Crucial control measures to contain China’s first Delta variant outbreak
Lei Luo¹, Zifeng Yang²,³,⁴,⁵#, Jingyi Liang²,³,⁶#, Yu Ma¹#, Hui Wang¹#, Chitin Hon⁶#, Mei Jiang²#, Zhengshi Lin²,³, Wenda Guan²,³, Zhitong Mai²,³,⁵, Yongming Li²,³, Kailin Mai²,³, Zhiqi Zeng²,³, Chuanmeizi Tu²,³, Jian Song²,³, Bin Liu²,³, Yong Liu²,⁸, Jianfeng He⁷, Huiyuan Li⁸, Baisheng Li⁷, Hang Dong¹, Yutian Miao¹, Shujun Fan¹, Lirui Fan¹, Xingyi Liang⁹, Ke Li¹, Chun Chen¹, Huihong Deng⁷*, Zhicong Yang¹*, Nanshan Zhong²*  
# Lei Luo, Zifeng Yang, Jingyi Liang, Yu Ma, Hui Wang, Chitin Hon, Mei Jiang have contributed equally to this article.

Affiliation
1. Institute of Public Health, Guangzhou Medical University & Guangzhou Center for Disease Control and Prevention, Guangdong, China
2. State Key Laboratory of Respiratory Disease, National Clinical Research Center for Respiratory Disease, Guangzhou Institute of Respiratory Health, the First Affiliated Hospital of Guangzhou Medical University, Guangzhou, Guangdong, postcode, P.R. China
3. Guangzhou Laboratory, Bio-Island, Guangzhou, 510320, P.R. China.
4. Guangzhou key laboratory for clinical rapid diagnosis and early warning of infectious diseases
5. State Key Laboratory of Quality Research in Chinese Medicine, Macau Institute for Applied Research in Medicine and Health, Macau University of Science and Technology, Taipa, Macau SAR, China
6. Macau Institute of Systems Engineering, Macau University of Science and Technology, Macau SAR, China.
7. Guangdong Center for Disease Control and Prevention, Guangzhou, Guangdong, China
8. Kingmed Virology Diagnostic & Translational Center, Guangzhou Kingmed Center for Clinical Laboratory Co., Ltd.
9. Shunde urban and rural planning information research center, Foshan, Guangdong, China

*Corresponding authors
Dr. Huihong Deng. Guangdong Center for Disease Control and Prevention, Guangzhou, Guangdong, China.  
Email: sjkzx_denghuihong@gd.gov.cn; 
Dr. Zhicong Yang. Guangzhou Center for Disease Control and Prevention, Guangzhou, Guangdong, China.  
Email: gdgzcdc@163.com; 
Dr. Nanshan Zhong. National Clinical Research Center for Respiratory Disease, State Key Laboratory of Respiratory Disease, Guangzhou Institute of Respiratory Health, the First affiliated Hospital of Guangzhou Medical University, 151 Yanjiang Road, Guangzhou, Guangdong, 510120, China. Email: nanshan@vip.163.com

© The Author(s) 2022. Published by Oxford University Press on behalf of China Science Publishing & Media Ltd. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted reuse, distribution, and reproduction in any medium, provided the original work is properly cited.
Abstract

SARS-CoV-2 B.1.617.2(Delta) variant flared up in late May in Guangzhou, China. Transmission characteristics of delta variant were analyzed for 153 confirmed cases and two complete transmission chains with 7 generations were fully presented. A rapid transmission occurred in 5 generations within 10 days. The basic reproduction number ($R_0$) was $3.60$ (95%CI: 2.50-5.30). After redefining the concept of close contact, the proportion of confirmed cases discovered from close contacts increased from 43% to 100%. With the usage of yellow health code, the potential exposed individuals were self-motivated to take nucleic acid test and regained public access with negative testing result. Facing the massive requirement of screening, novel facilities like makeshift inflatable laboratories were promptly set up as a vital supplement and 17 cases were found with one pre-symptomatic. The dynamic adjustment of these three interventions resulted in the decline of $R_t$ from 5.00 to 1.00 within 9 days. By breaking the transmission chain and eliminating the transmission source through extending the scope of the close contact tracing, health code usage and mass testing, the Guangzhou Delta epidemic was effectively contained.

Keywords: COVID-19; Public health; Control measure; Close contact; Mass testing

Introduction

COVID-19 pandemic has been wreaking havoc the whole world since the beginning of 2020. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the culprit(1). Implementation of mass vaccination against SARS-CoV-2 with non-pharmaceutical control measures has proved to be effective in containing the pandemic development. However, one of the big challenges we are confronting at present is the fast mutation of SARS-CoV-2, some mutated viral variants produce second or third waves of COVID-19 in some countries, making great burdens on public health and society(2, 3).

