



# Clusters of 2019 coronavirus disease (COVID-19) cases in Chinese tour groups

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## Abstract

International travel may facilitate the spread of the novel coronavirus disease (COVID-19). The study describes clusters of COVID-19 cases within Chinese tour groups travelling in Europe January 16–28. We compared characteristics of cases and non-cases to determine transmission dynamics. The index case travelled from Wuhan, China, to Europe on 16 January 2020, and to Shanghai, China, on 27 January 2020, within a tour group (group A). Four groups with the same outbound flight (group B) or the same tourism venue (group D) and all Chinese passengers on the inbound flight (group C) were investigated. The outbreak involved 11 confirmed cases, 10 suspected cases and six tourists who remained healthy. Group A, involving seven confirmed cases and six suspected cases, consisted of familial transmission followed by propagative transmission. There was less pathogenicity with propagative transmission than with familial transmission. Disease was transmitted in shared outbound flights, shopping venues within Europe and inbound flight back to China. The novel coronavirus caused clustered cases of COVID-19 in tour groups. When tourism and travel opens up, governments will need to improve screening at airports and consider increased surveillance of tour groups—particularly those with older tour members.

## KEYWORDS

China, coronavirus, disease outbreaks, severe acute respiratory syndrome coronavirus 2, travel, virulence

Dechuan Kong, Yuanping Wang, Lu Lu, and Huanyu Wu should be considered joint first author.

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## 1 | INTRODUCTION

A novel coronavirus (SARS-CoV-2) was discovered in mainland China in December 2019 (Harapan et al., 2020; Wu et al., 2020). The World Health Organization (WHO) declared coronavirus disease (COVID-19) a pandemic on 11 March 2020 (World Health Organization, 2020d, 2020e). In many countries outside of China, the first cases were identified as tourists and students from the city of Wuhan travelling abroad. Similarly, the spread of SARS-CoV-2 throughout southwestern and central Asia has been facilitated by Iranian citizens and residents who were travelling outside of Iran (Tuite et al., 2020).

The Chinese Center for Disease Control and Prevention has shown that there is person-to-person transmission among close contacts since the middle of December 2019 (Li et al., 2020). In recent studies, clusters of COVID-19 cases have been principally identified in family settings (Bai et al., 2020; Chan et al., 2020). These patterns suggest that familial transmission—through living and eating together—is a key contributor to the spread of COVID-19. How disease is spread outside of close contacts is less clear.

Other infectious diseases with airborne transmission have reported clusters of cases outside of family settings. In 2009, a cluster of influenza A/H1N1 cases occurred in a tour group in tour bus in Sichuan province, China (Han et al., 2009). In the current COVID-19 pandemic, two cases were reported at a conference in Germany (Rothe et al., 2020). Another notable example has been the *Diamond Princess* cruise ship, which initially carried approximately 3,700 passengers and crew from more than 50 countries and regions. There have been more than 700 confirmed cases of COVID-19 in the ship. The spread of disease thought to be attributable to inappropriate containment measures in the ship (World Health Organization, 2020a).

The outbreak of COVID-19 in China coincided with Chinese New Year, or the Spring Festival, the most important holiday in China. During this time, Chinese people often travel domestically and abroad. Before Wuhan was closed off, it is believed that a couple of million local people left the city for travel, which could have facilitated the spread of COVID-19 to foreign countries. It is not as clear how well the infection is transmitted in tour groups outside of the familial

