

# Basic epidemiological parameter values from data of real-world in mega-cities: the characteristics of COVID-19 in Beijing, China

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## Research article

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# Abstract

**Background.** With the spread of SARS-CoV-2 worldwide, understanding the basic epidemiological parameter values of COVID-19 from real-world data in meta-cities is essential for disease prevention and control.

**Methods.** To investigate the epidemiological parameters in SARS-CoV-2 infected cases in Beijing, we studied all confirmed cases and close contacts in Beijing from 1 Jan to 3 Apr 2020. The epidemiological and virological characteristics were analyzed.

**Results.** A total of 602 cases were positive for SARS-CoV-2, including 585 confirmed case-patients and 17 asymptomatic infections. The imported cases were mainly from Wuhan and then predominantly from abroad. Among 585 confirmed case-patients, the median age was 39 years. About 13.68% were severe and critical patients. The mean incubation period was 6.31 days. The secondary attack rate among households was higher than social contacts (15.55 vs. 4.56%). The secondary attack rate of healthcare workers (HCWs) was higher than non-HCWs' (7.26 vs. 4.24%). The basic reproduction number was 2.0, and the average serial interval was 7.64 days. No significant genetic variant was found.

**Conclusions.** The transmissibility of SARS-CoV-2 was relatively high, especially among households and from HCWs, which should be focused on. So far, there is no evidence of widespread circulation of SARS-CoV-2 in communities in Beijing.

## Background

In December 2019, a new beta coronavirus (CoV) was first detected in Wuhan, Hubei, China, causing a cluster of unknown pneumonia patients. It spread rapidly throughout Hubei and then to other provinces and other countries, requiring a worldwide large-scale response. The World Health Organization (WHO) declared the outbreak a public health emergency of international concern on 30 January 2020[1]. The novel coronavirus has been named SARS-CoV-2 by International Committee on Taxonomy of Viruses and the disease it causes has been named "coronavirus disease 2019" (COVID-19)[2]. As of 12 Apr, 2020, the global number of confirmed cases of COVID-19 has surpassed 1,600,000, including more than 100,000 deaths due to acute respiratory failure or other related complications [3].

Currently, the minority of the population of China has been infected, which leaves the majority of China susceptible to infection. Beijing, the capital of China, which has a population of 21 millions residents including 8 millions of migrants is particularly at risk. Since the first case detected in Beijing on 19 Jan, the number of case imported from Wuhan increased soon. To prevent further spread, the Chinese government announced the lockdown (forced quarantine or in-and-outflow restriction) of Wuhan City on 23 Jan before the upcoming spring festival during which massive population movements were expected to take place. The knowledge of basic epidemiological parameter values from data of real-world in mega-cities is an urgent need. We report the epidemiological and virological findings of 602 cases with SARS-CoV-2 infection and the outbreak response conducted in Beijing from 1 Jan to 3 Apr 2020.

## Methods

### Outbreak Response

Protocols for COVID-19 diagnosis and treatment, surveillance, epidemiological investigation, management of close contacts, and laboratory testing were formulated, and relevant surveillance activities and epidemiological investigations conducted. All individuals with suspected SARS-CoV-2 infection were isolated in designated hospitals for treatment. The epidemiological investigation, contact tracing, and quarantine were conducted by Centers for Disease Prevention and Control (CDCs) at district level or municipal level. Close contacts were defined based on protocol made by National Health Commission of the People's Republic of China (NHCPRC). Without any efficient personal protective equipment, a person who had contact within one meter with a confirmed case after onset of symptoms was defined as close contact. The definition changed on 10 Feb in accordance with the WHO guidelines [4], from after symptom onset to 4 days before symptom onset, given evidence of presymptomatic transmission. Close contacts were required to be quarantined at home or in designated sites (for cases who have no separate room or imported cases from overseas for medical observation till 14 days after the last exposure. Besides standard contact tracing, big data and artificial intelligence (AI) were used to strengthen contact tracing. For enhanced surveillance to detect COVID-19 in influenza-like illness (ILI) cases, all samples from ILI cases reported in routine influenza virological surveillance system [5] were tested for SARS-CoV-2 by real-time RT-PCR since January 28.

### Case definitions

The case definitions of suspected and confirmed cases of COVID-19 were based on the standard protocol made by the NHCPRC. Some modifications in case definitions were made during the study period in Beijing. The definitions of suspected cases and confirmed cases in the different periods are shown in Supplementary Table 1. Among all confirmed cases, mild cases were defined as non-pneumonia cases, and moderate cases was defined as those with pneumonia but no oxygen therapy required. Severe cases were defined as those with dyspnea, respiratory frequency  $\geq 30$ /minute, blood oxygen saturation  $\leq 93\%$ ,  $\text{PaO}_2/\text{FiO}_2$  ratio  $< 300$ , and/or lung infiltrates  $> 50\%$  within 24–48 hours. Critical cases were those that exhibited respiratory failure, septic shock, and/or multiple organ dysfunction/failure.

Asymptomatic laboratory-confirmed case was defined a person infected with SARS-CoV-2 who does not develop any symptoms and signs until they were tested negative for SARS-CoV-2.

### Data sources

The demographic, epidemiological, clinical, and outcome data were obtained using a standardized questionnaire by interviewing patients and/or their family members/relatives, attending doctors and other healthcare providers, supplemented by patient medical records. All data were checked by two professionals.