The SARS-CoV-2 Delta (B.1.617.2) Variant of Concern (VOC) was first identified in India in October, 2020, and later spread quickly across India(4). As of 13 July 2021, World Health Organization (WHO) reports that at least 111 countries, territories and areas have detected Delta variant, which is expected to become the dominant one globally in the coming months. The high increase in case incidence is believed to be related to the increased transmissibility of the Delta variant(5); moreover, studies have shown reduced sensitivity of Delta to antibody neutralization, suggesting Delta spread may be associated with an immune escape(6-9).

An epidemic caused by Delta variant broke out on May 21, 2021, Guangzhou, China, which is the first Delta outbreak in the country. Guangzhou is the major economic center in Southern China with a population about 15 million. In the early stage of the epidemic, we found out that the epidemic was characterized by spatial clustering, short incubation period, strong infectivity and rapid transmission. However, conventional interventions carried out in the first COVID-19 epidemic in the early 2020, such as wearing facial masks, social distancing, tracing and testing the close contacts, and isolating the confirmed cases, were no longer blocking the transmission as quickly as possible. As a result, we implemented some new intervention
measures complementary to those mentioned above. At last, the epidemic was eliminated within 28 days with a relative small number of confirmed cases and without whole city lockdown, such that the impact on the society was minimized. Here, we present the Delta epidemiological characteristics and the control measures we adopted to contain the epidemic.

Results

Characteristics of Delta Transmission in Guangzhou

Between May 21 and June 18 2021, 48.8 million throat swab samples were collected and tested for nucleic acid of SARS-CoV-2, among which 153 cases were identified. The demographic characteristics of the confirmed cases were summarized in Table S1. All infections were related to different clustering and a significant number of infections were from household or community (81.53%) and restaurant (41.27%) (Table 1). The incubation time was short, with a median of 4.00 days (IQR: 3.00, 6.00) and the median serial time was 3.00 days (IQR: 2.00, 5.00). Besides, a low average Ct value of 22.62 (SD: ±6.37) was also observed (Table 1). The basic reproduction number ($R_0$) was 3.50 (95%CI: 2.00-5.62).

Table 1. Characteristics of Delta cases in Guangzhou, China from May 21 to June 18, 2021

| Characteristics                  | No. (%) | Ct value, mean (SD) |
|----------------------------------|---------|---------------------|
| **Total**                        | 153     | /                   |
| **Incubation period (days)—median(IQR)** | 4.00(3.00,6.00) | / |
| **Serial time (days)—median(IQR)** | 3.00 (2.00,5.00) | / |
| **Clustering**                   |         |                     |
| Household/Community              | 81 (52.94) | / |
| Restaurant                       | 41 (26.80) | / |
| School/ Workplace                | 12 (7.84) | / |
| Other                            | 19(12.41) | / |
| **Generation**                   |         |                     |
| First                            | 1(0.70) | 16.50(/)\textsuperscript{a} |
| Second                           | 2(1.40) | 14.03(1.67) |
| Third                            | 15(10.49) | 21.08(5.49) |
| Fourth                           | 37(25.87) | 21.46(6.06) |
| Fifth                            | 43(30.07) | 24.34(7.27) |
| Sixth                            | 43(30.07) | 22.94(5.68) |
| Seventh                          | 2(1.40) | 31.72(8.63) |
| **Total**                        | 143\textsuperscript{b} | 22.62 (6.37) |

\textsuperscript{a}There was only one patient in this generation. \textsuperscript{b}We excluded 10 cases who were unable to trace their previous and next generation and proportions of different generations was calculated by dividing the number of 143 instead of 153. IQR: Interquartile range; SD: Standard deviation; Ct: cycle threshold value.
Transmission scenario unraveled by in depth epidemiological investigation

