Epidemiological Traceability Investigation of a New Wave of COVID-19 Outbreaks in Beijing

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Research Article

Keywords: Coronavirus, 2019-nCoV, COVID-19, Transmission chain, Incubation period

Posted Date: June 1st, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-559763/v1>

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Abstract

Background: To investigate a new wave of COVID-19 outbreaks in Beijing at the end of 2020, and to analyze the infection situation and transmission chain of each generation.

Methods: Using a unified questionnaire, through the combination of field investigation and telephone survey, and with the help of trajectory big data technology to track the infected persons and close contacts for clues and case investigation. All nasal/pharyngeal swabs were collected and detected by real-time fluorescence quantitative RT-PCR method. The propagation relationship was analyzed by using the schematic diagram of transmission chain.

Results: The outbreak involved 21 infected persons (15 confirmed cases and 6 asymptomatic). The first case was only an index case rather than the source of infection. The infected persons were spread through family exposure, workplace exposure, public premises exposure, vehicle exposure, diet exposure and so on. The average incubation period was 4 days, and those who had contact during both the virus incubation period and the symptom period had a higher risk of infection ($\chi^2=30.688$, $P<0.001$). Unprotected family exposure, diet exposure, and exposure to small spaces, such as within transport, presented a higher risk of infection ($\chi^2=33.461$, $P<0.001$).

Conclusion: Against the background of global integration, the COVID-19 situation is still grim, still can not relax. While speeding up the recovery of the economy, "external defense input and internal defense rebound" is still the top priority in China's epidemic prevention and control work.

Introduction

In December 2019, the novel coronavirus disease 2019 (COVID-19) was first reported in Wuhan, China ^[1]. Soon after, the number of cases rose sharply and rapidly spread around the world. As of 27 January 2021, there have been more than 100 million confirmed cases of the coronavirus worldwide, with a total of more than 2.14 million deaths. At present, China has basically succeeded in controlling the COVID-19 epidemic, but in the context of the global economic crisis, no country can manage alone or stand aloof. After a long period of calm in Beijing, a new wave of COVID-19 outbreaks had resurfaced since the discovery of a local asymptomatic patient on December 23, 2020. The infected person was only an index case. Due to taking the postgraduate entrance examination, the novel coronavirus nucleic acid test was performed on December 22 and the result was positive on December 23. As of December 30, this epidemic situation altogether infected 21 people, involving the spread of shared housing, transportation, homes, units, shopping malls, restaurants and other places. By analyzing the transmission chain and the transmission of each generation of cases, this study provided a reference for COVID-19 scientific prevention and control.

Methods

All definitions of COVID-19 infected persons and close contacts referred to diagnosis and treatment protocol for novel coronavirus pneumonia (Trial version 8) [2]. In this study, according to the exposure period (time period from first to last contact), before or after the onset of the previous generation of infected persons, was divided into 3 categories: only incubation period exposure, incubation period and symptom period exposure, only symptom period exposure. According to the contact between the close contacts and the infected persons, exposure was divided into 5 categories: family exposure (e.g. husband-and-wife relationship), diet exposure, workplace exposure (e.g. co-worker relationships, and co-tenancy also falls into this category), vehicle exposure, public premises exposure (e.g. market, shopping malls, supermarkets, hotels, etc.), then compared the differences between different categories. Using a unified questionnaire to obtain information through telephone surveys, face-to-face surveys, and access to medical records. Follow-up and screening of all close contacts of each case from 4 days before onset to isolation (the asymptomatic patient was 4 days before sampling and testing). Epidemiological investigations of all infected people and close contacts, collection of information such as clinical characteristics and exposure history. Nasal/pharyngeal swabs were collected, and the novel coronavirus nucleic acid was detected by real-time fluorescence quantitative RT-PCR method. In addition, combined with trajectory big data analysis means, draw a schematic representation of the transmission chain to guide the traceability of the epidemic situation. The principle is to use the base station to actively obtain the instantaneous location information of the infected person's mobile phone, and to compare the trajectory overlap of the other infected persons at the same time, then infer whether there is any possible contact between them. Statistical analysis was carried out using SPSS 25.0 software (SPSS Inc., Chicago, IL, USA), and the comparison of rates was made by chi-square test. P-value was two-sided and $P < 0.05$ was considered statistically significant.

Results

Look for clues to the outbreak's origins

Clue 1. C1, a asymptomatic patient, due to taking the postgraduate entrance examination, was tested for novel coronavirus nucleic acid on December 22 and diagnosed on December 23.