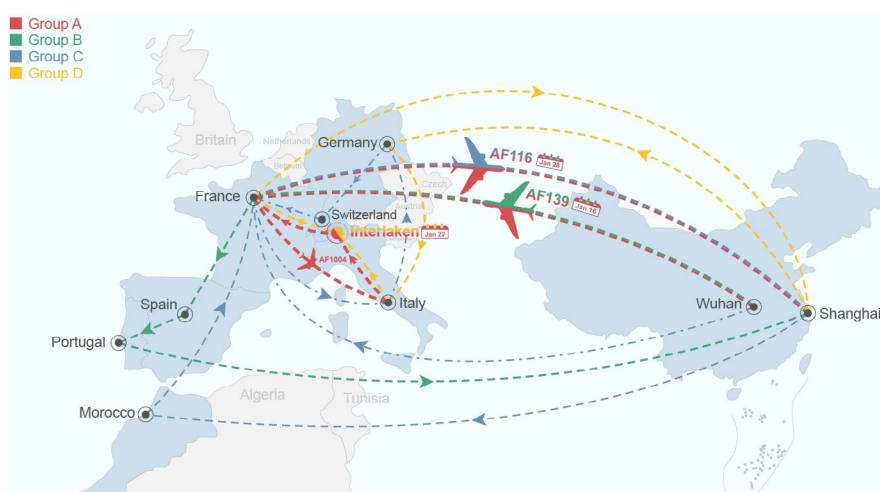
setting. Our study describes clusters of COVID-19 cases within four groups travelling in European countries from January 16 through 28.

## 2 | MATERIALS AND METHODS

This study conducted a retrospective look at four cohorts of individuals. The index case was a 69-year-old Chinese man who had travelled from the city of Wuhan, China, to Paris, France, on 16 January 2020 and back to Shanghai, China, on 27 January 2020, within a tour group of totally 34 members (group A). During the travel, a total of seven confirmed cases and six suspected cases were documented within the tour group. Group A were on three flights, AF139 (Wuhan–Paris), AF1004 (Paris–Rome) and AF116 (Paris–Shanghai). We examined two other groups based on these flights and travel plans. Group B consisted of 25 Chinese tourists from Wuhan to Paris, sharing the flight AF139 with the group A. Group C was composed of approximately 200 Chinese passengers from Paris to Shanghai, sharing the flight AF116 with the group A. We also examined group D, tour group sharing the same tourism venue of Interlaken, Switzerland as the group A on January 22, 2020 (Figure 1).

We retrospectively tabulated the number of confirmed cases, suspected cases and other non-cases in the four groups to determine potential transmission dynamics. This epidemiological investigation was conducted by experienced investigators in Pudong New Area Center for Disease Control and Prevention (CDC), Huangpu District CDC, Hongkou District CDC and Shanghai Municipal CDC. First, we extracted detailed travel information from the investigation reports, including arrival and departure dates of cities, hotels and seats in flight, which were provided and checked by both tour group members and travel agencies. Second, we compared travel itineraries to determine if there was connection between groups. Third, we collected routine clinical examinations and virological testing results from hospitals for suspected cases and the Shanghai Public Health Clinical Center for confirmed cases.

The case definition of COVID-19 came from national guidelines (General Office of National Health Commission, 2020). Cases could



**FIGURE 1** Map of travel for four groups of Chinese tourists in January–February 2020

have epidemiological evidence, that is travelling or living in Hubei province or communities with a confirmed case of COVID-19, or having contact with a confirmed case of COVID-19 or having contact with patients with fever and/or respiratory symptoms from Hubei province or communities with confirmed case of COVID-19 within 14 days. Cases' clinical evidence could include fever and/or respiratory symptoms, pneumonia-related radiological finding, normal or reduced white blood cell count or reduced lymphocyte count. A suspected case was defined by at least one of epidemiological criterion combined with at least two clinical criteria or clinical evidence combined with zero epidemiological evidence. A confirmed case was defined by a positive RT-PCR test.

Based on their exposure history, we categorized cases as having familial or propagative (i.e. within tour group) transmission. We calculated the proportion of pathogenicity by group by counting the number of individuals with a sign or symptom of disease.

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

### 3 | RESULTS

#### 3.1 | Transmission dynamics in group A

##### 3.1.1 | Exposure

The index case and his wife and parents-in-law lived in two separate apartments in a city 310 km away from Wuhan, in Hubei province. On January 10, they went to Wuhan for a Schengen visa application and then had a dinner taking wild eel (*Monopterus albus*) at the aquatic food corner of Huanan Seafood Wholesale Market where initial cases were reported in the beginning of the COVID-19 epidemic (Li et al., 2020). It is likely that some of the family members were exposed to SARS-CoV-2.

