

Study on the Epidemiological Characteristics of SARS-CoV-2 Infection Based on Population of Zunyi, China

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Research

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Abstract

Background

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a new type of virus that firstly confirmed in Wuhan, China recently. SARS-CoV-2 mainly spread through droplets. Infection characteristics data of SARS-CoV-2 is still limited, especially about asymptomatic infection, familial aggregation infection and infection risk in family member.

Methods

From 2nd January 2020 to 23th February 2020, we have screened 22,729 throat swab samples from individuals with either have contact history of imported personnel, out-of-city travel or residence history or flu-like symptoms during the past 14 days. SARS-CoV-2 RNA was extracted and detected by real-time PCR. Data were analyzed using SPSS version 19 (IBM, Armonk, NY, USA). The results were confirmed by the Pearson χ^2 test; $P \leq 0.05$ was considered statistically significant.

Results

35 SARS-CoV-2 positive patients were found, 22 were asymptomatic infection, and 13 were familial aggregation infection. Odds ratio of SARS-CoV-2 infection risk between family aggregated close contacts and overall close contacts was 29.40 (95% confidence interval: 13.99 - 62.205, $\chi^2 = 140.23$, $P \leq 0.001$); odds ratio of SARS-CoV-2 infection risk between family aggregated close contacts and non-family aggregated close contacts was 703.50 (95% confidence interval: 89.53 - 5527.95, $\chi^2 = 282.659$, $P \leq 0.001$). One SARS-CoV-2 positive patient infected 2.08 (25/12) people on average under social control without separate isolation.

Conclusions

Social control is effective in SARS-CoV-2 inhibition, but self-isolation and screening should be added as supplementary means to avoid familial aggregation infection and find out asymptomatic patients.

Introduction

An infection of new novel coronavirus (severe acute respiratory syndrome coronavirus 2, SARS-CoV-2) was confirmed in Wuhan, China near December 2019 [1]. Soon, SARS-CoV-2 infection cases were reported in other provinces and other countries [2,3]. By 2nd March 2020, China alone had about 80000 confirmed SARS-CoV-2 cases. SARS-CoV-2 infection had been declared by WHO as a global public health emergency [4,5].

SARS-CoV-2 is a kind of single positive strand RNA virus, and is highly homologous with SARS-CoV and middle east respiratory syndrome coronavirus (MERS-CoV) [5,6]. SARS-CoV-2 is mainly transmitted by droplets and contact, has strong infectivity [7].

At present, there are few data about the family aggregated infection and asymptomatic infection of SARS-CoV-2. The infection ability of SARS-CoV-2 is limited to model calculation, there is little observation data. Guizhou province launched the first level response to major public health emergencies at 24th January 2020 [8]. Strict personnel flow control measures were carried out in Zunyi, residents need necessary reasons to go out and register at the community gate to control the contact opportunities between people; dispersive SARS-CoV-2 infected patients make it possible for virus transmission route retrospection (35 confirmed patients distributed in 6.13 million people, in 10 families of different areas, no mutual infection) [9,10]. This study aimed to screen SARS-CoV-2 infection in Zunyi, to trace the infection route, to estimate infection risk in close contacts, and to analyze the early clinical symptoms of SARS-CoV-2 patients.

Methods

Patients

People/patients in Zunyi met the following standards were screened: have travel or residence history out of Zunyi within 14 days; have contact history with people from city out of Zunyi within 14 days; have fever, cough, muscle soreness, fatigue, diarrhea and other symptoms according to Chinese Center for Disease Control and Prevention SARS-CoV-2 diagnosis treatment guidance "Diagnosis and treatment of novel coronavirus pneumonia (trial version sixth)" or WHO guidance [11, 12]; had contact history with suspected or confirmed SARS-CoV-2 patients within 14 days [11, 12]. People/patients with fever, have travel or residence history in Wuhan, had contact history with confirmed SARS-CoV-2 patients within 14 days were key screening targets for SARS-CoV-2, two SARS-CoV-2 RNA detections are required at a 24-hour interval. Medical staffs involved in SARS-CoV-2 positive patients' treatment were in 3-levels of biological safety protection and were detected for SARS-CoV-2, too.

