as statistically significant.

In our survey, 45.3% of the participants were male and the ratio of genders was 1:1.21. The average age of the elderly was 72.2 ± 8.5 years (range: 60–102 years) with a similar average age in both genders. As for education, 67.5% of the elderly had schooling of 9 years or less (equivalent to junior high school or below), and 15.4% had schooling of 13 years and above (equivalent to a college or tertiary education). Among the older participants, the smoking rate was 16.2% (26.4% for men and 7.8% for women). An estimated 49.6% of the elderly suffered from chronic diseases including 69.0% having hypertension and those with diabetes, osteoporosis, and tumors accounted for 15.5%, 15.5% and 15.5%, respectively. An estimated 69.0% of surveyed individuals were chronically taking 3 or more medications. During the pandemic, 72.6% of the elderly reported that they did not pay attention to diet and nutrition, and 95.7% of the elderly did not deliberately take nutritional supplements. In our study, 21.4% of the elderly did not know their weight and 61.5% neglected waist circumference. A proportion of 15.2% in those who knew their weight reported an increased weight, while 22.2% had reductions in weight. There were statistically significant differences between gender, age, education, health status, and change of body weight between the 2 communities ($p<0.05$) (Table 1).

During the community closure period, the elderly reported that basic food and drink were mainly supplied by local community (83.8%) and family reserves (70.1%). There was a higher proportion of online purchasing in Community A (36.8%) than in Community B (13.3%) with statistically significant differences ($p<0.01$). The elderly in Community A also reported a statistically higher proportion of food reductions (43.9%) than in Community B (1.7%; $p<0.01$), and also a higher proportion of the elderly ate two meals per day or less in community A than community B (38.6% *vs.* 5.0%, $p<0.01$). Furthermore, only 21.4% of the elderly met the recommended 1,500 mL of daily water intake (Table 1).

About 83.8% of the elderly consumed rice or wheat products once or more per day, and 82.1% consumed fresh vegetables more than one time a day. The proportion of the elderly who consumed red meat and poultry once a week or more was 69.2%. The frequency of egg consumption of the elderly was 63.3% of at least once a day and 28.2% of 1–6 times a week. However, the proportions of elderly consuming soybeans, milk, and aquatic food products (including freshwater fish, marine fish, shrimp, crab, shellfish and other animal aquatic products excluding seaweed, kale, etc.) less than once a week were 73.5%, 61.6%, 60.6%, respectively. Red meat and poultry intake frequency of more than once a day among males was significantly higher than that in female (52.8% *vs.* 34.4%, $p<0.01$). Potatoes consumption frequency of more than once per day among individuals aged 80 years and above was significantly lower than that of individuals aged 70–79 years and individuals aged 60–69 years (10.7%, 20.0%, 16.3%; $p<0.05$). However, there were no statistically significant differences of intake frequency of specific foods between the elderly in better health status and those living with chronic diseases. When compared with before community closures, the proportions of elderly consuming dramatically less aquatic food products, soybeans, and fresh fruit after community closures were 70.9%, 70.9%, and 53.0%, respectively. Subgroup analysis showed that the consumption of rice/wheat products and coarse grains was significantly reduced among females than in males (rice/wheat products: 21.9% *vs.* 5.7%, coarse grains: 46.9% vs. 24.5%, $p<0.05$), but healthy individuals consumption of eggs, red meat, and poultry were reportedly more significantly reduced than in individuals with chronic diseases (eggs: 22.0% *vs.* 6.9%; red meat and poultry: 44.1% *vs.* 32.8%; $p<0.05$)(Table 2).

Table 3 showed that 85.5%, 83.8%, 79.5%, 73.5%, 70.9%, and 60.7% of the elderly consumed milk, potatoes, coarse grains, soybeans, fresh fruits, and aquatic food products lower than recommended levels. Females also showed much higher rates of not consuming recommended amounts of rice/wheat products, red meat, and poultry when compared to males (rice/wheat products: 23.4% *vs.* 7.6%; red meat and poultry: 45.3% *vs.* 13.2%).

DISCUSSION

This investigation demonstrated that dietary nutrition status of the elderly was affected during the COVID-19 pandemic in Wuhan as their consumption of aquatic food products, soybeans and fresh fruits decreased significantly. Furthermore, unreasonable and unbalanced diet structure combined with decreased physical activity will increase the risk of chronic diseases. Therefore, the elderly should maintain balanced diet as well as an active lifestyle during the pandemic.

During the period of community closure in Wuhan, early of foods reservs such as rice, flour, oil, vegetables, eggs, meats, and poultry were often prioritized at the family level. These basic foods provided adequate energy and moderate levels of protein to prevent severe energy-protein malnutrition from occurring in the short term. In addition, community food supplies were

TABLE 1. Characteristics of participants in two communities during the period of community closure.

variables	Community A (n=57)	Community B (n=60)	Total (n=117)
Female (n, %)	37 (64.9)	27 (45.0)[*]	64(54.7)
Age (mean ± sd)	69.4±8.4	74.8±7.7[†]	72.2±8.5
Age group (n, %)			
60–69 years	31 (54.4)	18 (30.0)[†]	49 (41.9)
70–79 years	17 (29.8)	23 (38.3)	40 (34.2)
80 years and above	9 (15.8)	19 (31.7)	28 (23.9)
Education level (n, %)			
Primary school and below	30 (52.6)	9 (15.0)[†]	39 (33.3)
Junior high school	11 (19.3)	29 (48.4)	40 (34.2)
Senior high school	6 (10.5)	14 (23.3)	20 (17.1)
College or other tertiary education	10 (17.6)	8 (13.3)	18 (15.4)
Smoking (n, %)	9 (15.8)	10 (16.7)	19 (16.2)
Living with chronic diseases[§] (n, %)	16 (28.1)	42 (70.0)[†]	58 (49.6)
Hypertension (n, %)	10 (62.5)	30 (71.4)	40 (69.0)
Diabetes (n, %)	4 (25.0)	5 (11.9)	9 (15.5)
Osteoporosis (n, %)	5 (31.2)	4 (9.5)	9 (15.5)
Tumors (n, %)	5 (31.2)	4 (9.5)	9 (15.5)
Chronic use of 3 or more medications (n, %)	13 (81.2)	27 (64.3)[*]	40 (69.0)
Paid attention to diet and nutrition (n, %)	6 (10.5)	26 (43.3)[**]	32 (27.4)
Taking nutritional supplements (n, %)	1 (1.8)	4 (6.7)	5 (4.3)
Current self-reported body weight (mean±sd)	59.4±14.2	62.3±11.0	61.0±12.5
Former self-reported body weight (mean±sd)	59.9±13.9	63.3±11.1[†]	61.8±12.4
Body weight change during community closure[¶]			
No change (n, %)	15 (48.4)	30 (73.2)[*]	45 (62.5)
Weight gain (n, %)	8 (25.8)	3 (7.3)	11 (15.2)
Weight loss (n, %)	8 (25.8)	8 (19.5)	16 (22.2)
Self-reported waist circumference (mean±sd)	84.9±14.3	87.7±12.3	86.8±12.9
Food sources (n, %)			
Local community supplies	45 (79.0)	53 (88.3)	98 (83.8)
Family reserves	39 (68.4)	43 (71.7)	82 (70.1)
Online purchase	21 (36.8)	8 (13.3)[†]	29 (24.8)
Food intake reduction during community closure (n, %)	25 (43.9)	1 (1.7)[†]	26 (22.2)
Consuming 2 meals per day or fewer during community closure (n, %)	22 (38.6)	3 (5.0)[†]	25 (21.4)
Water intake of at least 1,500 mL per day (n, %)	8 (14.0)	17 (28.3)	25 (21.4)

[*]: Comparison of variables between two communities, $p<0.05$.

[†]: Comparison of variables between two communities, $p<0.01$.

[§]: Chronic diseases included cardiovascular and cerebrovascular diseases, cancer, diabetes, and chronic respiratory diseases.

[¶]: The weight change was calculated among those who had known their body weights both before and after community closure.

a complementary addition for household food stocks. But due to different community management, there were differences in the variety and quantity of the food supply, which potentially influenced the food intake of the elderly. Due to limits in the food supply and insufficient intake of fresh fruits, soybeans, and aquatic food products, the elderly inevitably experienced a lack of high-quality protein, calcium, vitamins, and essential fatty acids, so increasing the variety of available food should be a priority as the communities return to normalcy. In addition, high-quality protein plays an important role in improving immunity of the

TABLE 2. Intake frequency of specific foods and reductions* among elderly participants during the period of community closure.