##### 3.1.2 | Familial transmission

On January 16, the family joined the tour group A and boarded the flight AF139. The index case's father-in-law (zero case), the index case, the index case's wife (case 2) and mother-in-law (case 1) successively had symptoms on January 22, 26, 27 and 28. The zero case developed severe symptoms and was hospitalized in Paris on January 25, and was taken care of by his daughter (case 2). These two were labelled as the 4th and 5th cases in France. The index case and case 1 went back to China on January 27 and were immediately diagnosed as COVID-19 confirmed cases. The timeline was listed in Figure 2.

##### 3.1.3 | Tour group transmission

Group A was placed under quarantine once they arrived back in Shanghai, China. Among the rest ( $n = 30$ ) of the group, a total of nine members successively developed symptoms from January 28 through

February 9 in quarantine, including three confirmed cases and six suspected cases. The cases and their family members/ accompanying friends are described in Figure 2. Clinical examinations and virological testing results are presented in Table 1. Pathogenicity in the group transmission (9/30) was lower compared with the familial transmission (3/3). Similarly, pathogenicity seemed to be weakened as all of the family were confirmed cases (3/3), whereas the following cases in the group transmission included both confirmed (3/9) and suspected (6/9) cases.

Tour group transmission may have occurred in the following scenarios. (1) On the outbound flight Wuhan—Paris and connecting flight Paris—Rome, the nine cases had inconsistent seat proximity to the family (Figure 3) and no contact with one another, except for the guide (case 3). (2) During the tour, the members moved by bus. Generally, they gathered in smaller groups including family members and accompanying friends. They reported inconsistent and limited contact with one another and did not precisely recall the seat proximity in bus. The guide had regular contact with adult members and helped arrange the hospital admission of the zero case in Paris. (3) On the inbound flight Paris—Shanghai, all of the confirmed and suspected cases had seats within two rows (Figure 3). Furthermore, suspected cases had nearer seat proximity to the family cases, compared with the other three confirmed cases (case 3, 4, 5) which may be attributable to the suspected cases being less contagious. Considering time sequence of onset and exposure/ contact history, we inferred that there was initially a familial transmission, followed by a propagative transmission within the group, which possibly occurred during the tour and on the inbound flight.

In addition, we identified that five members had close contact with the cases, who remained healthy during the 12-day tour in Europe and in 14-day quarantine in Shanghai (Figure 2). Similarly, some members who had seats close to the confirmed cases remained healthy (Figure 3).

#### 3.2 | Group A connection to Group B, C and D

##### 3.2.1 | Outbound flight Wuhan – Paris

On AF139, there was a cluster consisting of two COVID-19 confirmed cases and one suspected case, which all belonged to tour group B (Table 1). They shared the same outbound flight from Wuhan with group A and then had different itineraries in Europe (Figure 2). On board, the cases in group B had a seat proximity of >3 rows to the family in group A. At this point, the zero case did not have any symptoms. The onset of disease in the first case (case 12) in group B occurred on January 29, which was 7 days later than the zero case in group A. Thus, we could not completely exclude the connection to group A.

##### 3.2.2 | Inbound flight Paris—Shanghai

On AF116, there were approximately 200 Chinese passengers (group C; they shared the same flight but not belonged to a same tour group), in which two were diagnosed as suspected case in