### Laboratory testing

Upper and lower respiratory tract specimens, urine, blood, stool, and saliva specimens were obtained from patients. RNA was extracted and amplified by real-time reverse transcriptase polymerase chain reaction (RT-PCR) with SARS-CoV-2-specific primers and probes obtained from NHCPRC or with commercial kits (Bio-germ Inc., Shanghai, China and ABT Inc., Beijing, China)[6]. According to NHCPRC protocol, a case tested with a cycle threshold (Ct) value less than 37 was defined as a positive result; otherwise, they were treated as negative results or successive tests were needed. Cases testing positive for both target genes (open reading frame 1ab and nucleocapsid protein) were determined as laboratory-confirmed cases. For those cases tested by a commercial kit (Bio-germ Inc., Shanghai, China and ABT Inc., Beijing, China), the results were determined following the manufacturer's instructions. Upper and lower respiratory tract specimens from confirmed cases were used for viral genome sequencing. Next-generation sequencing (NGS) was achieved based on a metagenomics strategy followed by Illumina sequencing (Illumina Inc., San Diego, CA, USA). Output data were assembled by a viral genome-targeted assembly pipeline with a homology search E-value of  $1e^{-10}$ . Full genome sequences used in the current study are available on request. Sequence alignment was achieved by MAFFT[7]. The Neighbor-Joining (N-J) method with a bootstrap of 1000 was used for phylogenetic analysis.

## Statistical analysis

We used descriptive statistical methods to analyze the epidemiological characteristics of confirmed cases with SARS-CoV-2 infection. Monte Carlo approach was applied to simulate 1000 times and estimate the average incubation period and its confidential interval. Data analysis was performed using SPSS statistical software package version 20.0 (IBM SPSS Inc., Chicago, IL, USA) and GraphPad Prism version 7.0 (GraphPad Software., San Diego, CA, USA). All statistical tests were 2-sided, and statistical significance was set at *P* value less than 0.05.

## Ethics Approval

Data collection and analysis of cases and close contacts were determined by the NHCPRC to be part of a continuing public health outbreak investigation, and as such was granted exemption from the institutional review board.

## Results

### Epidemiological characteristics of confirmed cases

From 1 Jan 2020 to 3 Apr 2020, respiratory specimens from 7,432 suspected cases were tested for SARS-CoV-2, and 602 (8.10%) were tested positive for SARS-CoV-2. Among 602 laboratory-confirmed SARS-CoV-2 infections, 585 were confirmed case-patients with symptoms and signs and 17 were asymptomatic COVID-19 cases. The proportion of asymptomatic infection was 2.82% (95% CI: 1.50–4.15).

The epidemic curve in Beijing by date of confirmation and onset was shown in Fig. 1A. Cases were firstly confirmed on 19 Jan, and then the number of cases rapidly grew to 30 Jan, peaked between 31 Jan and 1 Feb, and then steadily declined between 30 Jan and 18 Feb. However, the number of reported cases

fluctuated due to a local cluster (14 cases) that occurred in a company on 25 Feb in Beijing and imported cases from abroad. Since the first cases imported from abroad on 29 Feb, the number of imported cases from overseas increases rapidly. To effectively treat and manage the imported cases overseas, Xiaotangshan Hospital was launched on 16 Mar. On 23 Mar, nine cities designated as points of first entry for international passenger flights bound for Beijing. To detect more potential cases, all international passengers arriving in Beijing were required to be tested and quarantined at designated facilities on 25 Mar. The number of imported case from overseas in Beijing ranked first in China on 29 Mar. As of 3 Apr, a total of 169 cases had been identified in Beijing. However, only 4 local cases were identified at the same time. And besides one local case was related to one imported case from abroad, no local cases had been reported for 27 days.

As shown in Fig. 1B, among 585 confirmed case-patients, 124 (21.20%) were imported from Wuhan, 76 (12.99%) were imported from other regions outside Wuhan in China, 169 (28.89%) were imported from overseas, 1 (0.17%) was a secondary case of imported cases from overseas, 201 (34.36%) were local cases and 14 (2.39%) were under investigation. The epidemic in Beijing has been undertaken in two main phases. The first phase, started on 19 Jan when the first two cases were confirmed and ended on 28 Feb. The second phase, started on 29 Feb when the first imported case from overseas was identified. At the beginning of the first phase (before 1 Feb), the majority of confirmed cases were imported cases from Wuhan (61.00%, 97/159), while the proportion of imported cases from Wuhan had decreased since 1 Feb (one week after the lockdown of Wuhan)(16.07%, 27/168) ( $\chi^2 = 70.065$ ,  $P < 0.001$ ). At the beginning of the second phase (before 6 Mar when the last local cases identified), imported cases from overseas and local cases coexisted, and then the imported cases from overseas occurred dominated.

Of 585 confirmed case-patients, 268(45.81%) cases were male. The male-to-female ratio was 0.85:1. The incidence of males was slightly lower than females, 2.45/100,000 and 2.91/100,000, respectively (Fig. 2). The median age of confirmed cases was 39 years old (range, 0.5 to 94; interquartile range, 27 to 56). About 19% (114/585) were 60 or above, and 7.86% (46/585) were children < 18 years, among which 34.78% (16/46) were children under five years old (Table 1). A total of 17 (2.91%) cases aged 80 years or above. The incidence rate of the population 60 years old or above (6.91/100,000) was the highest compared to the other three groups, followed by the 18–59 years old group (5.55/100,000), the 5–17 years old group (0.50/100,000), and children under five years old (0.25/100,000).