Food items	Gender (%)		Age group (%)			Healthy status[†] (%)		Total (%)
	Male	Female	60–69 years	70–79 years	80 years and above	Yes	No	
Rice/wheat products								
≥ once/day	92.5	76.6	79.7	82.5	92.9	83.1	84.5	83.8
1–6 times/week	7.5	12.5	16.3	10.0	–	11.9	8.6	10.3
1–3 times/month	–	4.7	2.0	5.0	–	3.4	1.7	2.6
≤ once/month	–	6.2	2.0	2.5	7.1	1.6	5.2	3.3
Reduction	5.7	21.9[§]	14.3	17.5	10.7	15.3	13.8	14.5
Coarse grains								
≥ once/day	24.5	17.1	22.5	17.5	21.4	22.0	19.0	20.5
1–6 times/week	20.8	26.6	16.2	37.5	17.9	15.3	32.8	23.9
1–3 times/month	17.0	26.6	28.6	15.0	21.4	22.0	22.3	22.2
≤ once/month	37.7	29.7	32.7	30.0	39.3	40.7	25.9	33.4
Reduction	24.5	46.9[§]	36.7	45.0	25.0	37.3	36.2	36.8
Potatoes								
≥ once/day	17.0	15.6	16.3	20.0	10.7[§]	17.0	15.5	16.2
1–6 times/week	39.6	40.7	44.9	47.5	21.4	37.3	43.1	40.2
1–3 times/month	30.2	28.1	28.6	27.5	32.1	30.5	27.6	29.1
≤ once/month	13.2	15.6	10.2	5.0	35.8	15.2	13.8	14.5
Reduction	34.0	39.1	36.7	40.0	32.1	44.1	29.3	36.8
Fresh vegetables								
≥ once/day	88.7	76.6	83.7	75.0	89.3	81.4	82.8	82.1
1–6 times/week	11.3	15.6	14.3	20.0	3.6	15.3	12.1	13.7
1–3 times/month	–	6.3	2.0	5.0	3.6	3.3	3.5	3.3
≤ once/month	–	1.5	–	–	3.5	–	1.6	0.9
Reduction	32.1	34.4	30.6	40.0	28.6	30.5	36.2	33.3
Fresh fruits								
≥ once/day	32.1	26.6	32.7	22.5	32.1	28.8	29.3	29.1
1–6 times/week	43.4	32.8	42.9	37.5	28.6	33.9	41.4	37.6
1–3 times/month	18.9	29.7	20.4	27.5	28.6	28.8	20.7	24.8
≤ once/month	5.6	10.9	4.0	12.5	10.7	8.5	8.6	8.5
Reduction	45.3	59.4	51.0	60.0	46.4	52.5	53.5	53.0
Eggs								
≥ once/day	71.7	56.3	63.3	62.5	64.3	57.6	69.0	63.3
1–6 times/week	24.5	31.3	28.6	27.5	28.5	33.9	22.4	28.2
1–3 times/month	1.9	9.4	6.1	7.5	3.6	5.1	6.9	6.0
≤ once/monthh	1.9	3.0	2.0	2.5	3.6	3.4	1.7	2.5
Reduction	7.6	20.3	16.3	17.5	7.1	22.0	6.9[§]	14.5
Aquatic food products**								
≥ once/dayy	11.3	9.4	10.2	10.0	10.7	11.9	8.6	10.3
1–6 times/week	35.9	23.4	30.6	25.0	32.1	32.2	25.9	29.1
1–3 times/month	39.6	39.1	38.8	42.5	35.8	33.9	44.8	39.2
≤ once/month	13.2	28.1	20.4	22.5	21.4	22.0	20.7	21.4
Reduction	67.9	73.4	71.4	75.0	64.3	66.1	75.9	70.9

TABLE 2. (Continued)

Food items	Gender (%)		Age group (%)			Healthy status[†] (%)		Total (%)
	Male	Female	60–69 years	70–79 years	80 years and above	Yes	No	
Red meat and poultry								
≥ once/day	52.8	34.4[¶]	42.9	40.0	46.4	35.6	50.0	42.7
1–6 times/week	34.0	20.3	30.6	22.5	25.0	30.5	22.4	26.5
1–3 times/month	7.6	31.3	20.4	20.0	21.4	18.6	22.4	20.5
≤ once/month	5.6	14.0	6.1	17.5	7.2	15.3	5.2	10.3
Reduction	34.0	42.2	40.8	37.5	35.7	44.1	32.8[§]	38.5
Milk								
≥ once/day	20.8	9.4	14.3	7.5	25.0	11.9	17.2	14.5
1–6 times/week	22.6	25.0	22.5	25.0	25.0	20.3	27.6	23.9
1–3 times/month	20.8	23.4	26.5	25.0	10.7	20.3	24.1	22.2
≤ once/month	35.8	42.2	36.7	42.5	39.3	47.5	31.1	39.4
Reduction	24.5	45.3	38.8	40.0	25.0	39.0	32.8	35.9
Soybeans								
≥ once/day	9.4	3.1	6.1	2.5	10.7	6.8	5.2	6.0
1–6 times/week	24.5	17.2	22.5	17.5	21.4	23.7	17.2	20.5
1–3 times/month	39.6	32.8	30.6	42.5	35.7	33.9	37.9	35.9
≤ once/month	26.5	46.9	40.8	37.5	32.2	35.6	39.7	37.6
Reduction	69.8	71.9	73.5	80.0	53.6	64.4	77.6	70.9

*: The proportion of the elderly whose food intake frequency less than they did before community closure.

[†]: Healthy status was defined as whether the elderly had living with chronic diseases.

[§]: Comparison of each variable in different subgroups, *p*<0.05.

[¶]: Comparison of each variable in different subgroups, *p*<0.01.

[**]: Aquatic food products included freshwater fish, marine fish, shrimp, crab, shellfish and other animal aquatic products excluding seaweed, kale, etc.

TABLE 3. Elderly participants failing to reach the recommended intake levels of specific foods during the period of community closure* (%)

Food items	Gender		Age group			Healthy status[†]		Total
	Male	Female	60–69 years	70–79 years	80 years and above	Yes	No	
Rice/wheat products	7.6	23.4[§]	20.4	17.5	7.1	17.0	15.5	16.2
Coarse grains	75.5	82.8	77.6	82.5	78.6	78.0	81.0	79.5
Potatoes	83.0	84.4	83.7	80.0	89.3	83.1	84.5	83.8
Fresh vegetables	11.3	23.4	16.3	25.0	10.7	18.6	17.2	18.0
Fresh fruits	67.9	73.4	67.4	77.5	67.9	71.2	70.7	70.9
Eggs	28.3	43.8	36.7	37.5	35.7	42.4	31.0	36.8
Aquatic food products[¶]	52.8	67.2	59.2	65.0	57.1	55.9	65.5	60.7
Red meat and poultry	13.2	45.3[**]	26.5	37.5	28.6	33.9	27.6	30.8
Milk	79.3	90.6	85.7	92.5	75.0	88.1	82.8	85.5
Soybeans	66.0	79.7	71.4	80.0	67.9	69.5	77.6	73.5

*: the recommended intake frequency of rice/wheat products, coarse grains, potatoes, fresh vegetables, fresh fruits, eggs, and milk were more than once a day, while intake of aquatic products, red meat, poultry, and soybeans of more than once a week were defined as meeting the recommendations.

[†]: Health status was defined as whether the elderly were living with chronic diseases.

[§]: Comparison of each variable in different subgroups, *p*<0.05.

[¶]: Aquatic food products included freshwater fish, marine fish, shrimp, crab, shellfish and other animal aquatic products excluding seaweed, kale, etc.

[**]: Comparison of each variable in different subgroups, *p*<0.01.

elderly during the pandemic (*2*). Fish, poultry, eggs, milk, lean meat, and soybean products are primary sources of high-quality protein, but marinated/processed fish and meat products should be avoided for the potential of increasing cardiovascular disease risk in the elderly.

Elderly individuals often suffer from hypertension, diabetes, or other non-communicable cardiovascular diseases and must take multiple medications regularly. They paid more attention to their health in case of emergencies, so drug stockpiles and medical resources should always be prioritized by themselves or by the community (*3*). However, their nutritional status was often neglected, and food intake correspondingly decreased, especially when combined with digestive dysfunction and loss of appetite during the pandemic. For elderly with hypertension or diabetes, adequate coarse grains, vegetables, and soybeans could benefit for their blood glucose and blood pressure (*4*–*5*). Chinese dietary guidelines also recommended that a daily diet should contain an adequate amount of these plant-based foods (*2*).

There are some limitations in our study. First, although there was variation in age, gender, education, lifestyles, and other characteristics of the elderly involved in our study, findings from this survey were not representative of the elderly living in closed communities in Wuhan. Second, given the self-reported information nature of this survey, the results were subjected to some level of recall bias or mistakes. Third, data in this study were based on information provided by participants, so the results were also influenced by some level of subjectivity. Nevertheless, the study reflected the nutritional and health status of the elderly during the COVID-19 pandemic and can be used to inform elderly individuals' health maintenance and promotion in Wuhan.

doi: 10.46234/ccdcw2020.120

Corresponding authors: Qing Yu, yuqing@nipd.chinacdc.cn; Gangqiang Ding, dinggq@chinacdc.cn.