Close contacts were confirmed by investigating contacted persons and activity tracks of confirmed SARS-CoV-2 patients. Phone calls, door notices and media announcements were used for recruiting contacts and close contacts. In this study, close contacts were divided into family (live with SARS-CoV-2 patients without respiratory tract protection or isolation) and non-family close contacts.

The present study was approved by the Affiliated Hospital of Zunyi Medical University Ethics Committee; the approval number was KLL-2020-008. Informed consent was obtained from person or guardian.

SARS-CoV-2 RNA detection

Throat swabs were collected and transported at 4°C in RNA storage solution (Zeesan Biotech, Xiamen, Fujian) for SARS-CoV-2 screening. All samples were detected within 6 hours after sample collection. SARS-CoV-2 RNA was extracted and purified by a kit named "Virus DNA/RNA Extraction Kit (CDC)" (Xi'an Tianlong Science and Technology, Xi'an, China; batch number: 20021410T014) according to the instruction. SARS-CoV-2 RNA was detected by real-time PCR using two kits named "Novel coronavirus

2019-nCoV RNA Detection Kit” (Daan Gene, Guangzhou, China; batch number: 2020001) and “Novel coronavirus 2019-nCoV RNA Detection Kit” (Shanghai GeneoDX Biotech, Shanghai, China; batch number: COV2020008) according to the instructions. Samples were detected by “Novel coronavirus 2019-nCoV RNA Detection Kit” (Daan Gene, Guangzhou, China) firstly, suspected positive (cycle threshold exceeded but near the cut off threshold of the kit) and positive samples were detected by both the two real-time PCR kits mentioned above again. Negative and positive controls were included in every experiment.

Data analysis

Data were analyzed using SPSS version 19 (IBM, Armonk, NY, USA). The results were confirmed by the Pearson χ^2 test; $P \leq 0.05$ was considered statistically significant.

In infection route tracing, contact relationship was prioritized in determine the infection route, then time interval from contact to onset or diagnosis; the mean incubation period was 5.2 days (95% confidence interval 4.1 - 7.0) [13].

Results

From 2nd January 2020 to 23th February 2020, 21052 people/patients and 22729 samples were detected for SARS-CoV-2 positive patients and close contacts were collected more than one time were detected for SARS-CoV-2 RNA. Age of 19447 people/patients were recorded, the average age was 34.11 ± 16.56 years old, age range was from 1 day to 94 years old. Among all the people/patients, 35 (35/21052, 0.17%) were SARS-CoV-2 positive. The average age of 35 SARS-CoV-2 positive patients was 45.43 ± 21.37 years old, age range was from 3 to 84 years old; 18 were female and 17 were male. The SARS-CoV-2 positive rates in different groups were shown in Table 1. Self-isolation and virus transmission of all 5 SARS-CoV-2 positive cases came from epidemic focus (Wuhan) were shown in Table 2.

| Group | Positive cases | Number of the whole group | Positive rate |
|---------------------------|----------------|---------------------------|---------------|
| All people/patients | 35 | 21052 | 0.17% |
| fever | 9 | 3249 | 0.28% |
| Cough and other symptoms | 9 | 627 | 1.44% |
| All symptoms | 13 | 3876 | 0.34% |
| People with Wuhan history | 5 | 236 | 2.12% |
| Medical staffs | 0 | 50 | 0 |
| Close contacts | 25 | 516 | 5.04% |
| Family close contacts | 24 | 46 | 50.98% |
| Non-family close contacts | 1 | 470 | 0.22% |

Table 1 Positive rate in different groups.