Table 1

Epidemiologic Characteristics of 585 confirmed case-patients with SARS-CoV-2 Infection in Beijing, China.

<b>Characteristic</b>	<b>Csese (n = 585) No./total no. (%)</b>
<b>Sex</b>	
Male	268/585(45.81)
Female	317/585(54.19)
<b>Age group</b>	
0-	16/585(2.74)
5-	30/585 (5.13)
18-	427/585 (72.99)
60-	112/585 (19.15)
<b>Imported cases</b>	368/585 (62.91)
<b>Exposure history</b>	
Huabei Seafood Wholesale Market	0/585(0.00)
History of residence or travel	368/585(62.91)
History of residence or travel in Wuhan	124/585(21.20)
History of residence or travel in other regions outside Wuhan in China	76/585(12.99)
History of residence or travel	169/585(28.89)
Contact with confirmed or suspected cases	201/585(34.36)
Contact with confirmed or suspected cases from abroad	1/585(0.17)
Under investigation	14/585(2.39)
<b>Health care worker</b>	17/585(2.91)
<b>Case of severity</b>	
Mild	212/585(36.24)
Moderate	291/585(49.74)
Severe	66/585(11.28)
Critical	16/585(2.74)

The median age of 46 children < 18 years was 7 years old (interquartile range, 3 to 13). The sex ratio was 0.84:1. The proportion of asymptomatic infection among children < 18 years and adults was 4.17% and 2.71% ( $\chi^2 = 0.343$ ,  $P = 0.558$ ). Among 585 confirmed case-patients, 17 cases (2.91%) were healthcare workers (HCW). Epidemiological investigations suggested that 7 cases were infected due to health care activities and the remaining 10 were infected due to close contact with household cases rather than in a health care setting according to data from epidemiological investigation.

Of all confirmed case-patients, 36.24% were mild, 49.74% were moderate, 11.28% (64/585) were severe cases and 2.74% (16/585) were critically ill. The proportion of severe and critical cases decreased from 21.35% before 1 Feb to 7.24% after 1 Feb (Fig. 3A). The association between illness severity and age was shown in Fig. 3B. It was shown that illness severity aggravated with age (Supplementary Table 2,  $\chi^2 = 50.576$ ,  $P < 0.001$ ). A total of 8 cases deceased (with a crude case-fatality rate of 1.37%), among which 7 deaths were old adults over 60 years and 1 death was a 50-year-old man. The case fatality rate for males was 1.87% (5/268) and 0.95% (3/317) for females. The case fatality rate for  $\geq 80$  age group was 29.41% (5/17). All of the deaths had comorbid conditions, of which 75% (6/8) had hypertension or cardiovascular disease. Among 46 children < 18 years, 28 (60.87%) were mild, 17 (36.96%) were moderate and 1 (2.17%) was severe. The severe case was a three-year-old child with leukemia.

## Medical care timelines

The median duration from onset of symptoms to their first medical visit was estimated to be 3 days ( $P_{2.5}$ - $P_{97.5}$ : 0–17). The median duration from first medical visit to case confirmation was estimated to be 5 days ( $P_{2.5}$ - $P_{97.5}$ : 1.00-19.53).

## Incubation estimates

We reviewed the records of the confirmed cases and found 37.43% (219/585) had clear history of contacts with cases prior to symptom onset; based on which we estimated that the mean incubation period was 6.31 days (95% CI: 6.03–6.58) and the median was 5.68 days ( $P_{2.5}$ - $P_{97.5}$ : 5.23–6.06).

## Close contacts

By 3 Apr, a total of 4,007 close contacts were quarantined, 186 were confirmed with SARS-CoV-2 infection, with an overall secondary attack rate of 4.56% (95% CI: 3.99–5.29). The secondary rate was higher among family members or relatives (15.55%, 111/714) than that among social contacts (2.23%, 75/3363) ( $\chi^2 = 239.852$ ,  $P < 0.001$ ).

Among 441 close contact of HCWs, 32 were confirmed with SARS-CoV-2 infection, with an overall secondary attack rate of 7.26%, which was higher than that of non-HCWs', with a secondary attack rate of 4.24% (154/3636) ( $\chi^2 = 8.243$ ,  $P = 0.004$ ).

## Clusters

Till 3 Apr, a total of 117 clusters occurred, involving 391 confirmed cases. Among 391 cases, 246 (66.31%) occurred in family, 56 from abroad (15.09%), 28 (7.55%) in health care facilities, 28 (7.55%) in public areas and 13 (3.50) in mixed areas. Before 18 Feb, clusters mainly occurred in family and then were predominantly from abroad after 28 Feb (Fig. 4A).

The 91 family clusters involved 246 confirmed cases. The median number of involved cases of family clusters was 3 (Range, 2–7; IQR, 2–3). To estimate the basic reproduction number and serial interval in families, we identified 38 family clusters where one single index case was introduced. Since the 38 index cases caused 76 secondary cases among 193 family close contacts, we estimated that  $R_0$  in family clusters was 2.00 (95% CI: 1.63–2.39). And the average serial interval was estimated at 7.64 (95% CI: 6.43–8.93) days. The median serial interval was 6.00 (range, 0–34; IQR, 3.25–11.00) days (Fig. 4B).