---

[1] National Institute for Nutrition and Health, Chinese Center for Disease Control and Prevention. Beijing, China; [2] Jiangxia Disease Control and Prevention Center, Hubei, China; [3] Chinese Center for Disease Control and Prevention, Beijing, China; [4] National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention (National Center for International Research on Tropical Diseases); Key Laboratory of Parasite and Vector Biology, National health and Family Planning Commission; WHO Collaborating Center for Tropical Diseases, Shanghai, China. .

Submitted: April 28, 2020; Accepted: June 15, 2020

REFERENCES

1. World Health Organization. Report of the WHO-China joint mission on coronavirus disease 2019 (COVID-19), February 16-24, 2020. https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report.pdf. [2020-04-28].
2. Chinese Nutrition Society. Dietary guideline of the elderly in China 2016. Beijing: People's Medical Publishing House, 2016 . (In Chinese).
3. Wu J. An important but overlooked measure for containing the COVID-19 epidemic: protecting patients with chronic diseases. China CDC Weekly 2020; 2(15): 249-50. http://weekly.chinacdc.cn/en/article/id/45571a77-8d7a-4c78-82cb-463c72f0e7c8.
4. Micha R, Shulkin ML, Peñalvo JL, Khatibzadeh S, Singh GM, Rao M, et al. Etiologic effects and optimal intakes of foods and nutrients for risk of cardiovascular diseases and diabetes: systematic reviews and meta-analyses from the Nutrition and Chronic Diseases Expert Group (NutriCoDE). PLoS One 2017; 12(4): e0175149. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5407851/.
5. Bechthold A, Boeing H, Schwedhelm C, Hoffmann G, Knüppel S, Iqbal K, et al. Food groups and risk of coronary heart disease, stroke and heart failure: a systematic review and dose-response meta-analysis of prospective studies. Crit Rev Food Sci Nutr 2019; 59(7): 1071-90. https://pubmed.ncbi.nlm.nih.gov/29039970/.

Notes from the Field

Reemergent Cases of COVID-19 — Xinfadi Wholesales Market, Beijing Municipality, China, June 11, 2020

Wenjie Tan[1,3,&,#]; Peihua Niu[1,&]; Xiang Zhao[1,&]; Yang Pan[2,&]; Yong Zhang[1,3,&]; Lijuan Chen[2]; Li Zhao[1]; Yanhai Wang[1]; Dayan Wang[1,3]; Jun Han[1,3]; George F. Gao[1,4]; Chun Huang[2,#]; Wenbo Xu[1,3,#]; Guizhen Wu[1,3,#]

No new local coronavirus disease 2019 (COVID-19) cases were reported in Beijing for over 56 days before the reemergent COVID-19 cases that were reported on June 11, 2020, and more than 200 confirmed cases have been reported as of June 20 in Beijing. All confirmed COVID-19 cases were associated with Xinfadi Wholesale Market. Here, we reported the phylogenetic characteristics of the COVID-19 viruses (also known as severe acute respiratory syndrome coronavirus 2, SARS-CoV-2, and human coronavirus 2019, HCoV-19) sequenced from the clinical specimens of 2 human cases and 1 environmental sample.

We conducted whole-genome sequencing of COVID-19 viruses using the Illumina NextSeq 550 platform. A total of 3 whole genomes of COVID-19 virus were submitted to GISAID website and these sequences were named as nCoV Beijing IVDC-001 (EPI_ ISL_469254, from the first confirmed case in a 53-year-old male), -002 (EPI_ ISL_469255, from another confirmed case in a 25-year-old male), -003 (EPI_ ISL_469256, from environmental sample), respectively. These genomes (Beijing Xinfadi strains) showed 99.96%–99.97% nucleic acid identity to the reference strain hCoV-19/Wuhan/IVDC-HB-01/2019|EPI_ISL_402119|2019-12-30 that was isolated from Wuhan on January 7, 2020 (*1*). A total of 7 nucleotide variations were identified among the 3 whole genomes of Xinfadi strains, including C241T, C3037T, C14408T, A23403G, G28881A, G28882A, and G28883C, which were consistent with the characteristics of Branch 1 of the L-lineage from Europe (Figure 1) and different from the previous pandemic COVID-19 virus in Wuhan (Dec-2019) and Beijing (Feb-2020), which belong to the S-lineage (*2*). Additional genetic variations were also identified among these Xinfadi strains including the C6026T mutation in all 3 genomes of the virus, C12085T and A29694C in nCoV Beijing IVDC-001 and A11910G, A29694C, and G29868A in nCoV Beijing IVDC-003.

Among them, C6026T (P1291S), C14408T (P4715L), A23403G (D614G), and the GGG mutated to AAC at position 28881–28883 (R203K, R203R, G204R), caused amino acid substitutions that were located on ORF 1ab (6026, 14408), S protein (23403), and N protein (28881–28883), respectively. Some amino acid mutations (ORF1ab: P1291S, P4715L; S: D614G; N: R203K, G204R) in the COVID-19 virus may change its biological characteristics significantly. For example, the D614G mutation of the COVID-19 S protein caused by A23403G may increase the ability of the virus to infect cells (*3*).

The genome sequences of these Xinfadi strains provide strong evidence that the reemergent of COVID-19 cases in Beijing may be caused by an imported source of infections, suggesting that it is not continuous transmission of the local COVID-19 virus strain. It is worth noting that these Xinfadi strains have high homology with several genomes from the recently imported COVID-19 cases in northeastern China (Shulan strain, Heilongjiang strains) (*4*–*5*) that also belong to Branch 1 of L-lineage from Europe (Figure 1). Furthermore, the whole genome sequence analysis of the COVID-19 virus further confirmed that the source of the virus in this outbreak did not spread from natural animal hosts or intermediate animal hosts to humans.

COVID-19 cases are associated with the Xinfadi Wholesale Market, the virus could be transmitted from person to person via the respiratory tract or direct contact of the contaminated environment at market. The source of the virus needed to be further determined based on epidemiological, serological, and etiological monitoring.

Fundings: This work was supported by the National Key Research and Development Program of China (2016YFD0500301, 2020YFC0840900).

doi: 10.46234/ccdcw2020.132

[#] Corresponding authors: Wenjie Tan, tanwj@ivdc.chinacdc.cn; Huang Chun, huangch@bjcdc.org; Wenbo Xu, xuwb@ivdc.chinacdc.cn; Guizhen Wu, wugz@ivdc.chinacdc.cn.