Through large scale and arduous epidemiological investigation with multipronged approach, among 153 cases with positive viral nucleic acid test, 143 cases had clear epidemiological link (Fig. 1a) except ten cases with uncertain exposure history. To illustrate how the virus propagated among people, we present two complete transmission chains (7 generations) as examples (Fig. 1b, c). Both transmission chains were initiated with the same patient (Patient G1) of this outbreak, which took place in Liwan District. Patient G1 was a 71 years old female, she did not feel well on May 18, visited the fever clinic on May 20; the diagnosis of SARS-CoV-2 infection was confirmed the next day by routine nucleic acid test with a Ct value of 23.73. Patient G2 on both transmission chains was the same person, who was not an acquaintance of G1; instead, they dined in the same restaurant, brushed past each other (within several seconds, separated by about 6 feet) without direct contact. G2 also had a high viral load with a Ct value of 20.23. Thus, high viral loads of patients G1 and G2 implied Delta infectivity was strong. Other cases in chain I were infected through family and community clustering. Between the earliest date of symptom onset of G2 (May 22) and that of G6 (June 2), a rapid transmission was seen with virus spreading through 5 generations within 10 days (Fig. 1b). The trajectories of the viral propagation after patient G2 separated. Similar to chain I, cases on chain II had a space-time intersection in a restaurant and the virus was further transmitted among family members and classmates in the following days (Fig. 1c). In addition to the close epidemiological relationship, further evidence of phylogenetic analysis of the viral nucleic acid sequences support the cases on each chain were closely related. (Fig. S1).
Fig. 1 Epidemiological linking network and two transmission chains confirmed by epidemiology investigation and whole genome sequencing. a, One hundred and forty-three cases are shown in the network. Cases in each generation are shown in circles with different colors. The first-generation patient (red
circle, G1) is in the middle of the network. b, Transmission chain I. There are five cases in the sixth generation. G6.1 was a family member of G5, G6.2 was one of the classmates of G6.1. G6.3, G6.2 and G6.1 were the neighbors of G6.4. c, Transmission chain II. Highlighted in white represents the time before this epidemic onset, blue, red and green represents the second, third and fourth stages of the epidemic, respectively; The yellow boxes indicate the epidemiological relationships between generations. G: generation of transmission.

Temporal and spatial distributions of Delta cases across 4 stages in Guangzhou

This epidemic started from Liwan district and discretely spread over six districts: 127 Cases were found in Liwan, 8 cases in Haizhu, 10 cases in Nansha, 4 cases in Panyu, 3 cases in Baiyun, and 1 case in Yuexiu. Among 127 cases in Liwan district, 70.08% (89 cases) were in Baihedong subdistrict, and 23.62% (30 cases) in Zhongnan subdistrict. The daily confirmed cases per ten million people in Liwan district increased from 19.85 before May 28 to 109.15 between May 29 and June 5, then decreased to 73.71 between June 6 and June 12, and continued to decline thereafter (Figure 2).

Fig. 2 The case finding source at each stage.

Cases finding source includes fever clinic, close contact, key place and community.

*Key place refers to where confirmed cases had stayed 4 days before the symptom onset

Renovated interventions against Delta variant

The outcome of close contact redefinition

After realizing the high infectivity of the Delta strains, we therefore redefined close contact to contain those who were potentially at risk of infection. The number of close contact increased from 378 in the first stage to 5,992 in the fourth stage (Table 2). We discovered that the confirmed cases were mainly detected through four channels, including the fever clinic, close contact, key places and community (Fig. 2). With the close
contact redefinition, the proportion of close contact as the source of confirmed cases ultimately increased from 43% to 100% through four stages of the epidemic.

**Epidemic control with health code**

After extending the scope of close contact tracing, the conduction of epidemiological investigation slowed down due to limited manpower. Thus, people with exposure risk were classified and differentially managed (Fig. 3). Totally 600,441 potential exposed and exposed were identified and labeled with yellow health code according to case investigation and exposure risk classification. Individuals assigned a yellow code were considered as having potentially exposed or exposed to positive cases, and could not access public places; thus prompted them to take nucleic acid test on their own initiative. As long as these people obtained negative nucleic acid test results, they returned to usual life with restrictions lifted off. Among all identified potential exposed and exposed, a couple with yellow code participated in community screening test with one of their family members, they were all later confirmed COVID-19 diagnosis and became the first 3 cases in Nansha District. After they were isolated, 4 family members and 3 close contacts of them were subsequently confirmed Delta virus infection and isolated promptly, including 1 pre-symptomatic case (Fig. S2). Except for this cluster, no more cases were found in Nansha District. Thus, the progress of COVID-19 outbreak in Nansha District was quickly contained.