Two clusters occurred in hospitals, involving 38 confirmed cases. One cluster occurred in the cardiac intensive care unit (CICU) and intensive care unit (ICU) of a general hospital in Beijing, involving 35 cases, among which 7 were HCWs. Another clusters in hospital involved 3 cases including one hospitalized patients and her two relatives providing medical assistants.

## **SARS-CoV-2 testing among ILI cases**

From 28 Jan to 3 Apr 2020, a total of 3,267 specimens were collected, no SARS-CoV-2 viral RNA was identified.

## **Viral RNA in clinical samples**

Among all 585 confirmed case-patients, 936 specimens from 243 cases were available for analysis, including 612 pharyngeal swabs, 7 nasal swabs, 5 saliva specimens, 219 sputa specimens, 2 serum/plasma specimens, 22 urine specimens, and 69 fecal specimens. 354 pharyngeal swabs, 7 nasal swabs, 156 sputa specimens, and 28 fecal specimens showed positive results in real-time RT-PCR tests. The RNA positive rate of throat swabs in mild, ordinary, severe and critical cases was 58.73%, 55.17%, 62.07%, and 76.47%, respectively ( $\chi^2 = 4.050$ ,  $P = 0.256$ ). In contrast to these, the RNA positive rate of sputum in mild, ordinary, and severe cases was 63.08%, 75.86%, and 70.27%, respectively ( $\chi^2 = 3.329$ ,  $P = 0.189$ ). No viral RNA was found in urine and serum/plasma, urine and saliva.

## **Phylogenetic analysis of SARS-CoV-2 in Beijing**

A total of five viral full genomes were obtained during the study period. Phylogenetic analysis suggested all tested viruses belonged to lineage B of the genus beta-coronavirus, and is genetically closely related to SARS-CoV-2 isolates in Wuhan (Fig. 5). It showed high genetic similarity among all tested viruses of 99.97% – 99.99%. It was of importance that all five viruses carried 442L, 472F, 479Q, 487N, and 491Y in viral S gene receptor-binding subdomain.

## **Discussion**

The transmission of COVID-19 in Beijing was initially imported from Wuhan, Hubei of China, then generated subsequent community clusters in local areas of Beijing, dominated by intrafamilial transmission. Later, after the epidemic was controlled in China, imported cases were predominantly from abroad. Our results could provide important epidemiological and genetic parameters in the real-world outside Wuhan for further analysis, including evaluations of the impact of control strategy and predictions of COVID-19 dissemination in large cities. We also show the importance of enhanced surveillance and testing capacity in a mega-city where a very small proportion of the population are immune to the virus. Until a vaccine is available, this is critical to prevent new epidemics from arising.

We estimated basic epidemiological parameters from family clusters where exposure and infection details were well characterized. We estimated an average serial interval of 7.64 days based on the data of 38 family clusters, which was similar to Li's[8]. We further bring up the 95% CI from 5.3–19.0 to a higher precision of 6.43–8.93 due to the larger sample size. We also obtained a similar estimate of  $R_0$  approximately 2 (95% CI: 1.63–2.39) to Li's (indicating that each patient was able to further infect 2 persons on average) [8]. Some estimates of  $R_0$  used reporting date of cases, and are not as reliable as  $R_0$  estimates from case data which have date of symptom onset. The  $R_0$  for SARS-CoV-2 was similar to SARS. In contrast, the estimated  $R_0$  of SARS coronavirus ranged from 1.1 to 4.2 with most estimates between 2 and 3[9–11]. However, the major difference with COVID 19 is pre- and asymptomatic transmission, which makes disease control far more challenging. The previous models highly relied on the assumptions underpinning the models, the timing of diagnosing and reporting of confirmed cases.

We estimated the secondary transmission of COVID-19 in 2,902 close contacts. The secondary attack rate of household was statistically higher than that of social contact (16.59% vs. 3.41%,  $P < 0.001$ ). This suggests that disease control around contact tracing should focus on spread from person to person among household close contacts as the highest risk. Thus, the implementation of prevention and control measures in household is particularly required. The household secondary attack rate of COVID-19 was slightly higher than SARS in Beijing, 2003[12, 13]. This might imply that the transmissibility of SARS-CoV-2 was higher than SARS. Due to the atypical or unspecific presence of mild infection or asymptomatic infection, the family members had been fully exposed to cases before they were confirmed, and this increased the risk of infection among household close contacts. In addition, we found that the secondary attack rate of HCWs was relative higher than that of non-HCWs' which implied that we should focus on the prevention among HCWs who might cause potential clusters or outbreaks both in healthcare facilities and families.

On 23 Jan, the Chinese government officially announced the implementation of lockdown in Wuhan City. We showed that from 1 Feb, about 1 incubation period from the lockdown, the proportion of cases with a travel history to Wuhan progressively declined, indicating impact of lockdown in Wuhan on the epidemic in Beijing.

The laboratory findings for SARS-CoV-2 infection pointed out the preference of lower respiratory tract samples in PCR testing. The positive rate of sputum was slightly higher than that of pharyngeal swab in

moderate and severe cases. Our previous quantitative study also showed the relatively high viral loads in sputum with a median of  $7.52 \times 10^5$ [14]. Recent reports also suggested some other type of sample for SARS-CoV-2 RNA testing [15, 16], including nasopharyngeal swabs, saliva samples and tear samples. The performances of these specimens need further assessment since the viral RNA was not found in urine samples and saliva samples in our study.