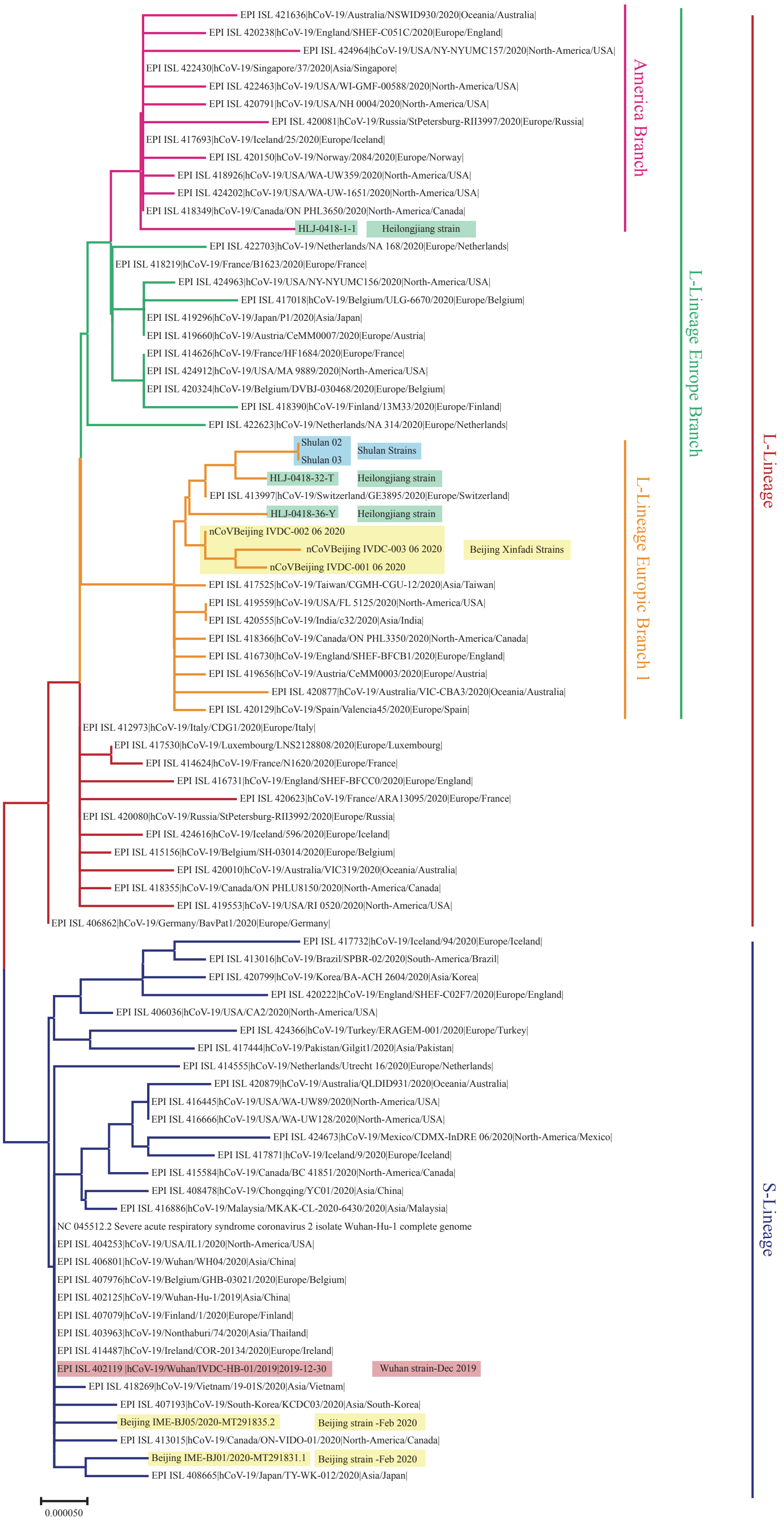


FIGURE 1. Phylogenetic tree based on the genome sequences of the COVID-19 virus. The genome of the COVID-19 virus from Beijing Municipality and Wuhan City were highlighted in shades of yellow and orange, respectively. The recent reemergence of COVID-19 virus in northeastern China (Shulan and Heilongjiang) that was associated with imported cases was also highlighted in shades of blue and green, respectively. S- or L-lineage of the COVID-19 virus were marked and colored on the right.

---

[1] Key Laboratory of Biosafety, National Health and Family Planning Commission, National Institute for Viral Disease Control and Prevention, China CDC, Beijing, China; [2] Beijing Center for Disease Control and Prevention, Beijing, China; [3] Center for Biosafety Mega-Science, Chinese Academy of Sciences, Wuhan, Hubei, China; [4] Chinese Center for Disease Control and Prevention, Beijing, China.
[&] Joint first authors.

Submitted: June 21, 2020; Accepted: June 23, 2020

REFERENCES

1. Lu RJ, Zhao X, Li J, Niu PH, Yang B, Wu HL, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet 2020;395 (10224):565 – 74. http://dx.doi.org/10.1016/S0140-6736(20)30251-8.
2. Tang XL, Wu CC, Li X, Song YH, Yao XM, Wu XK, et al. On the origin and continuing evolution of SARS-CoV-2. Nat Sci Rev 2020;7(6):1012 – 23. http://dx.doi.org/10.1093/nsr/nwaa036.
3. Daniloski Z, Guo XY, Sanjana NE. The D614G mutation in SARS-CoV-2 Spike increases transduction of multiple human cell types. bioRxiv 2020. http://dx.doi.org/10.1101/2020.06.14.151357.
4. Xu J, Zhang Y, Zhao X, Wang DY, Dai WP, Jiao GY, et al. A Reemergent Case of COVID-19 — Harbin City, Heilongjiang Province, China, April 9, 2020. China CDC Weekly, 2020, 2(25):460 – 2. http://weekly.chinacdc.cn/en/article/doi/10.46234/ccdcw2020.127.
5. Chen C, Zhao X, Wang DY, Li J, Wang A, Wu DL, et al. The Initial Case of COVID-19 — Shulan City, Jilin Province, China, May 8, 2020. China CDC Weekly, 2020, 2(25):458 – 9. http://weekly.chinacdc.cn/en/article/doi/10.46234/ccdcw2020.115.

Notes from the Field

Diet and Nutrition of Healthcare Workers in COVID-19 Epidemic—Hubei, China, 2019

Jian Zhang[1]; Shanrong Lai[2]; Quanjun Lyu[3]; Pianhong Zhang[4]; Dagang Yang[5]; Juan Kong[6]; Yumei Qi[7]; Wei Yuan[8]; Shan Zeng[9]; Pengkun Song[1]; Titi Yang[1]; Li Li[1]; Jinglei Wang[10]; Yujing Liu[10]; Tanxi Ge[10]; Qi Zhang[10]; Ganyu Feng[1]; Ailing Liu[1]; Gangqiang Ding[1,#]

From late January to March, more than 42,000 doctors, nurses, public health workers, and health administrators across China went to Hubei Province to assist in the response to coronavirus disease 2019 (COVID-19). There are many studies on nutrition status of affected people amid natural disasters or pandemics (*1–3*), but the diet and nutrition status of healthcare workers receive little attention. The aim of this article is to provide evidence for addressing this issue by investigating food supply and nutrition status during the COVID-19 response period. The subjective survey was conducted from March 19 to April 1, 2020. The questionnaire composed of 9 questions including participants' occupation, body weight changes during the COVID-19 response, assessments of the amount and diversity of foods, meal tastes, changes in fitness due to consumption, dietary suggestions, and overall satisfaction for the meals. Healthcare workers randomly sampled from 27 provincial-level administrative divisions (PLADs) participated in the online survey excluding workers from Hubei Province, workers participating for less than 30 days in the COVID-19 response, and workers participating in the response in their hometown. A total of 1,048 valid responses were used in the final analysis. All statistical analyses were performed using SPSS 22.0 (SPSS, Inc., Chicago, IL, USA).

The participants were 57.9% females and 42.1% males, 30.7% doctors, 54.1% nurses, 11.2% public health workers, and 4.0% others. The age range was 22–60 years, and 96.6% of the surveyed subjects were aged below 50 years. The average age was 37.6±7.3 years for men and 33.8±7.2 years for women.

Participants with self-reported weight gain were 26.2% of the total including 27.4% of males and 25.4% of females, 27.6% of doctors, 25.2% of nurses, 26.5% of public health workers, and 28.6% of others. Participants with self-reported weight loss were 22.9% of the total including 20.0% of males and 25.0% of females, 19.3% of doctors, 26.1% of nurses, 17.9% of public health workers, and 21.4.% of others (Figure 1).

Nearly 65% of the healthcare workers thought that the box meals they were provided could meet their nutrition requirements, and more than 80% of them gave scores of ≥8 point in a 10-point overall assessment of the meals (Figure 2) despite some complaints about the taste. Approximately 30% of the healthcare workers thought that the dishes were too greasy, and 16.8% of them complained that the dishes were too salty. The proportion suggesting reducing edible oil, salt, and red meat were 48.4%, 42.0%, and 33.4%, respectively. More than 50% of the healthcare workers

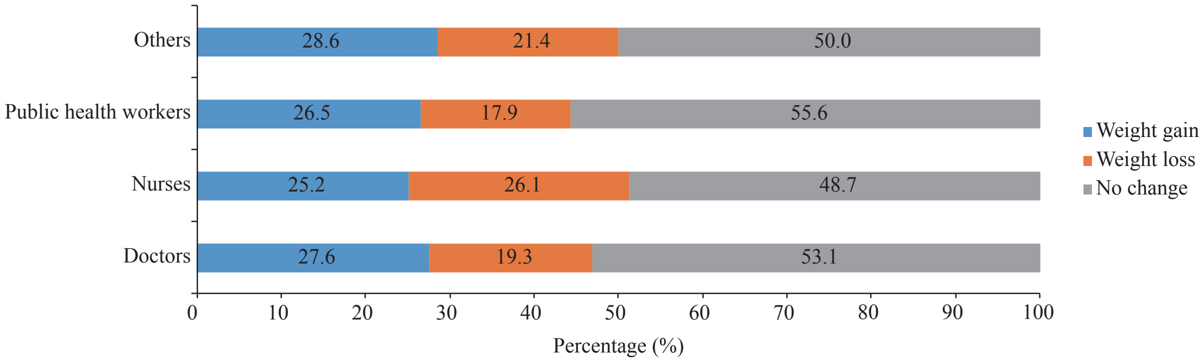


FIGURE 1. The percentage of self-reported body weight gain/loss/no change in healthcare workers during COVID-19 response in Hubei Province (%).