Note: fever was the most important symptom in guidance and previous study [11, 13], and fever was easy to perform in compulsory examination, so patients with fever was more than other symptoms.

| Patient number | Performed self-isolation or not | Family member infected/Family member | have clinical symptoms or not [observation time] | Positive or negative by the end of observation | Have basic susceptible diseases [14] or not. |
|----------------|---------------------------------|--------------------------------------|---|--|--|
| Patient 01 | ☐ | 0/4 | ☐ | Negative | ☐ |
| Patient 02 | ☐ | 0/5 | ☐ | Negative | ☐ |
| Patient 03 | ☐ | 0/4 | ☐ | Negative | ☐ |
| Patient 05 | ☐ | 8/10 | ☑41 days☑ | Positive | ☑diabetes☑ |
| Patient 08 | ☐ | 3/4 | ☐ | Negative | ☐ |

Table 2 Summary of human-to-human transmissions on 5 Wuhan-imported cases.

Note: “Family member” and “Family member infected” did not include Patient 01, 02, 03, 04 and 05. Observation end time was 3 March 2020. “☑” means yes, “☐” means no. “Positive” or “Negative” mean SARS-CoV-2 RNA positive or negative.

In this study, 35 SARS-CoV-2 positive cases distributed in 10 families, 4 were alone sick (patients 01, 02 and 03 self-isolated, patient 04 live alone), the remains 31 distributed in 6 families and caused familial cluster infection. Most of the SARS-CoV-2 positive cases (31/35, 88.57%) were familial cluster infection. The SARS-CoV-2 transmission routes in the families were investigated and shown in Additional file 1.

Based on confirmed transmission routes, the infection risk odds ratio (OR) between family close contacts and all close contacts was analyzed and shown in Table 3, the infection risk OR between family and non-family close contacts was analyzed and shown in Table 4.

| Group | Positive number | Negative number | OR (95% CI) |
|----------------------------------|-----------------|-----------------|---|
| Family aggregated close contacts | 24 | 16 | 29.40 (13.99 - 62.21); $\chi^2 = 140.228$, $P < 0.001$ |
| Overall close contacts | 25 | 490 | 1 |

Table 3 Odds ratio of SARS-CoV-2 infection risk between family aggregated close contacts and overall close contacts.

Note: OR means odds ratio, CI means confidence interval. The first positive case in each family was not counted.

| Group | Positive number | Negative number | OR (95% CI) |
|--------------------------------------|-----------------|-----------------|---|
| Family aggregated close contacts | 24 | 16 | 703.50 (89.53 - 5527.95); $\chi^2 = 282.66$, $P < 0.001$ |
| Non-family aggregates close contacts | 1 | 469 | 1 |

Table 4 Odds ratio of SARS-CoV-2 infection risk between family aggregated close contacts and non-family aggregated close contacts.

Note: OR means odds ratio, CI means confidence interval. The first positive case in each family was not counted.

Fever (9/35) and cough (9/35) were the most common early clinical symptoms, but asymptomatic infections (22/35) were the main SARS-CoV-2 positive cases. Early clinical features of all the 35 SARS-CoV-2 positive patients were analyzed and shown in Table 5.

| Clinical symptoms | Number of symptomatic patients | Ratio (35 positive cases in total) |
|------------------------|--------------------------------|------------------------------------|
| fever | 9 | 25.71% (9/35) |
| cough | 9 | 25.71% (9/35) |
| Muscle soreness | 4 | 11.43% (4/35) |
| diarrhea | 1 | 2.86% (1/35) |
| abdominal pain | 1 | 2.86% (1/35) |
| Vomit | 1 | 2.86% (1/35) |
| fatigue | 1 | 2.86% (1/35) |
| Asymptomatic infection | 22 | 62.86% (22/35) |

Table 5 Clinical symptoms of 35 positive patients.

Note: Some patients have multiple clinical symptoms.

In family 05 to family 10, counting from the first positive case in every family, there were 12 times of SARS-CoV-2 transmission, from 12 infection sources to 25 patients in total. One SARS-CoV-2 positive patients infected 2.08 (25/12) people on average.