None of the 3,267 samples from ILI cases based on routine ILI surveillance was tested positive for SARS-CoV-2. This provides confidence that COVID-19 has not spread widely in Beijing, China.

Little genetic variance were found in SARS-CoV-2 viruses in Beijing. When the virus jumped directly from bats to human or via some unknown intermediate hosts is still unclear[17, 18],The genomic analysis suggested the SARS-CoV-2 had a relatively low estimated mean evolutionary rate of  $1.79 \times 10^{-3}$  to  $1.82 \times 10^{-3}$  substitutions per site per year[19], which was in consistent with our results. However, the increased genetic diversity of SARS-CoV-2 in human hosts over time cannot be neglected.

Our analysis had several limitations. First, if the close contacts of confirmed cases in Beijing traveled to other provinces outside Beijing, the health condition of those close contacts might not be obtained and updated even the information of close contact was transferred to corresponding provinces. This might bias the secondary attack rate of close contact and thus lead to lower  $R_0$  estimates. Second, detailed information on such exposure history as frequency, intensity, and duration for all cases was not available. This may influence the estimates of the incubation period. Third, the relationship between index cases and their quarantined close contact was not well-recorded, which limited the analysis of secondary attack rates by different relationships. A strength of the study is the well-established surveillance systems such as ILI surveillance, which were able to provide enhanced capability to study the epidemiology and exclude substantial community transmission.

In conclusion, we found that the human-to-human transmissibility of SARS-CoV-2 was relatively high, and the secondary attack rate of household contact was higher than that of social contact. The lockdown (quarantine) of Wuhan City was effective to halt the spread of the SARS-CoV-2. So far, there was no obvious evidence implying a widespread of SARS-CoV-2 in community in Beijing.

## Conclusion

The transmissibility of SARS-CoV-2 was relatively high, especially among households and from HCWs, which should be focused on since they might cause potential clusters or outbreaks both in healthcare facilities and families. The lockdown of Wuhan City was effective in halting the spread of the COVID-19 to Beijing. So far, there is no evidence of widespread circulation of SARS-CoV-2 in community in Beijing.

## List Of Abbreviations

CoV: coronavirus; COVID-19: coronavirus disease 2019; AI: artificial intelligence; ILI: influenza-like illness; RT-PCR: reverse transcriptase polymerase chain reaction; NGS: Next-generation sequencing; N-J: Neighbor-Joining; CI: confidential interval; HCWs: healthcare workers;

## Declarations

### Ethics approval and consent to participate

Data collection and analysis were determined by the National Health Commission of the People's Republic of China to be part of the continuing public health investigation of an emerging outbreak and thus the informed consent and ethics approval was waived by institutional review board and human research ethics committee of Beijing CDC.

### Consent for publication

Not applicable.

### Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

### Competing interests

No potential conflicts of interest were disclosed.

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### Contributors

Concept and design: PY and QW.

Acquisition, analysis, or interpretation of data: All Authors.

Drafting of the manuscript: XW, YP and CRM.

Critical revision of the manuscript: PY and QW.

Laboratory testing: YP, DZ, LC.

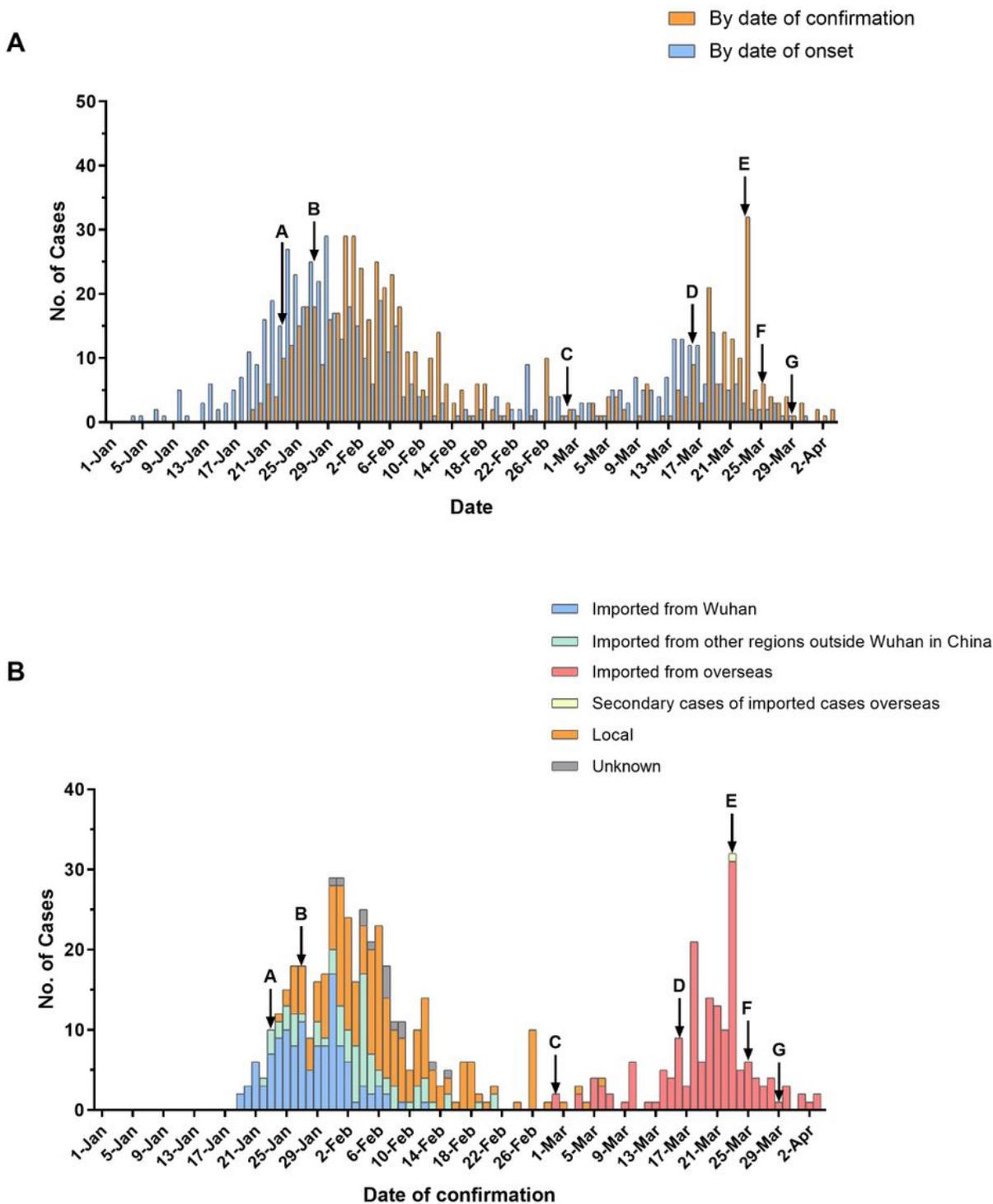
Data management and statistical analysis: XW, LJ, XL.