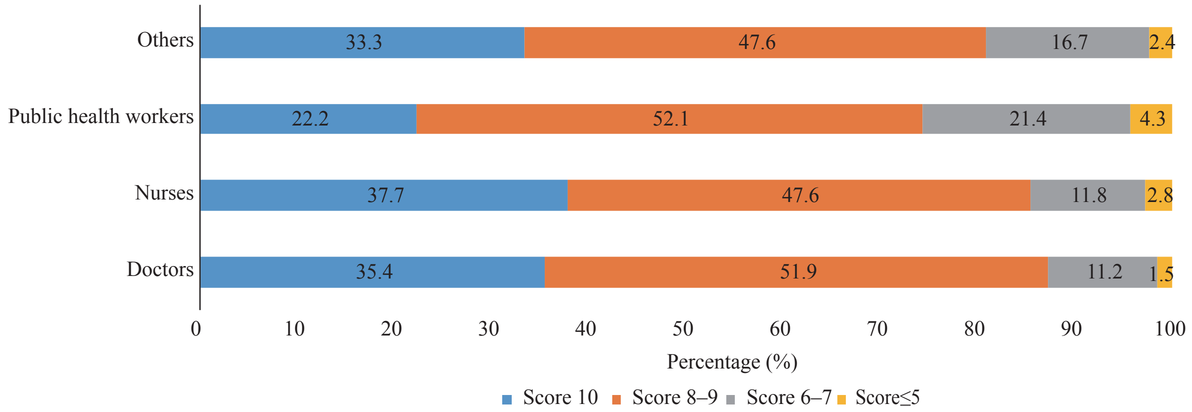


FIGURE 2. The percentage of assessment score from healthcare workers of overall satisfaction for meals during the COVID-19 response in Hubei Province.

asked for more vegetables, coarse grains, fruits, nuts, and soybeans.

As far as we know, this is the first survey on the diet and nutrition for healthcare workers during the pandemic. Our data showed that even in a short period of 1–2 months, participant body weight changed, which was an important nutritional index. Although self-reported, the results suggested that a large proportion of healthcare workers had unbalanced diets throughout the response. In addition, 13.5% of the healthcare workers complained of mild discomfort after consumption, and 8 persons, including 6 females and 2 males, experienced severe discomfort and needed medication.

Daily diet has great influence on the health of medical workers, especially during the response period with heavy work intensity and physical and mental exhaustion. Our results suggested that some dietary problems existed such as energy intake imbalance and excessive use of oil and salt (*4*) in the meals provided to healthcare workers. Therefore, more effective approaches should be taken to improve nutritional quality for workers in public health crises in the future.

Acknowledgments: Thanks to the participation of all COVID-19 response healthcare workers and strong support from the National Health Commission of the People's Republic of China. Thanks to all members of the epidemiological investigation team of China CDC for their efforts in this investigation.

doi: 10.46234/ccdcw2020.121

[#] Corresponding author: Gangqiang Ding, dinggq@chinacdc.cn.

---

[1] National Institute for Nutrition and Health, Chinese Center for Disease Control and Prevention, Beijing, China; [2] Fujian Disease Control and Prevention, Fuzhou, Fujian, China; [3] Public Health College, Zhengzhou University, Zhengzhou, Henan, China; [4] The Second Affiliated Hospital of Zhejiang University School of Medicine, Hangzhou, Zhejiang, China; [5] Hospital affiliated to Guizhou Medical University, Guiyang, Guizhou, China; [6] Shengjing Hospital of China Medical University, Shenyang, Liaoning, China; [7] Tianjin Third Central Hospital, Tian Jin, China; [8] Zhabei Central Hospital of Jingan District, Shanghai, China; [9] Jiang Su Province Hospital, Nanjing, Jiangsu, China; [10] Chinese Center for Disease Control and Prevention, Beijing, China.

Submitted: May 12, 2020; Accepted: June 11, 2020

REFERENCES

1. Aguayo VM, Sharma A, Subedi GR. Delivering essential nutrition services for children after the Nepal earthquake. Lancet Glob Health 2015;3(11): e665–6. https://www.ncbi.nlm.nih.gov/pubmed/?term=Aguayo+VM%2C+Sharma+A%2C+Subedi+GR.
2. Clark WA, Cress EM. Nutritional issues and positive living in human immunodeficiency virus/AIDS. Nurs Clin North Am 2018;53(1): 13–24. https://www.ncbi.nlm.nih.gov/pubmed/?term=William+Andrew+Clark%2C%C2%A0Eileen+M+Cress.
3. Zick SM, Snyder D, Abrams DI. Pros and cons of dietary strategies popular among cancer patients. Oncology 2018;32(11): 542–7. https://www.ncbi.nlm.nih.gov/pubmed/?term=Zick+SM%2C+Snyder+D%2C+Abrams+DI.
4. Yu DM, He YN, Fang HY, Xu XL, Wang X, Yu WT, et al. Salt intake among Chinese adults in 2010-2012. Chin J Prev Med 2016;50(3): 217–20. https://www.ncbi.nlm.nih.gov/pubmed/26957237. (In Chinese).

Outbreak Reports

The Source of Infection of the 137th Confirmed Case of COVID-19 — Tianjin Municipality, China, June 17, 2020

COVID-19 Field Response Group[1]; Laboratory Testing Group[1]; Ying Zhang[1,#]

Summary

What is already known on this topic?

Following 110 days of no new confirmed cases of COVID-19 in Tianjin Municipality, a case was confirmed on June 17, 2020. A total of 136 local cases had been reported previously.

What is added by this report?

The 137th case was found in a dishwasher working in the western dining room of a hotel in Tianjin. Epidemiological investigations and laboratory research indicated that this case was likely transmitted from an asymptomatic individual that had recently visited several public places in Beijing Municipality and was working as a chef in the same workplace as the patient. Sequencing and analysis found that the COVID-19 virus genome found in the 137th case was 100% identical to sequences from the recent outbreak in Beijing's Xinfadi Agricultural Product Wholesale Market.

What are the implications for public health practice?

A combination of meticulous epidemiological investigation and detailed laboratory research can promptly identify the source of COVID-19.

BACKGROUND

After no local cases had been reported for 110 consecutive days in Tianjin Municipality, a confirmed case of coronavirus disease 2019 (COVID-19) was reported on June 17, 2020 in a 22-year-old male with no notable medical conditions. A total of 136 cases had previously been confirmed within Tianjin. The patient was employed as a kitchen assistant in the western dining room of a 5-star hotel, and within a 14-day period before onset of illness, he had not traveled to any other provincial-level administrative divisions (PLADs) or countries and had no known contact with suspected or confirmed cases, overseas returnees, or persons with similar respiratory symptoms cases. The patient developed fever (maximum temperature 38 °C), dry throat, and slight cough beginning on the morning of June 16, 2020 at approximately 8:00 am. He was transferred to Haihe Hospital for isolation and treatment after a COVID-19 nucleic acid test was positive on June 17. He was diagnosed as a COVID-19 confirmed case and was classified as mild by an expert group.

INVESTIGATION AND RESULTS

To prevent further spread of the disease and find the source of infection, Tianjin Municipal CDC organized relevant professionals to conduct epidemiological investigations and laboratory tests to identify the source of infection as rapidly as possible. Persons included in this investigation were the 137th confirmed COVID-19 patient in Tianjin, his family members and colleagues, residents of his apartment building, and hotel guests including non-Chinese nationals at his place of employment.

The patient was investigated with the "Epidemiological Questionnaire for COVID-19 Cases," and others were investigated with a checklist that included basic personal information, clinical conditions, travel history, contact with others, and suspected exposures in the previous 14 days (*1–3*). Type and frequency of contact with the patient were determined.

Throat swabs and blood samples were obtained from all investigated subjects. Environmental samples from the patient's residence and workplace were obtained including samples from door handles, faucets, kitchenware, refrigerators, garbage cans, air conditioners, sewers, clothes, stoves, sealed meat products, and aquatic equipment in the hotel. Samples from the environment, food, and food packaging from hotel suppliers were also obtained for testing.

Nucleic acid samples were extracted from throat, nasopharyngeal, and anal swabs using viral DNA/RNA extraction kits (Xi'an Tianlong Science and Technology, China), and initially stored at −70 °C.

COVID-19 virus (also known as SARS-CoV-2 and 2019-nCoV) detection was conducted via real-time reverse transcriptase polymerase chain reaction (RT-PCR) using nucleic acid detection kits (Shanghai BioGerm Medical Technology, China) according to the manufacturer instructions. ULSEN® SARS-CoV-2 whole genome capture kits (MicroFuture, Beijing, China) were used for COVID-19 virus genome enrichment as described by the manufacturer. Amplified products were purified by Agencourt AMPure XPKit (Beckman Coulter, Brea, CA, USA) and then subjected to library preparation by Nextera® XT DNA Library Preparation Kit (Illumina, San Diego, CA, USA). Whole genome sequencing was carried out using a MiniSeq™ Sequencing System (Illumina, San Diego, CA, USA).

Resulting sequences were assembled with CLC Genomics Workbench 20.0.3 (Qiagen, Hilden, Germany). Sequence alignments and phylogenetic analysis were performed with MEGA X software, and a neighbor-joining tree was assembled with bootstrap values determined from 1,000 replicates. All comparison sequences, including the most recent Beijing outbreak sequences (i.e., ESP_ISL_469 254, ESP_ISL_469 255, and ESP_ISL_469 256), were downloaded from the EpiFlu database of the Global Initiative on Sharing All Influenza Data (GISAID; gisaid.org) and from GenBank (ncbi.nlm.nih.gov/genbank/).