Clue 2. B3 appeared symptoms on December 16, symptoms aggravated (fever symptoms appeared) to the hospital for novel coronavirus nucleic acid detection on December 23, confirmed on December 25. Her close contact, A1 (tenant, living in different rooms), was diagnosed with asymptomatic patient on December 25 after receiving routine nucleic acid tests among close contacts.

Clue 3. C4 developed symptoms on December 23, December 24 to participate in the company's unified organization of novel coronavirus nucleic acid detection, confirmed on December 25. Her close contacts, D3 (husband, cohabitation), B2 (taxi and shopping together), C5 (taxi and shopping together), C2 (taxi driver), D4 (C5's husband, contacted on December 19) were diagnosed one after another on December 25 and 26 after receiving routine nucleic acid tests from close contacts. For safety reasons, C3 (B2's husband) was also tested for nucleic acid on December 25 and confirmed on December 26. After C2's

diagnosis, his close contacts, D1 (dinner together) and D2 (taking on his taxi) were diagnosed on December 28 and 30 respectively, with D2 being asymptomatic. Later, C3, D3, D4's eight colleagues (E1, E2, E3, E4, E5, E6, E7, and E8) were diagnosed from December 27 to 30, among which E1, E5 and E6 were asymptomatic.

Clue 4. B1 appeared cold symptoms on December 18, only self-purchased drugs did not seek medical treatment, until December 30, the village organized a full staff of novel coronavirus nucleic acid detection, medical staff in the patient's home to collect nucleic acid samples for testing, confirmed on the same day.

Contact each clue. With the help of track big data, A1 visited a shirt store in a shopping mall on December 13, and B2 had close contact with him as a clerk in the shirt store. On the same day, at the toilet door of the mall, A1 and B1 also had close contact. Then on December 17, C1 also went to the shirt store and had close contact with B2.

Analysis of the transmission chain

A total of 21 infected persons (15 confirmed cases and 6 asymptomatic patients) in this outbreak, with A1 (Malaysian nationality, November 26 from Indonesia to Fuzhou, after 14 days of intensive medical isolation observation, from Fuzhou to Beijing on December 10) as the first generation case; 3 persons infected through shared housing and in-store exposure for the second generation; 5 persons infected by shared transportation, family life and in-store exposure for the third generation; and 4 persons infected by shared transportation, dinner and family life for the fourth generation. Finally, through joint work, 8 persons were infected (due to the relationship between 8 persons and the third generation case C3, the fourth generation cases D3 and D4 as colleagues, there was the possibility of infection by the previous generation cases, or even between each other, so it became difficult to define the generation). The incidence and relationship of each generation were shown in Fig. 1.

Infectious analysis at different stages of disease

Incubation period was calculated for exposure to 1 infected person and only 1 exposure. 6 persons (B1, B2, C2, C4, C5, D1) were eligible for this analysis, of which 3 had an incubation period of 3 days, 1 person 5 days, 1 person 7 days and 1 person 8 days, with a median of 4 days. Because C3 had been in contact with B2 (C3's wife, the source of infection for C3) for a long time, B2 had earlier onset than D3 and D4, so C3's colleagues were classified as C3's close contacts. To analyze the infection caused by the contact between the close contacts and the previous generation cases at different stages of the disease, and to compare the infection rate (number of infections divided by number of exposed persons) by Chi-square Segmentation method, there were statistically significant differences ($\chi^2 = 30.688, P < 0.001$). Only incubation period exposure, infection rate was 0.30% (9/3012), no person infection during symptom period exposure only (0/125), the overall infection rate in both groups was 0.29% (9/3146), well below incubation period and symptom period exposure infection rate of 2.53% (11/435).

Infectious analysis of different modes of exposure

The infection rates from different exposure patterns were family exposure 7.32% (3/41), diet exposure 10% (1/10), workplace exposure 0.67% (9/1345), vehicle exposure 1.79% (4/224) and public premises exposure 0.15% (3/1961). There were statistically significant differences in infection rates by Chi-square Segmentation method ($\chi^2 = 33.461, P < 0.001$), the risk ranges from high to low, with family exposure, diet exposure and vehicle exposure being higher than workplace exposure, the lowest infection rate from public premises exposure.

Discussion

In this outbreak, the earliest occurrence C1 was only an index case. Through the trajectory big data analysis means, deep search, isolation and control of close contacts, we set up a link between the various transmission chains, and ultimately traced the source of the infected person A1 returning from Indonesia. A1 in Jakarta to Fuzhou flight, next to a COVID-19 case, and then infected. Later, the virus samples of the confirmed case were analyzed by gene sequence analysis, and the results were compared with the virus gene sequences of the infected persons in this epidemic situation. It was confirmed that all of them belonged to the Branch II (North American branch) of the European L genotype, and compared with the virus carried by A1, the nucleotide sequence similarity was 99.99%. A1 conducted 14 days of centralized medical isolation observation in Fuzhou, during which 5 nucleic acid tests and 2 serological tests were carried out, might be due to too small viral load, the results were negative, which was also consistent with A1 as an asymptomatic patient. This showed that even under strict epidemic prevention and control measures, there were still various uncertain factors.