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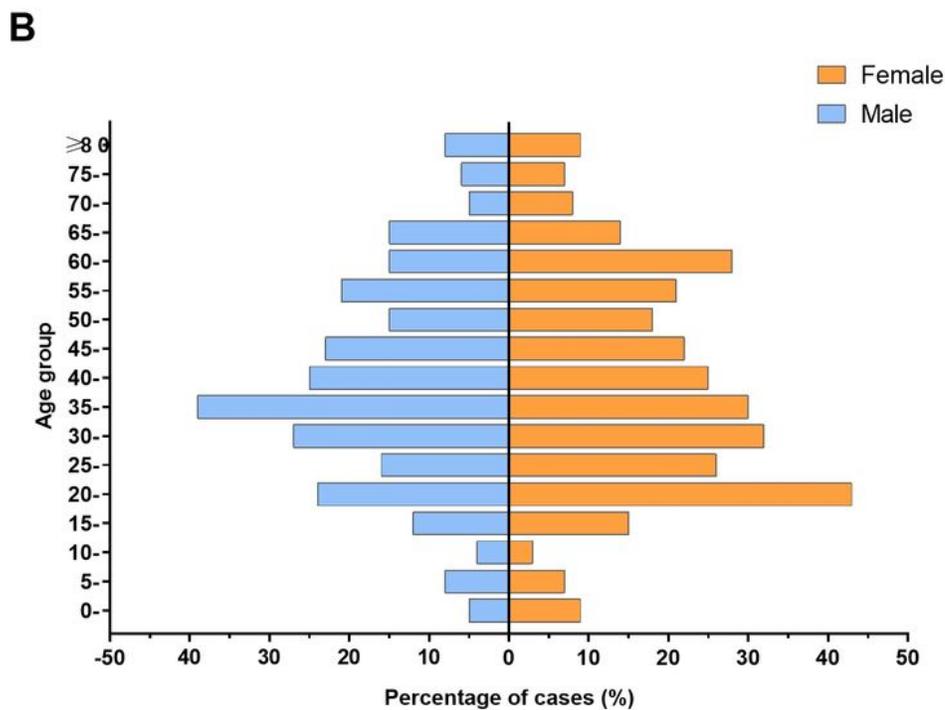
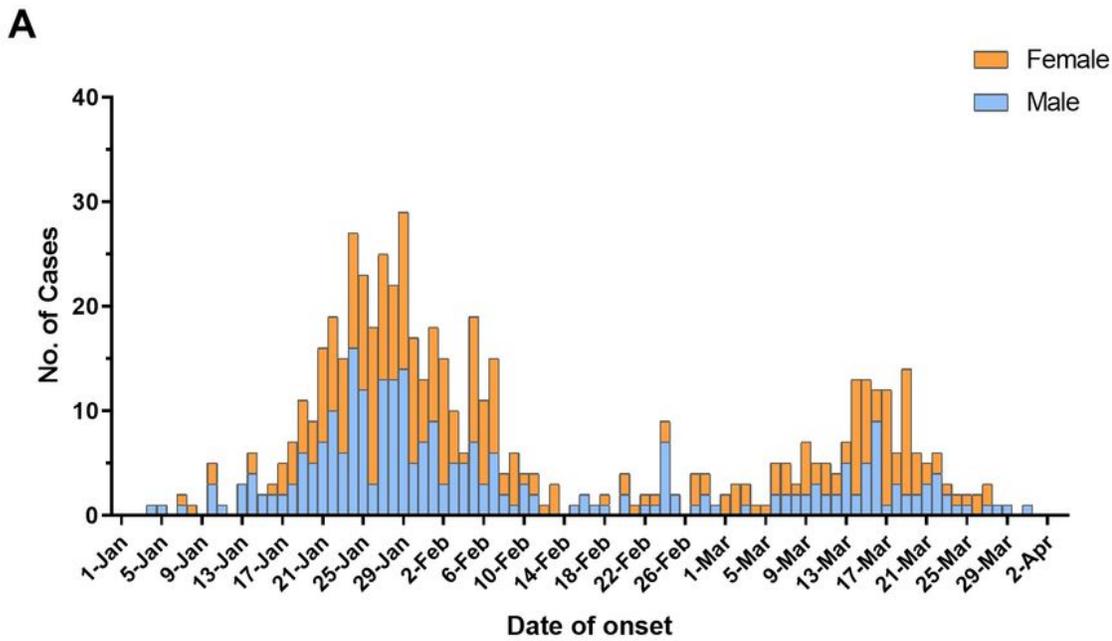
## Figures