A total of 246 environmental and food specimens were collected during the investigation. This total included 144 environmental samples of 18 types of sources (e.g., door handles, kitchenware items, etc.) and 102 food samples (i.e., food and food packaging for frozen and fresh seafood, beef, mutton, and vegetables). All 246 specimens had negative viral nucleic acid test results.

A total of 1,137 contacts were investigated for suspected exposure (e.g., family members, colleagues, neighbors, hotel guests, etc.). No individuals had travel history to Xinfadi Agricultural Product Wholesale Market in Beijing Municipality or other high-risk areas or contact with persons with travel history to mid- to high-risk areas in Beijing. No individual had travel history overseas or contact with foreign travel returnees. In addition, no individual had contact with confirmed COVID-19 cases or persons experiencing COVID-19 or related respiratory symptoms.

On June 17, a total of 750 throat swab specimens and 365 serum specimens from persons with suspected exposures were collected and tested for both viral nucleic acids and virus-specific antibodies. All test results were negative.

On June 19, 55 employees in the dining room of the hotel were tested a second time. All viral nucleic acid test results were negative. All antibody test results were also negative, except one. A chef who worked in the western dining room of the hotel tested positive for IgM antibody specific to COVID-19 virus. After three consecutive tests, the IgM antibody result remained positive.

As a result, the chef who tested positive for anti-COVID-19-virus IgM antibodies was then further investigated as a possible source, and he reported having had no symptoms and was therefore preliminarily designated as a confirmed asymptomatic COVID-19 patient. He had visited his girlfriend in Beijing many times in the past month. While in Beijing on June 8, he took the subway and spent time in public places including restaurants, bars, and a theater. While in the workplace in the hotel in Tianjin, the chef and the patient had several exposures while in the smoking room on the ground floor. In addition, there was also an instance of close (less than 0.5 meters) communication between the chef and the patient on June 10 where the patient wore a mask but the chef did not. The patient was also responsible for cleaning the tableware in the employee's dining room and had resulting contact with the chef during the daily lunch. Therefore, it was hypothesized that the source may have been infected in public places in Beijing, returned to work normally due to his asymptomatic status while in Tianjin, and then infected the case through frequent close contact at work.

Furthermore, COVID-19 virus RT-PCR test results on throat, nasopharyngeal, and anal swab samples were all positive with cycle threshold (Ct) values of 16.0/18.0 (ORF1ab/N), 23.0/24.4, and 35.0/35.0, respectively. As the Ct values of the anal swab sample was too high to acquire whole genome sequences, we chose throat (FH-124-Y) and nasopharyngeal (FH-124-B) swab samples for genome sequencing. The whole genome of FH-124-Y was 29,868 nt, and FH-124-B was 29,803 nt, with a shortage in 5'-NTR and 3'-polyA tail. The genome sequences of FH-124-Y and FH-124-B were found to be 100% identical and were both named Tianjin/137/2020.

Phylogenetic analysis has revealed that all known COVID-19 virus genomes fall into two major clades, or lineages, named S and L (Figure 1). We found that Tianjin/137/2020 belonged to the Europe Branch of

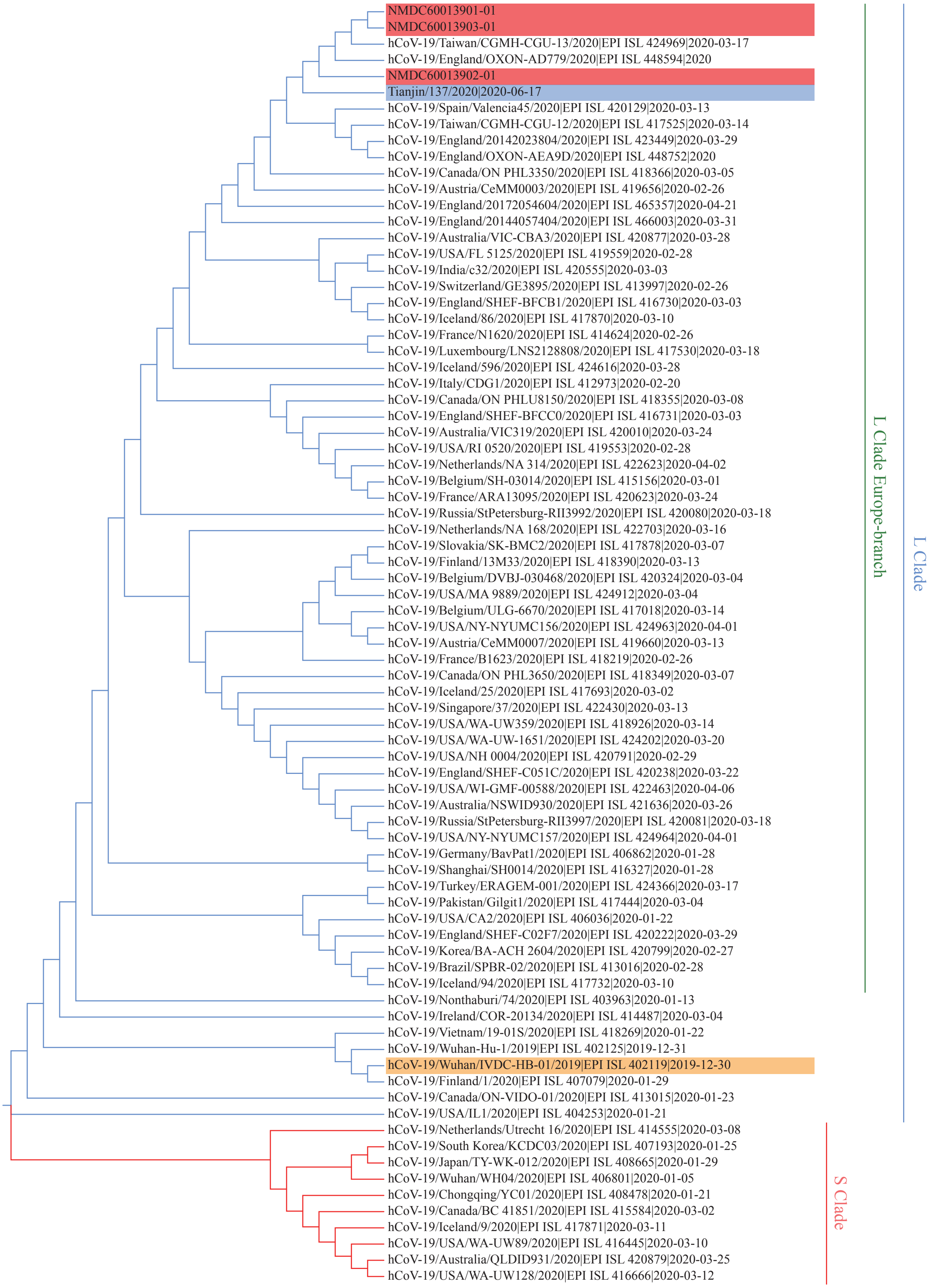


FIGURE 1. Phylogenetic tree based on the whole genome sequences of COVID-19 virus. The COVID-19 virus genome of the cases in Beijing Municipality and Tianjin City were highlighted in shades of red and blue, respectively. The reference sequence Wuhan-Hu-1 (NC_045512) were highlighted in orange. S- or L-clade of COVID-19 virus were marked and colored on the right.

the L-Lineage, and that it was most closely related to the Beijing strain ESP_ISL_469 255 (*4*), to which it was 100% identical at the nucleotide level.

DISCUSSION

The 137th patient had no contact with individuals who arrived in Tianjin from abroad or other PLADs before illness onset. Foreigners who stayed in the hotel where the patient had worked were isolated for 14 days; their tests for COVID-19 virus nucleic acids and serum antibodies were all negative. Closed-loop isolation management was implemented for all foreign personnel, and the possibility of the patient acquiring infection from these individuals was excluded.

No new local cases were reported in Tianjin for over 110 days. Family members, colleagues, neighbors, and hotel guests were investigated. None of them had any suspicious symptoms, and the results of nucleic acid and serum antibody tests were negative. Therefore, the possibility that other unknown local cases were the source was excluded.

Local CDC professionals collected hundreds of specimens from surfaces in the patient's residence and workplace and from meat, seafood, and other food products in the hotel. They also collected environmental and product-related samples from the hotel's supplier. All samples were subjected to nucleic acid testing and all results were negative, thereby excluding the possibility that surface or food contamination was the source.