Timeline

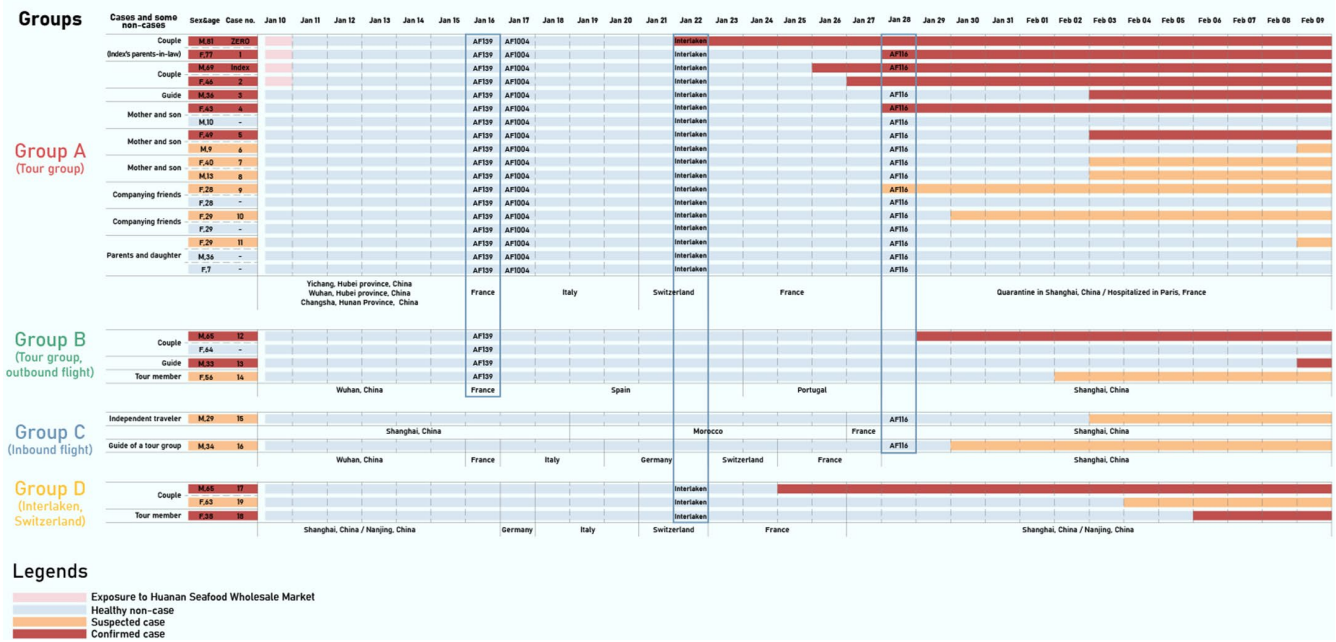


FIGURE 2 Timeline of novel coronavirus disease (COVID-19) diagnosis in four groups of Chinese tourists in January–February 2020

quarantine after arrival in Shanghai (Figure 2; Table 1). Case 15 was an independent traveller, and case 16 was a guide of a tour group of 19 members (the rest of the tour group have not developed symptoms). Their seats were <3 rows away from the cases in group A. Neither of them reported travel or living history in Hubei province/communities with confirmed case of COVID-19; contact with confirmed case of COVID-19; or contact with patients with fever and/or respiratory symptoms from Hubei province/communities with confirmed case of COVID-19, within 14 days before the onset. They might have a connection to group A.

3.2.3 | During the tour

We identified another group of 41 tourists (group D), which had been visiting Interlaken, Switzerland, in the afternoon of January 22, sharing the same shopping venue with the group A. The group D was not placed under quarantine after they arrived in Shanghai. Later, two confirmed cases and one suspected case were successively diagnosed, which composed a cluster (Figure 2; Table 1). The dates of onset of symptoms were January 30 for confirmed case 17 and February 4 for suspected case 19; date of onset of symptoms was unavailable for confirmed case 18. Unfortunately, we could not identify all the Chinese tour groups that visited Interlaken on January 22 or check the Chinese COVID-19 cases who had visited Interlaken on January 22. So far, we have recognized only the cases in group A and D, which suggests they might have an epidemiological linkage, though we had contacted and investigated another two Chinese tour groups which had no confirmed or suspected cases (not listed in the study).

4 | DISCUSSION

A large concern is if SARS-CoV-2 is able to efficiently spread in settings beyond the family or other sustained close contact. We reported three clusters of COVID-19 confirmed cases in three tour groups travelling in European countries and one cluster of suspected cases on one flight in late January 2020. The outbreak in total involved 11 confirmed cases, 10 suspected cases and more than two hundred persons placed in quarantine. In group A, the cluster was initiated by a familial transmission, followed by spread of disease to 13 out of 34 members in the 12-day tour. Group A was characterized by lower pathogenicity in the following group transmission, compared with the familial transmission which might be attributable to exposure to the Huanan Seafood Wholesale Market.