**Figure 1**

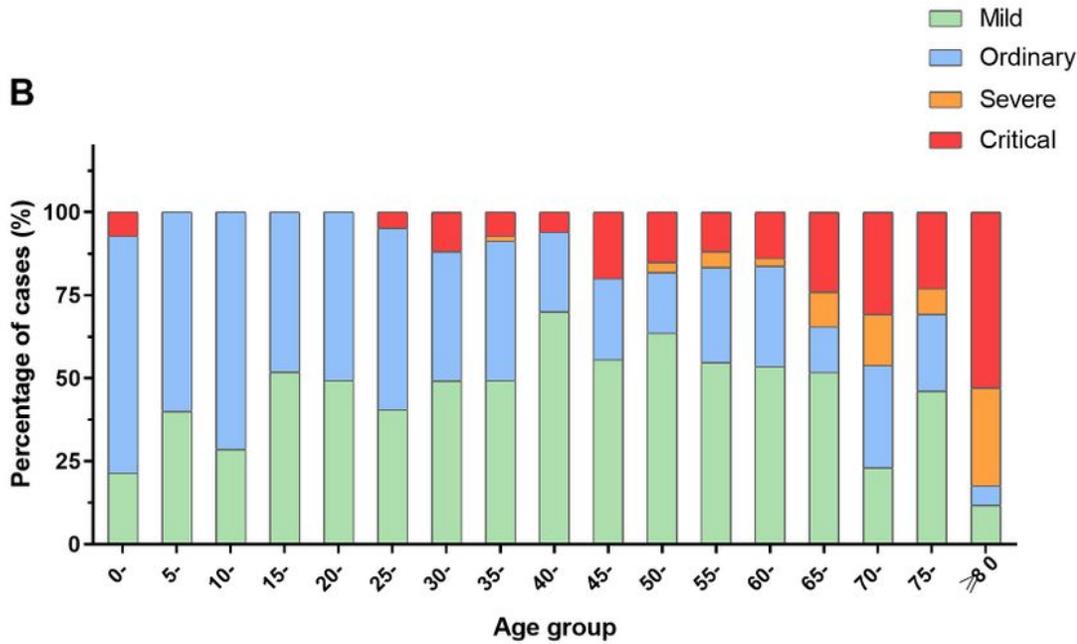
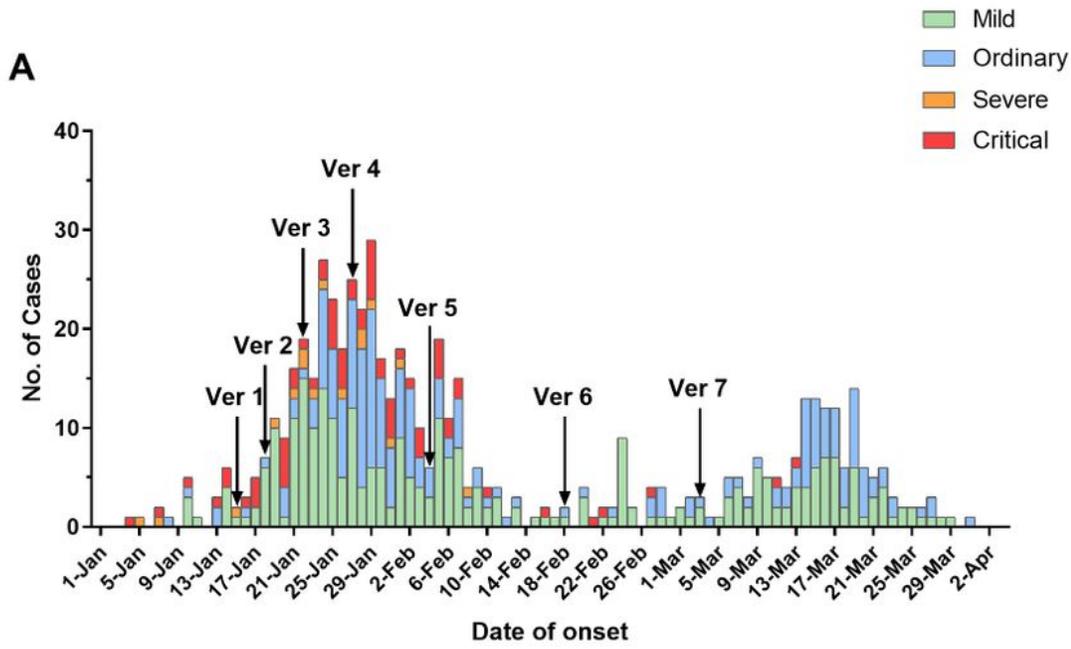
Epidemiologic Characteristics of 585 confirmed cases with SARS-CoV-2 infection Note: Local cases include the secondary cases of imported case outside in China, excluding secondary cases of imported case from abroad. A: Wuhan was locked down on 23 Jan. B: First fatal cases occurred on 27 Jan. C: First imported case from overseas identified on 29 Feb. D: Xiaotangshan Hospital launched for imported cases from overseas on 16 Mar. E: Nine cities designated as points of first entry for international passenger