The serological test result of 1 of 55 hotel dining room employees was positive for COVID-19-virus-specific IgM antibody. This individual worked as a chef in the western dining room of the hotel but had reported no COVID-19-like symptoms. The chef had been to Beijing many times in the past month to see his girlfriend. In particular, he visited restaurants and bars, a theater, and other public places in Beijing on June 8. He had close communication with the patient on June 10, during which, the chef did not wear a mask. During the typical work day, the two men met in the employees' dining room during the daily lunch and often smoked together in the smoking room on the ground floor of the hotel several times.

COVID-19 virus genomes fall into two major types (L and S), defined by two different SNPs at nucleotide 8,782 and 28,144. Strains that exhibit a "CT" haplotype at these two sites are designated as L type and strains that exhibit a "TC" haplotype are designated as S type. Although the L type is more prevalent (≥70%) than the S type (≥30%), the S type is evolutionarily older (*5*).

Our phylogenetic tree clearly showed the separation of the 2 lineages. Tianjin/137/2020 and ESP_ISL_469255 (from the Beijing outbreak) clustered together in the L-Lineage of the Europe-Branch. Beijing strains ESP_ISL_469254, ESP_ISL_469256, Taiwan strain CGMH-CGU-13, and England strain OXON-AD779, were also found tightly clustered, indicating that Tianjin/137/2020 was closely related to the Beijing and Europe strains rather than local strains identified during the first wave of the epidemic in China, which initiated the epidemic in Wuhan.

Evidence from the epidemiological investigations, nucleic acid and antibody tests, and whole genome sequencing indicated that the chef was most likely infected with COVID-19 virus in public places in Beijing. The chef was asymptomatic and went back to work, transmitting the virus to the 137th patient. Therefore, we believe that this patient in Tianjin is linked to the Xinfadi Agricultural Product Wholesale Market in Beijing by traditional and molecular epidemiology.

doi: 10.46234/ccdcw2020.122

Corresponding author: Ying Zhang, sjkzxcrbyfkzs@tj.gov.cn.

---

[1] Tianjin Center for Disease Control and Prevention, No.6 Huayue Road, Hedong District, Tianjin, China.

Submitted: June 28, 2020; Accepted: July 02, 2020

REFERENCES

1. Chinese Center for Disease Control and Prevention. Guidelines for COVID-19 Epidemiological Investigations. China CDC Weekly 2020;2(19):327 – 8. http://dx.doi.org/10.46234/ccdcw2020.083.
2. Chinese Center for Disease Control and Prevention. Guidelines for Investigation and Management of Close Contacts of COVID-19 Cases. China CDC Weekly 2020;2(19):329 – 31. http://dx.doi.org/10.46234/ccdcw2020.084.
3. Chinese Center for Disease Control and Prevention. Technical Guidelines for COVID-19 Laboratory Testing. China CDC Weekly 2020;2(19):332 – 6. http://dx.doi.org/10.46234/ccdcw2020.085.
4. Tan WJ, Niu PH, Zhao X, Pan Y, Zhang Y, Chen LJ, et al. Reemergent Cases of COVID-19 Xinfadi Wholesales Market, Beijing Municipality, China, June 11, 2020. China CDC Weekly 2020. http://dx.doi.org/10.46234/ccdcw2020.132.
5. Tang XL, Wu CC, Li X, Song YH, Yao XM, Wu XK, et al. On the origin and continuing evolution of SARS-CoV-2. Natl Sci Rev 2020;7(6):1012 – 23. http://dx.doi.org/10.1093/nsr/nwaa036.

Insights

Professor Jian Lu's Interdisciplinary Approach to Modeling the COVID-19 Pandemic

Peter Hao[1]; Shicheng Yu[1]; Yu Chen[2]; Feng Tan[1,#]

Editorial Our new column *Insights* is an ongoing series of interviews prepared by the *China CDC Weekly* team with researchers, policymakers, experts, and other leaders that strives to disseminate experiences, knowledge, and perspectives in global and public health with a wider community. At the discretion of the *Weekly*'s team, these interviews will be written into articles, shared as videos, and/or presented as transcripts to best promote plain-language principles and to ease understanding of non-specialized academic readers.

Our first publication in *Insights* is an interview with Professor Jian Lu, the City University of Hong Kong's Chair Professor of the Department of Biomedical Sciences, Department of Material Science and Engineering, and Department of Mechanical Engineering, conducted on June 15, 2020. Prof. Lu has used his interdisciplinary expertise to create a new approach for modeling the COVID-19 pandemic by drawing comparisons between infection propagation and mechanical vibration. For more information, please read below.

As the coronavirus disease 2019 (COVID-19) pandemic was becoming a major public health emergency in late January 2020, Professor Jian Lu of the City University of Hong Kong was queried by friends in a WeChat group to predict the number of cases in the coming days. Prof. Lu, the chair professor of three departments including Biomedical Sciences, Material Science and Engineering, and Mechanical Engineering, saw in this academic challenge an opportunity to utilize his interdisciplinary expertise and contribute to the global understanding of the pandemic.

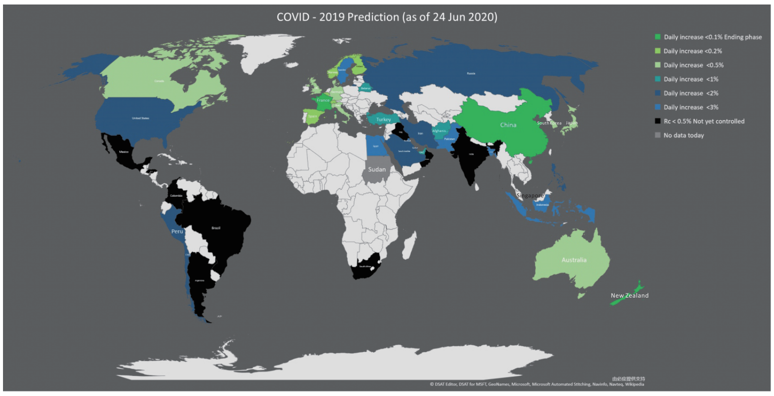
Where many existing models have relied on epidemiological and biostatistical principles to find an R_0, the basic reproductive number indicating the number of infections coming from one case, Prof. Lu believed that the modeling of R_0 relied on many difficult-to-estimate parameters such as the effectiveness of social distancing measures and case-finding capabilities. Having a separate skillset, Prof. Lu saw a chance to use only publicly available case numbers to formulate the propagation of the COVID-19 pandemic analogously to a vibration mechanical system. Being an expert in fracture mechanics and experimental mechanics, Prof. Lu saw similarities to assessing the strength of new materials and Moore's Law, the observation that transistor density on a microchip doubles every two years but has no inherent material explanation, and applied these lines of thinking by viewing the country and regional health systems as pseudo-materials with the COVID-19 pandemic applying stress and propagating failure.

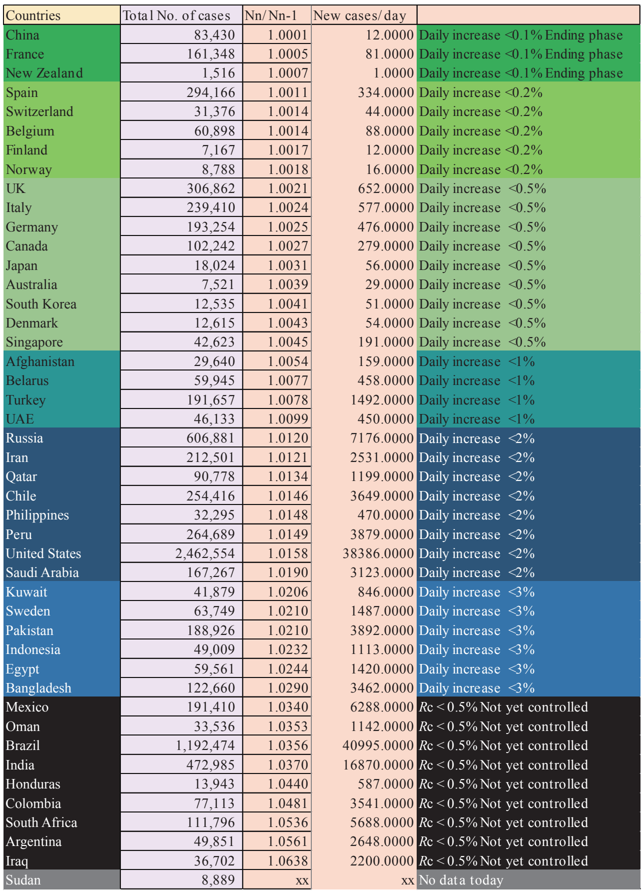
The following is his equation: $N(D_n)_{total} = N(D_{n-1})_{total} \times (R_{n-1} - R_c \times D_n)$; where D_n is the number of days starting from the first day of simulation to day n; $N(D_n)_{total}$ is the total number of infected cases till day n; R_{n-1} is the case increase rate prior to day n; and R_c is the reduction coefficient of daily cases increase rate (*1*).