![Fig. 3 Exposure risk classification and graded management](https://academic.oup.com/nsr/advance-article/doi/10.1093/nsr/nwac004/6510839)

*Public access included public transportation usage and public places entrance. **Visiting NAT refers to door-to-door sampling process conducted by three-people groups. ***The exposed individuals were suggested to quarantine at home. NAT - nucleic acid test
Mass testing
With the range of potential risk population extended, previously routine nucleic acid testing capacity could not reach our requirement. In addition to the testing volume composed of those from CDC, hospital and third-party laboratories, novel facilities-makeshift inflatable laboratories were established in several gymnasiums. The maximum daily testing number of these labs increased from 120,000 to 180,000, and samples were received around the clock and issued results in 6 to 10 hours, this manipulation significantly improved the speed of screening. Besides, the mobile testing vehicles were also introduced in risk areas such as Liwan District to save the sample transporting time and restrict the people at risk moving around. With the joint effort of various institutes, the cumulative testing number reached 48.80 million samples within a month, including 34.07 million samples citywide and 14.73 million samples from risk areas (Fig. S3). Seventeen positive cases outside the risk areas were found through mass testing including 1 pre-symptomatic case.

Effectiveness of epidemic control
With the facilitation of new approaches, the median interval between symptoms onset and isolation shortened from 0.44 days to -11.50 days on average (Fig. 4a), indicating the infected cases had been isolated even before symptom onset. Moreover, the interval between close contacts identified and isolation shortened from 2 days at the early stages to less than a day at the end (Fig. 4b). These data suggested that the infected cases were under controlled before the symptom onset, the transmission risk was cut off timely and effectively. Although the effective reproduction number (Rt) was sharply increased at the beginning of the second stage with a peak of 5.00 on May 29, it quickly declined subsequently and less than 1.00 on June 7, 2021. In total, cases of COVID-19, and Rt were reduced effectively along with 4 stage intervention (Table 2, Fig. 4c).
Fig. 4 Effectiveness of epidemic control

a, Interval between symptom onset and isolation among close contacts. b, Interval between close contacts identification and isolation. c, \( R_t \) throughout the epidemic. Grey columns represent daily reported cases. The blue line represents the dynamic change of \( R_t \) and the surrounding purple area refers to 95% CI of \( R_t \). The light blue vertical lines separate the epidemic course into four stages.

Discussion

SARS-CoV-2 Delta variant have rapidly spread worldwide, becoming the dominant epidemic strain. Epidemiology of Delta strain in Guangzhou is characterized by spatial clustering, short incubation period, strong infectivity and rapid transmission. With close contact redefinition, implementation of health code and mass testing, plus routine control measures, time taken to isolate confirmed cases and \( R_t \) have rapidly declined. Within 28 days the first Delta outbreak in China was contained.

In light of 153 confirmed cases, a majority of them show strong relation to the same space, mainly in restaurants and household. Additionally, the incubation period estimated in present study is shorter than that in previous studies (4.0 vs.5.2(10, 11)). Besides, an average of Ct value 22.62 is observed, lower than that of SARS-CoV-2 B.1.1.7 lineage reported by Frampton(12) and van Loon W(13). Moreover, the average serial interval was 3 days, which is consistent with that reported by previous study(14). Different from the epidemic caused by SARS-CoV-2 wild-type strain in Guangzhou last year(15), the strong infectivity of Delta strain necessitates intervention measures to be modified and more specific and effective.
In the early stage of epidemiological investigation, we considered primary close contact as people living together, or having contact at a certain distance (≤ 2 meters) for more than 15 minutes with confirmed cases, which is consistent with the definition implemented by USA(16), UK(17) and Singapore(18). However, a brush-into-infection case occurred in public enclosed space suggesting possible aerosol transmission could not be overlooked(19). In view of this situation, we redefined the concept of close contact to include whoever is with an infected person in same places such as office, building, and entertainment venues or, those who had been with an infected person 4 days before the disease onset. It’s this new strategy that expanded our surveillance scope and controlled the risk of transmission as early as possible. As can be seen in our result, the source of confirmed cases was gradually narrowed into the key surveillance population.

Rapid development and utilization of mobile health applications has been seen since the beginning of COVID-19 in many territories and jurisdictions throughout five continents with government support(20-22). Up to August, 2020, 63 mobile apps had been used, the functionality of them includes contact tracing, self symptom checking, GPS location tracing, exposure notification, awareness raising and information sharing, etc. In our study, having close contacts been redefined, more people with exposure risk need investigation (Table 2). Execution of both targeted tracing of close contacts and comprehensively screening the potential exposed could be a big challenge under limited time and manpower. Therefore, we started to use a mobile app at stage 2, the stratified health code designation greatly facilitated and accelerated contact tracing process (table 2, Fig. 3 &4). Our experience on mobile app application proves that modern technology is requisite for epidemic control like other countries do.

To improve the screening speed and ensure testing volume, mass testing was implemented in many countries. Similar to German government action(23), we realized the great importance on expanding testing capacity. Not only hospitals and CDC, but also third-party laboratories have participated in the battle against Delta. Moreover, we applied makeshift inflatable laboratories and mobile testing vehicles synchronously into mass testing, reaching 180 thousand testing volume per day. This strategy also has been dynamically adjusted from citywide to risk areas in order to precisely block the channels of transmission.