flights bound for Beijing on 23 Mar. F: All international passengers arriving in Beijing must be tested and quarantined at designated facilities on 25 Mar. G: The number of imported case from overseas in Beijing ranked first in China on 29 Mar,



**Figure 2**

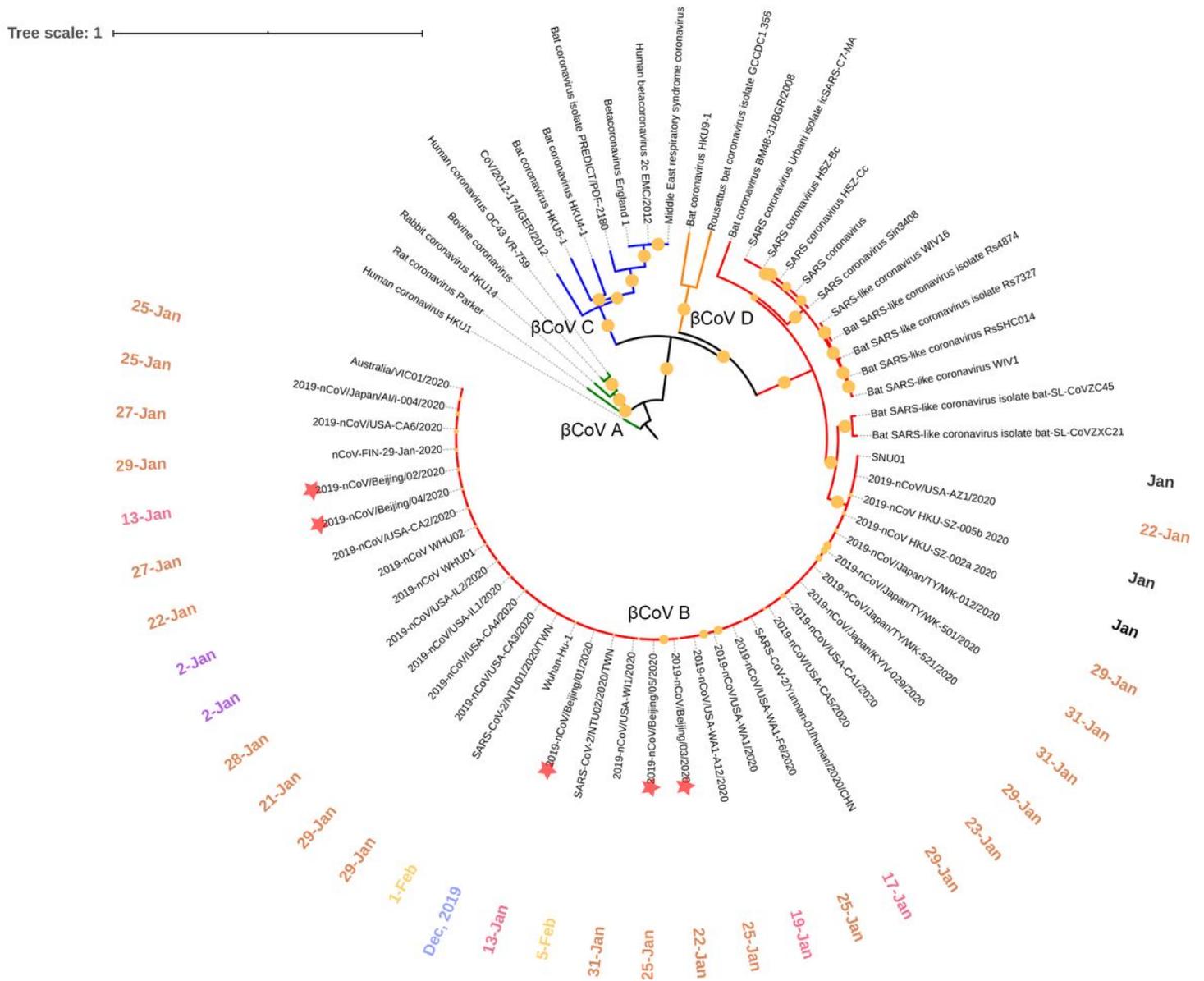
The age and sex distribution of 585 confirmed case-patients with SARS-CoV-2 infection



**Figure 3**

The clinical severity of 585 confirmed case-patients with SARS-CoV-2 infection Note: Ver: Version. The different version of definition for confirmed cases were marked.





**Figure 5**

The phylogenetic tree of SARS-CoV-2 in Beijing, China, 2020. The tree was constructed by the N-J method using the HKY model with bootstrap values determined by 1000 replicates. The bootstraps are shown at the branch point. The isolated time was colored at tags.

## Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [20200505SupplementalTable12.pdf](#)