Prof. Lu's equation was used to display two vital components in his model: the rate of increase in daily cases and the reduction coefficient R_c of the increase rate in daily cases. As shown in Figure 1, the rate of increase in daily cases was mapped to display the rate of growth in individual countries and regions. Countries that were shaded green have reached the final stages of propagation and were close to overcoming the pandemic within their borders. However, countries that were bluer with rates of increase <2% and <3% were still experiencing high levels of growth, and countries that were shaded black have R_c's that were <0.5%, which indicates the pandemic was still not controlled within the country's borders. The countries modelled as having uncontrolled growth were, as of June 24, 2020, The Republic of Columbia, Republic of India, The Federative Republic of Brazil, Republic of the Philippines, Sultanate of Oman, The Republic of South Africa, The Republic of Honduras, The Republic of Argentina, and Republic of Iraq.

In his daily updates, Prof. Lu also included additional graphs modeling the propagation of COVID-19 at several different R_c's and tracked the real propagation within individual countries and several states of the USA. As shown in Figure 2, a higher R_c value indicated stronger control and the projected curves reached a lower cumulative number of cases. The red curve indicated the real progression of the pandemic using publicly available data and showed shifts in which R_c threshold the USA's curve was in, which intuitively suggested that the propagation of COVID-19 can alter based on the tightening or loosening of response measures. Prof. Lu's approach, therefore, means that R_0 can be considered as dynamic and as taking into account the response to virus propagation.

Prof. Lu and his team will diligently continue updating their modeling of these countries and regions until the end of the pandemic. For more detailed information, please visit their website: http://personal.cityu.edu.hk/jianlu/.





Countries	Total No. of cases	Nn/Nn-1	New cases/day	
China	83,430	1.0001	12.0000	Daily increase <0.1% Ending phase
France	161,348	1.0005	81.0000	Daily increase <0.1% Ending phase
New Zealand	1,516	1.0007	1.0000	Daily increase <0.1% Ending phase
Spain	294,166	1.0011	334.0000	Daily increase <0.2%
Switzerland	31,376	1.0014	44.0000	Daily increase <0.2%
Belgium	60,898	1.0014	88.0000	Daily increase <0.2%
Finland	7,167	1.0017	12.0000	Daily increase <0.2%
Norway	8,788	1.0018	16.0000	Daily increase <0.2%
UK	306,862	1.0021	652.0000	Daily increase <0.5%
Italy	239,410	1.0024	577.0000	Daily increase <0.5%
Germany	193,254	1.0025	476.0000	Daily increase <0.5%
Canada	102,242	1.0027	279.0000	Daily increase <0.5%
Japan	18,024	1.0031	56.0000	Daily increase <0.5%
Australia	7,521	1.0039	29.0000	Daily increase <0.5%
South Korea	12,535	1.0041	51.0000	Daily increase <0.5%
Denmark	12,615	1.0043	54.0000	Daily increase <0.5%
Singapore	42,623	1.0045	191.0000	Daily increase <0.5%
Afghanistan	29,640	1.0054	159.0000	Daily increase <1%
Belarus	59,945	1.0077	458.0000	Daily increase <1%
Turkey	191,657	1.0078	1492.0000	Daily increase <1%
UAE	46,133	1.0099	450.0000	Daily increase <1%
Russia	606,881	1.0120	7176.0000	Daily increase <2%
Iran	212,501	1.0121	2531.0000	Daily increase <2%
Qatar	90,778	1.0134	1199.0000	Daily increase <2%
Chile	254,416	1.0146	3649.0000	Daily increase <2%
Philippines	32,295	1.0148	470.0000	Daily increase <2%
Peru	264,689	1.0149	3879.0000	Daily increase <2%
United States	2,462,554	1.0158	38386.0000	Daily increase <2%
Saudi Arabia	167,267	1.0190	3123.0000	Daily increase <2%
Kuwait	41,879	1.0206	846.0000	Daily increase <3%
Sweden	63,749	1.0210	1487.0000	Daily increase <3%
Pakistan	188,926	1.0210	3892.0000	Daily increase <3%
Indonesia	49,009	1.0232	1113.0000	Daily increase <3%
Egypt	59,561	1.0244	1420.0000	Daily increase <3%
Bangladesh	122,660	1.0290	3462.0000	Daily increase <3%
Mexico	191,410	1.0340	6288.0000	Rc < 0.5% Not yet controlled
Oman	33,536	1.0353	1142.0000	Rc < 0.5% Not yet controlled
Brazil	1,192,474	1.0356	40995.0000	Rc < 0.5% Not yet controlled
India	472,985	1.0370	16870.0000	Rc < 0.5% Not yet controlled
Honduras	13,943	1.0440	587.0000	Rc < 0.5% Not yet controlled
Colombia	77,113	1.0481	3541.0000	Rc < 0.5% Not yet controlled
South Africa	111,796	1.0536	5688.0000	Rc < 0.5% Not yet controlled
Argentina	49,851	1.0561	2648.0000	Rc < 0.5% Not yet controlled
Iraq	36,702	1.0638	2200.0000	Rc < 0.5% Not yet controlled
Sudan	8,889	xx	xx	No data today

FIGURE 1. Professor Jian Lu's daily update of his COVID-19 pandemic model using publicly available data. The color scheme indicated the rate of increase in daily cases in countries and regions, and if the rate of increase had a significantly low reduction coefficient of the increase rate R_c, the country was shaded black.

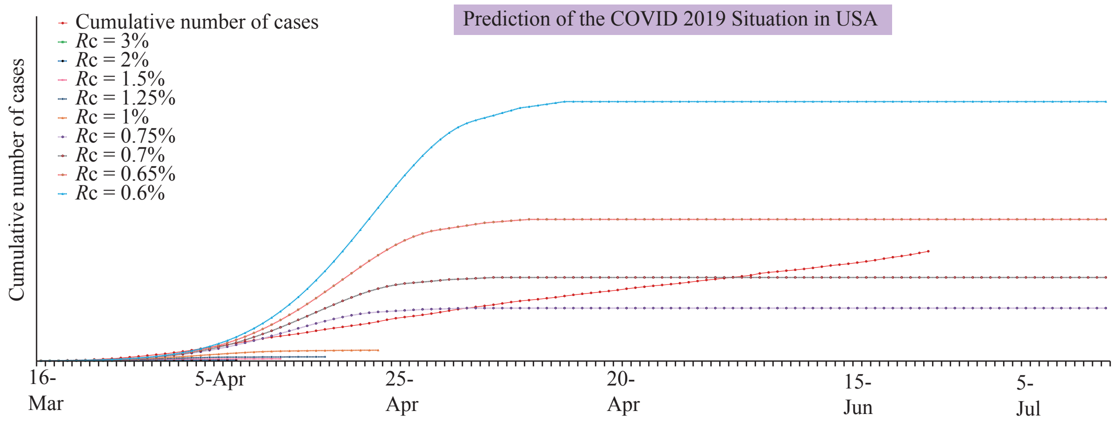


FIGURE 2. Professor Jian Lu's modeling of COVID-19 progression in the United States. The real progression was indicated by the red curve, and the other curves projected the progression at various reduction coefficients, R_c, of the rate of increase of daily cases. This curve indicated that COVID-19 is still not adequately controlled as the red line has exceeded the projected lines of R_c=0.75% and R_c=0.7%. Professor Jian Lu's models of other countries and of several states in the USA are available at his homepage: http://personal.cityu.edu.hk/jianlu.

doi: 10.46234/ccdcw2020.134

[#] Corresponding author: Feng Tan, tanfeng@chinacdc.cn.

---

[1] Chinese Center for Disease Control and Prevention, Beijing, China; [2] National Institute of Environmental Health, Chinese Center for Disease Control and Prevention, Beijing, China.

Submitted: June 25, 2020; Accepted: June 28, 2020

REFERENCES

1. Lu Jian. A new, simple projection model for COVID-19 pandemic. medRxiv 2020. http://dx.doi.org/10.1101/2020.03.21.20039867.

Jian Lu, PhD
Chair Professor of the Department of Mechanical Engineering
Chair Professor of the Department of Materials Science and Engineering
Chair Professor of the Department of Biomedical Sciences
City University of Hong Kong

The inauguration of *China CDC Weekly* is in part supported by Project for Enhancing International Impact of China STM Journals Category D (PIIJ2-D-04-(2018)) of China Association for Science and Technology (CAST).

CCDC weekly

Vol. 2 No. 27 Jul. 3, 2020

Responsible Authority
National Health Commission of the People's Republic of China

Sponsor
Chinese Center for Disease Control and Prevention

Editing and Publishing
China CDC Weekly Editorial Office
No.155 Changbai Road, Changping District, Beijing, China
Tel: 86-10-63150501, 63150701
Email: ccdcwjournal@163.com

CSSN
ISSN 2096-7071
CN 10-1629/R1