In addition to the new measures mentioned above, routine prevention and control measures were executed (Table 2). Firstly, similar to the 2019 Wuhan epidemic(24), we have also imposed restrictions on the movement of people. People leaving Guangdong Province were requested with negative nucleic acid tests and green codes; no confirmed cases so far were found outside the border during this outbreak. Secondly, quarantine measures were adopted. We not only imposed self-quarantine on people with exposure risk as many countries did(25, 26), but also persuaded those with less well living condition to hotels for centralized quarantine. Thirdly, we temporarily halted the vaccination program to avoid people gathering and false-positive nucleic acid results in mass testing. Currently, animal surveillance is ongoing in regard to the cross-species infection(27, 28).

The mutation of the SARS-CoV-2 is accelerating, and the control of the pandemic is still challenging. The containment of the Delta epidemic in Guangzhou has taught us several lessons. First of all, because this outbreak was possibly initiated from an import case, it reminds us management of port cities and
independent travelers should be strengthened. Secondly, prevention and control strategies should adhere to current characteristics of the epidemic transmission and improve in accordance with the changing situation of the epidemic. Reasonably classifying risk levels, accurately delimiting control units, and taking measures as soon as possible is indispensable. Finally, to strike a good balance between epidemic control and socioeconomic development, it is necessary to call for more precise prevention and control measures to control outbreaks.

Conclusion

When a local epidemic breaks out caused by a highly infectious pathogen like SARS-CoV-2 Delta, it is necessary to timely adjust the prevention and control measures according to the epidemic situation. Precise prevention and control policies not only help the epidemic control, but also minimize the epidemic impact on society and economy.

Materials and methods

Source of data

Data of demographics of confirmed cases from May 18 to June 18, 2021, were extracted from the collection of Guangzhou Center for Disease Control and Prevention, including patients’ birth date, sex, residential district. The population size in each stratum was extracted from the Guangzhou 2019 Statistical Yearbook.

Diagnosis and epidemiological investigation of confirmed case

The collection and detection of nasopharyngeal swabs was performed strictly followed by the Prevention and Control Protocols of COVID-19 (Edition 8). Based on open reading frame 1ab (ORF 1ab) and nucleocapsid (N) protein genes in the SARS-CoV-2 genome, RT-PCR was performed according to the manufacturer’s specification (Da’An Gene Co., Ltd. Of Sun Yat-sen University)(29). If the cycle threshold (Ct) value of RT-PCR is <40, the sample is considered to be positive. The exposure histories of confirmed cases and their close contacts were obtained through an interview, public video monitoring systems and cell phone apps, etc. The sequence analysis of cases is shown in supplementary data.
Renovated measures implementation

(1) Update the concept of close contact to expand the scope of tracking
The original definition of close contact is the family members, or colleagues who are with the infected person two days before the onset of the disease, or people who had meals or meeting with the infected person within one meter distance. The new concept of close contact for Delta virus was described as: (a) whoever is either in the same space, the same workplace, or the same building, with the infected person; (b) those who had been with the infected person 4 days before the disease onset.

(2) Exposure risk classification and graded management with health code
Based on the possibility of exposure to the source of infection, people with exposure risk were classified and divided into four levels, including (i) risk-free population, (ii) potential exposed, (iii) exposed, and (iv) close contacts; definitions of these four groups and the detailed corresponding management measures are shown in Fig. 3.

(3) Set up makeshift inflatable laboratories
Multiple standardized makeshift inflatable laboratories were built in gymnasiums within 24 hours to increase the testing capacity. Each inflatable laboratory covers an area of about 210 square meters, which is divided into three areas: reagent preparation area, sample processing area and nucleic acid amplification area (Fig. S4).

According to the judgment and prediction on the epidemic trend, we literally divided the whole epidemic into four stages. A more detailed control measures in each stage could be found in Table 2.

Statistical analyses.
Normal distribution data such as Ct value were presented as mean (± standard deviation). Qualitative information such as the source of case finding was presented as percentage or frequency. Analysis of Variance (ANOVA) was performed in the comparison of interval calculation across four stages. All of the tests were two tailed, and a value of P < 0.05 represented statistical significance. The epidemiological parameters (R0 and Rt) calculation is shown in supplementary data.
Data availability
The data that support the findings of this study originate from Guangzhou Center for Disease Control and Prevention. Case data are derived from epidemiological investigation reports which are not publicly available.