The analysis of the transmission chain showed that D3, D4 and C3 were colleagues, although C3 might be infected earlier by his wife B2, then C3 subsequently infected D3 and D4 at work, further spreading within two families, that was almost impossible. Because D3 and D4 both developed symptoms later than their wives C4 and C5. And Fig. 2 showed that D3 and D4 were also more likely to be the next generation cases infected by their wives, while other colleagues developed later than them, might be the same generation.

In this outbreak, the average incubation period was 4 days, consistent with the average incubation period of about 5 days of novel coronavirus^[3-7], longer than the incubation period of influenza (1-3 days)^[8]. Research results shown that people infected with novel coronavirus were highly infectious at the end of the incubation period and beginning of onset. The infectious characteristics were similar to influenza A (H1N1) or seasonal influenza^[9], but SARS patients were not infectious before and at the beginning of the disease^[10-11]. Therefore, people who had been exposed during the incubation and symptom periods of novel coronavirus, naturally had a higher risk of infection. In addition, no protection such as family exposure, diet exposure, and small space exposure such as within a vehicle, had a greater risk of infection than other exposures. Finally, the overall infection rate of this epidemic was only 0.56% (20/3581), which might be related to the exposure of most people wearing masks, indicating that personal protection was effective in reducing the risk of virus infection.

The experience of this epidemic investigation: firstly, can not be “first impressions are strongest”, take it for granted that the first case found as the initial case, such as, in this epidemic the first case C1 was found only an index case; secondly, once the infected person was found, it was necessary to quickly search for close contacts, even secondary close contacts, and expand the search time range if necessary, such as the establishment of the transmission chain between A1 and B2, because of tracing B2's onset time forward for 1 week and checking her trajectory within a week; thirdly, the isolation observation and nucleic acid detection should be carried out as soon as possible, and the community where the case was located should implement personnel control immediately, limited social contact between community residents and outside, to prevent the spread of the epidemic situation, and carried out nucleic acid testing for all community residents as soon as possible. The outbreak involved only 21 infected persons, but 3581 close contacts were identified, as well as a larger number of secondary close contacts observed in the community, and nucleic acid tests were carried out on all persons. These measures effectively ensured that infected persons could be identified and controlled in the first place; finally, when the traditional epidemiological investigation methods exist that the respondents can not recall clearly, intentionally or unintentionally conceal the facts to cause difficulties in traceability, the use of trajectory big data and other modern means can effectively cooperate with the traditional epidemiological investigation to guide the traceability of the epidemic situation.

Conclusions

Since the end of December 2019, the first case of unexplained pneumonia had been found for one year, and the Chinese people had made great efforts and sacrifices to achieve the results of the current epidemic prevention and control. But even now, while speeding up the recovery of the economy, “external defense input and internal defense rebound”^[12], is still the top priority in China's epidemic prevention and control work. The outbreak also shows that the current COVID-19 situation is still grim, still can not relax. Against the background of global integration, the movement of people between countries has become more frequent, and the fight against COVID-19 is also the common responsibility and challenge of all countries in the world.

Declarations

Ethics approval and consent to participate

This investigation was carried out in accordance with the law of the People's Republic of China on the prevention and treatment of infectious diseases. The relevant units and individuals shall cooperate with them and shall not refuse. Thus, it was a minimum risk study that was not subject to the ethical approval of the institutional review committee. Even though, we still gave oral announcement of their rights to all patients before the investigation and obtained oral consent from all patients.

Consent for publication

Not applicable.

Availability of data and materials

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Funding

No funds to support the study.

Authors' contributions

CDW analyzed the data, and drafted the manuscript for the study. ZGX, HC, LJC, GP, and LXF were involved in data collection. All the authors read and approved the final manuscript.

Acknowledgements

The authors would like to thank all the infected persons and close contacts involved in the epidemic for their strong cooperation. Thanks also to the staff of the Center for Disease Control and Prevention for their extensive epidemiological investigation and guidance from superior departments.

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Figures

Figure 1. Exposure history and transmission path map of the COVID-19 epidemic.

Figure 1

Exposure history and transmission path map of the COVID-19 epidemic.

Figure 2. Epidemic curve of a COVID-19 outbreak in Beijing at the end of 2020 (5 days interval).

Figure 2

Epidemic curve of a COVID-19 outbreak in Beijing at the end of 2020 (5 days interval).