Discussion

SARS-CoV-2 broke out in Wuhan near December 2019, Guizhou Province launched the first level response to major public health emergencies at 24th January 2020, Zunyi implemented social control immediately to inhibit SARS-CoV-2 transmission [9]. But under social control, family aggregated infection appeared obviously. Extensive screening and separated isolation were made up, and proven to be effective. The last SARS-CoV-2 positive patients were found by screening at 15 February 2020, and until 3 March 2020, there wasn't new SARS-CoV-2 case found in Zunyi. There was no medical staff with 3-level biosafety protection being infected.

SARS-CoV-2 family aggregated infections were reported dispersedly mainly by only one family, data for comprehensive family aggregated infection analysis was limited [15,16]. In this study, we analyzed family aggregated infection in 10 families. Without self-isolation, chance of family close contacts being infected was 50.98% (24/46); the infection risk in family members close contacts was much higher than that of non-family members and all close contacts (shown in Table 3 and Table 4).

People from epidemic focus should be key monitoring and isolation objects. Patient 05 and patient 08 came back from Wuhan, but had not performed self-isolation, caused serious family aggregated infection. Especially patient 05 came back from Wuhan at 21th January 2020, infected 8 family members; nevertheless, patient 05 did not have clinical symptoms (observation deadline 3 March 2020), it is difficult to find him out by clinical symptoms. On the other hand, patients 01, 02 and 03 were also from epidemic focus, but performed self-isolation, and did not infected anybody else. So self-isolation was effective complementary mean for social control.

According to published researches and guidelines for SARS-CoV-2 diagnosis and treatment, fever was the main early clinical screening symptoms for SARS-CoV-2 [10, 12]. We screened 3249 patients with fever, found 9 (9/3249) SARS-CoV-2 positive cases only. In all SARS-CoV-2 positive patients of this study, positive cases with fever was only 25.71% (9/35), positive cases with fever and other early clinical symptoms were 37.15% (13/35). However, asymptomatic infections (62.86%, 22/35) were the main part of SARS-CoV-2 positive patients. Asymptomatic SARS-CoV-2 positive patient (patient 05) was proved to be infectious. Although it is convenient to distinguish SARS-CoV-2 high risk groups by temperature, a large part of asymptomatic SARS-CoV-2 carriers will be missed. So extensive screening was needed to find out asymptomatic infections.

In previous studies, basic reproduction number (R_0) of SARS-CoV-2 was calculated to be near 2.2 by models, meaning that every SARS-CoV-2 positive patient can spread infection to 2.2 other people on average [12]. In this study, we found that one SARS-CoV-2 positive patient infected 2.08 (25/12) people on average under social control without separated isolation, meant effective number of SARS-CoV-2 infection was 2.08 under only social control, it was still high. Separated isolation and extensive screening were still needed.

The results of the study had positive effect on the prevention of SARS-CoV-2. This study was performed under the measures of the first level response to major public health emergencies; the characteristics of SARS-CoV-2 can not represent all status under different interventions.

Conclusions

Social control is effective in SARS-CoV-2 inhibition, but self-isolation and screening should be added as supplementary means to avoid familial aggregation infection and find out asymptomatic patients. Under strict social control, family aggregated infection was the main infection type, one SARS-CoV-2 positive patient infected 2.08 people on average.

Abbreviations

SARS-CoV: Severe acute respiratory syndrome coronavirus

OR: odds ratio

MERS-CoV: middle east respiratory syndrome coronavirus

WHO: World Health Organization

CDC: Center for Disease Control and Prevention

PCR: polymerase chain reaction

Declarations

Ethics approval and consent to participate

The present study was approved by the Affiliated Hospital of Zunyi Medical University Ethics Committee; the approval number was KLL-2020-008. Informed consent was obtained from person or guardian.

Consent for publication

Not applicable.

Availability of data and materials

All data generated or analysed during this study are included in this published article and its supplementary information file.

Competing interests

The authors declare that they have no competing interests

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Authors' contributions

ZC and QL conceived and designed the study. ZC, QL, ZC, JX, JH, JZ, QZ, JZ, ZM, DX and XM performed the experiments. ZC and QL analyzed the data. ZC and QL wrote the paper. All authors read and approved the final manuscript.

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