Author contributions
Conceived study: Lei Luo, Zifeng Yang, Yu Ma, Hui Wang, Chitin Hon, Mei Jiang, Huihong Deng, Zhicong Yang, Nanshan Zhong

Designed study and experiments: Lei Luo, Zifeng Yang, Yu Ma, Hui Wang, Jianfeng He, Chitin Hon, Huihong Deng, Zhicong Yang

Performed experiments: Jingyi Liang, Mei Jiang, Hang Dong, Yong Liu, Huiyuan Li, Baisheng Li, Yutian Miao, Shujun Fan, Lirui Fan, Xingyi Liang, Ke Li, Chun Chen,

Interpreted data: Zhengshi Lin, Yongming Li, Zhitong Mai, Kailin Mai, Wenda Guan, Zhiqi Zeng, Mei Jiang, Chuanmeizi Tu, Jian Song, Bin Liu, Lei Luo, Zifeng Yang, Yu Ma, Hui Wang, Jianfeng He, Chitin Hon, Huihong Deng, Zhicong Yang, Nanshan Zhong

Manuscript preparation: Zhengshi Lin, Yongming Li, Zhitong Mai, Kailin Mai, Chuanmeizi Tu, Jian Song, Bin Liu, Lei Luo, Zifeng Yang, Yu Ma, Hui Wang, Nanshan Zhong

Acknowledgments
We thank Minfei Yu, Peikun Guan and Tong Wu for their technical support on phylogenetic analysis. This work was funded by National Key Research and Development Program of China (No.2021YFF0306006), Key Project of Medicine Discipline of Guangzhou (No.2021-2023-11) and Basic Research Project of Key Laboratory of Guangzhou (No.202102100001). We are sincerely grateful to all epidemiology investigators, staffs of local community office, medical workers and volunteers for their hard work in helping to control the epidemic outbreak.

Competing interests
The authors declare no competing interests.
| Timeline | Stage 1 (May 21 – May 28) | Stage 2 (May 29 – Jun 5) | Stage 3 (Jun 6 – Jun 12) | Stage 4 (Jun 13 – Jun 18) |
|----------|--------------------------|--------------------------|--------------------------|--------------------------|
| Launch control measures against COVID-19 epidemic | Graded cordons sanitaire execution | Started at Jun 1 | Concentrated annihilation and search for latent cases at citywide level | Close the loophole and consolidate the achievements |
| | | 
| | | Confirmed cases were isolated and close contacts were quarantined | Closed-off management<sup>a</sup> took effect of whole area of Zhongnan Street in Liwan District, and 37 COVID-19 discrete places and surrounding areas in the city where all infected people live and work | After Jun 14 |
| | | Closed key places, where confirmed cases had visited | Closed and controlled management<sup>a</sup> were launched in non-closed-off areas in 4 subdistricts in Liwan District; 2 neighborhoods in Haizhu District; 1 neighborhood in Panyu District; as well as the surrounding areas of key places where infected persons had been to. | Gradual lift off lockdown measures on eight subdistricts and communities in different districts (Haizhu, Tianhe, Baiyun, Huangpu, Panyu) |
| | | | Strict health management and closed-loop management of homes and working places<sup>a</sup> took effect in neighborhoods of 4 subdistricts of Liwan District | After Jun 16 |
| | | | After Jun 4 | Six neighborhoods included two in Yuexiu District, one in Panyu and three in Haizhu, lifted from lockdown |
| | | | 2 subdistricts in Liwan District were adjusted to closed-off management | |
| | | | 6 subdistricts in Liwan District were adjusted to closed and controlled management | |
| | | Mobile Laboratory Vehicle operated in Liwan District on May 21 | |
| | | Set up makeshift inflatable laboratories on Jun 2 | |
| | | Targeted testing | Red Health Code | Gave Red Health Code for PCC and SCC |
| | | First Round in Guangzhou (May 26 - Jun 8) Over 27.98 million throat swab samples were tested | Number of PCC | 378 |
| | | | Number of SCC | 1,517 |
| | | | Over 5.5 million throat swab samples were tested | 1,813 |
| | | | Mobile Laboratory Vehicle operated in Liwan District on May 21 | 3,476 |
| | | | Set up makeshift inflatable laboratories on Jun 2 | 4,980 |
| | | | | 7,758 |
| | | Mass Testing | Yellow Health Code | Gave Yellow Health Code for people who stayed for over one hour within 500 meters of key places at the same time as or in the key place at the same time as the infected up to Jun 17 |
| | | General screening | Total 60,752 people; 22,974 in Liwan District 7,653 in Haizhu District 2,390 in Panyu District 214 in Nansha District | Total 417,761 people; 92,757 in Liwan District 109,683 in Haizhu District 1,156 in Panyu District 4,796 in Nansha District |
| | | | Total 417,761 people; 92,757 in Liwan District 109,683 in Haizhu District 1,156 in Panyu District 4,796 in Nansha District | Total 117,634 people; 50,904 in Liwan District 33,284 in Panyu District 1,697 in Nansha District |
| | | | Total 417,761 people; 92,757 in Liwan District 109,683 in Haizhu District 1,156 in Panyu District 4,796 in Nansha District | Total 4,294 people; 86 in Liwan District 198 in Haizhu District 1,156 in Panyu District 216 in Nansha District |
| | | | | | |
| | | | | | |
| Conventional approaches | Schools close | Offline teaching suspended at kindergartens and training institutions | School opened on Jun 17 except those in risk areas |
| | | Offline teaching stopped at primary, middle and high schools except for the senior classes in middle and high schools with accommodation and fully enclosed management conditions on campus | |
| | | Yes (citywide) | |
| | | Entertainment venues close | Yes | From Jul 3, all indoor cultural and entertainment venues allowed to receive visitors up to 75% of capacity |
| | | Travel restriction | Yes, unless had a negative nucleic acid testing result in 72 hours | From Jul 3, the requirements of negative nucleic acid test result for traveling to other provinces lifted |
| | | No dine-in services | Yes | Yes |
| | | Closed wholesale market (except for farm produce market) | Yes | No, except risk areas |
| | | Vaccination strategy | Routine vaccination | Routine vaccination (except risk areas) |
| | | Deferring Routine Vaccination | Routine vaccination (except risk areas) | Routine vaccination (except risk areas) |
a, People self-quarantined and performed nucleic acid tests on the 1st to 7th, 10th and 14th day of quarantine. b, People could only enter but could not exit their own neighborhood and gatherings were strictly prohibited. Nucleic acid tests were performed on the 1st, 4th and 7th day. c, People could only travel between home and working places with negative nucleic acid test results within 24 hours. d, Primary close contacts (PCC) referred to people (1) whoever was either in the same space, same workplace or building with infected people; (2) those who had been with infected people 4 days before disease onset. Disease onset referred to date of symptom onset for symptomatic cases and sampling date of the first positive test result for pre-symptomatic case. e, Secondary close contacts (SCC) referred to close contacts of PCC. f, Risk areas included places with (1) more than 50 cumulative number of confirmed cases and at least one cluster was discovered within 14 days; (2) cumulative number of confirmed non-clustered cases exceeded 50 within 14 days; (3) newly reported confirmed cases within 14 days.

Reference

1. Lu, R, Zhao, X, Li, J, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet (London, England). 2020; 395(10224): 565-74.
2. Campbell, F, Archer, B, Laurenson-Schafer, H, et al. Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin. 2021; 26(24): 2100509.
3. Callaway, E. Delta coronavirus variant: scientists brace for impact. Nature. 2021; 595(7865): 17-8.
4. Singh, J, Rahman, SA, Ehtesham, NZ, et al. SARS-CoV-2 variants of concern are emerging in India. Nature medicine. 2021; 27(7): 1131-3.
5. WHO. Weekly epidemiological update on COVID-19 - 13 July 2021. https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---13-july-2021 (20 July 2021, date last accessed).
6. Planas, D, Veyer, D, Baidaliuk, A, et al. Reduced sensitivity of SARS-CoV-2 variant Delta to antibody neutralization. Nature. 2021; 596(7871): 276-80.
7. Lustig, Y, Zuckerman, N, Nemet, I, et al. Neutralising capacity against Delta (B.1.617.2) and other variants of concern following Comirnaty (BNT162b2, BioNTech/Pfizer) vaccination in health care workers, Israel. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin. 2021; 26(26): 2100557.
8. Wall, EC, Wu, M, Harvey, R, et al. Neutralising antibody activity against SARS-CoV-2 VOCs B.1.617.2 and B.1.351 by BNT162b2 vaccination. Lancet (London, England). 2021; 397(10292): 2331-3.
9. Liu, C, Gimn, HM, Dejnirattisai, W, et al. Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. Cell. 2021; 184(16): 4220-423.
10. Li, Q, Guan, X, Wu, P, et al. Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia. New England Journal of Medicine. 2020; 382(13): 1199-207.
11. Yang, L, Dai, J, Zhao, J, et al. Estimation of incubation period and serial interval of COVID-19: Analysis of 178 cases and 131 transmission chains in Hubei province, China. *Epidemiology and Infection*. 2020; 148: 1-19.

12. Dan, F, Rampling, T, Cross, A, et al. Genomic characteristics and clinical effect of the emergent SARS-CoV-2 B.1.1.7 lineage in London, UK: a whole-genome sequencing and hospital-based cohort study. *The Lancet Infectious Diseases*. 2021; 21(9): 1246-56

13. Loon, WV, Oumlssig, H, Burock, S, et al. Emergence of the SARS-CoV-2 B.1.1.7 lineage and its characteristics at an outpatient testing site in Berlin, Germany, January-March 2021. 2021; 27(7): 1931-4.

14. Meng, Z, Jianpeng, X, Aiping, D, et al. Transmission Dynamics of an Outbreak of the COVID-19 Delta Variant B.1.617.2 — Guangdong Province, China, May–June 2021. *China CDC Weekly*. 2021; 3(27): 584-6.

15. Luo, L, Liu, D, Liao, X, et al. Contact Settings and Risk for Transmission in 3410 Close Contacts of Patients With COVID-19 in Guangzhou, China: A Prospective Cohort Study. *Annals of Internal Medicine*. 2020; 173(11): 879-87.

16. America, Co. Appendices(Dedinition of Close Contact) https://www.cdc.gov/coronavirus/2019-ncov/php/contact-tracing/contact-tracing-plan/appendix.html#contact (7 December 2021, date last accessed).

17. UK, G. Guidance for contacts of people with confirmed coronavirus (COVID-19) infection who do not live with the person. https://www.gov.uk/government/publications/guidance-for-contacts-of-people-with-possible-or-confirmed-coronavirus-covid-19-infection-who-do-not-live-with-the-person (20 July 2021, date last accessed).

18. Ng, OT, Marimuthu, K, Koh, V. et al. SARS-CoV-2 seroprevalence and transmission risk factors among high-risk close contacts: a retrospective cohort study. *The Lancet Infectious Diseases*. 2020; 21(3): 333-43.

19. Setti, L, Pa Ssarini, F, Gennaro, GD, et al. Airborne Transmission Route of COVID-19: Why 2 Meters/6 Feet of Inter-Personal Distance Could Not Be Enough. *International Journal of Environmental Research and Public Health*. 2020; 17(8): 2932.

20. Davalbhakta, S, Advani, S, Kumar, S, et al. A Systematic Review of Smartphone Applications Available for Coronavirus Disease 2019 (COVID19) and the Assessment of their Quality Using the Mobile Application Rating Scale (MARS). *J Med Syst*. 2020; 44(9): 164.

21. O’Connell, J, Abbas, M, Beecham, S, et al. Best Practice Guidance for Digital Contact Tracing Apps: A Cross-disciplinary Review of the Literature. *JMIR Mhealth Uhealth*. 2021; 9(6): e27753.

22. Wikipedia. COVID-19 apps. https://en.wikipedia.org/w/index.php?title=COVID-19_apps&oldid=1057957363 (7 December 2021, date last accessed).

23. Pereira, AMM, Machado, CV, Veu, MB, et al. Governance and state capacities against COVID-19 in Germany and Spain: national responses and health systems from a comparative perspective. *Cien Saude Colet*. 2021; 26(10): 4425-37.

24. Yang, Z, Zeng, Z, Wang, K, et al. Modified SEIR and AI prediction of the epidemics trend of COVID-19 in China under public health interventions. *Journal of Thoracic Disease*. 2020; 12(3): 165-74.

25. Pratt, CQ, Chard, AN, LaPine, R, et al. Use of Stay-at-Home Orders and Mask Mandates to Control COVID-19 Transmission - Blackfeet Tribal Reservation, Montana, June-December 2020. *MMWR Morb Mortal Wkly Rep.* 2021; 70(14): 514-8.

26. Hsiang, S, Allen, D, Annan-Phan, S, et al. The effect of large-scale anti-contagion policies on the COVID-19 pandemic. *Nature*. 2020; 584(7820): 262-7.

27. Munnik, B, Sikkema, RS, Nieuwenhuijse, DF, et al. Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. *Science*. 2020; 371(6525): 172-7.
28. Patterson, EI, Elia, G, Grassi, A, et al. Evidence of exposure to SARS-CoV-2 in cats and dogs from households in Italy. *Nature Communications*. 2020; 11(1): 6231.

29. Luo, L, Liu, D, Liao, X, et al. Contact Settings and Risk for Transmission in 3410 Close Contacts of Patients With COVID-19 in Guangzhou, China: A Prospective Cohort Study. *Ann Intern Med*. 2020; 173(11): 879-87.