In our study, the first case in group D might have been infected through a casual meeting with the zero case in group A at a shopping venue. A similar finding had been reported in a previous study that reports that Chinese tourists wearing facial masks may have infected a Thai taxi driver (Pongpirul, Pongpirul, Ratnarathon, & Prasithsirikul, 2020). Thus, there may be two conditions facilitating efficient transmission, (1) confined space and (2) consistent close contact. However, we found five tour group members who remained healthy even after sustained contact with the cases, such as sharing same hotel rooms, taking dinner together and having neighbouring seats. One explanation is that children are less susceptible to the virus (del Rio & Malani, 2020). Further studies on how the virus transmits across different age groups are urgently warranted. This is especially important considering the possible role of pre-symptomatic transmission (Kong et al., 2020).

**TABLE 1** Clinical examinations and virological testing results

Case by sex and age	Case no.	Case type	Clinical examination				Virological testing				
			Body temperature (°C)	White blood cell (10 <sup>9</sup> /L)	Lymphocyte %	Chest CT	Nasal swab		Throat swab		
							ORF1 a/b	N	ORF1 a/b	N	
Group A											
M, 81	Zero <sup>a</sup>	Confirmed	NA	NA	NA	NA	NA	NA	NA	NA	NA
F, 77	1	Confirmed	36.5	5.8	41.5	Bilateral pneumonia	+	+	+	+	+
M, 69	Index	Confirmed	36.5	5.3	31.0	Bilateral pneumonia	-	-	+	+	+
F, 46	2 <sup>a</sup>	Confirmed	NA	NA	NA	NA	NA	NA	NA	NA	NA
M, 36	3	Confirmed	36.7	4.7	38.4	Bilateral pneumonia	+	+	+	+	+
F, 43	4	Confirmed	37.5	4.1	43.9	Unilateral pneumonia, left	+	+	+	+	+
F, 49	5	Confirmed	36.7	7.1	30.6	No obvious abnormality	-	-	+	+	+
M, 9	6	Suspected	36.5	10.8	31.9	NA	-	-	-	-	-
F, 40	7	Suspected	36.0	8.7	36.3	No obvious abnormality	-	-	-	-	-
M, 13	8	Suspected	36.0	5.2	42.0	Bilateral pneumonia	-	-	-	-	-
F, 28	9	Suspected	37.5	3.1	43.3	Unilateral pneumonia, left	-	-	-	-	-
F, 29	10	Suspected	36.8	5.5	37.1	No obvious abnormality	-	-	-	-	-
F, 29	11	Suspected	36.5	4.1	36.3	Unilateral pneumonia, left	-	-	-	-	-
Group B											
M, 65	12	Confirmed	37.9	6.5	32.1	Bilateral pneumonia	+	+	+	+	+
M, 33	13	Confirmed	36.1	5.1	46.6	Bilateral pneumonia	-	-	+	+	+
F, 56	14	Suspected	37.1	5.4	19.4	Unilateral pneumonia, right	-	-	-	-	-
group C											
M, 29	15	Suspected	36.5	5.3	34.0	No obvious abnormality	-	-	-	-	-
M, 34	16	Suspected	37.0	5.6	24.6	Bilateral pneumonia	-	-	-	-	-
Group D											
M, 65	17	Confirmed	37.5	5.0	20.6	Bilateral pneumonia	+	+	+	+	+
F, 38	18 <sup>b</sup>	Confirmed	NA	NA	NA	NA	+	+	+	+	+
F, 63	19	Suspected	38.0	7.6	30.0	Unilateral pneumonia, right	-	-	-	-	-

<sup>a</sup>The zero case and case 2 were hospitalized in Paris; thus, we did not obtain detailed clinical examination and virological testing results.

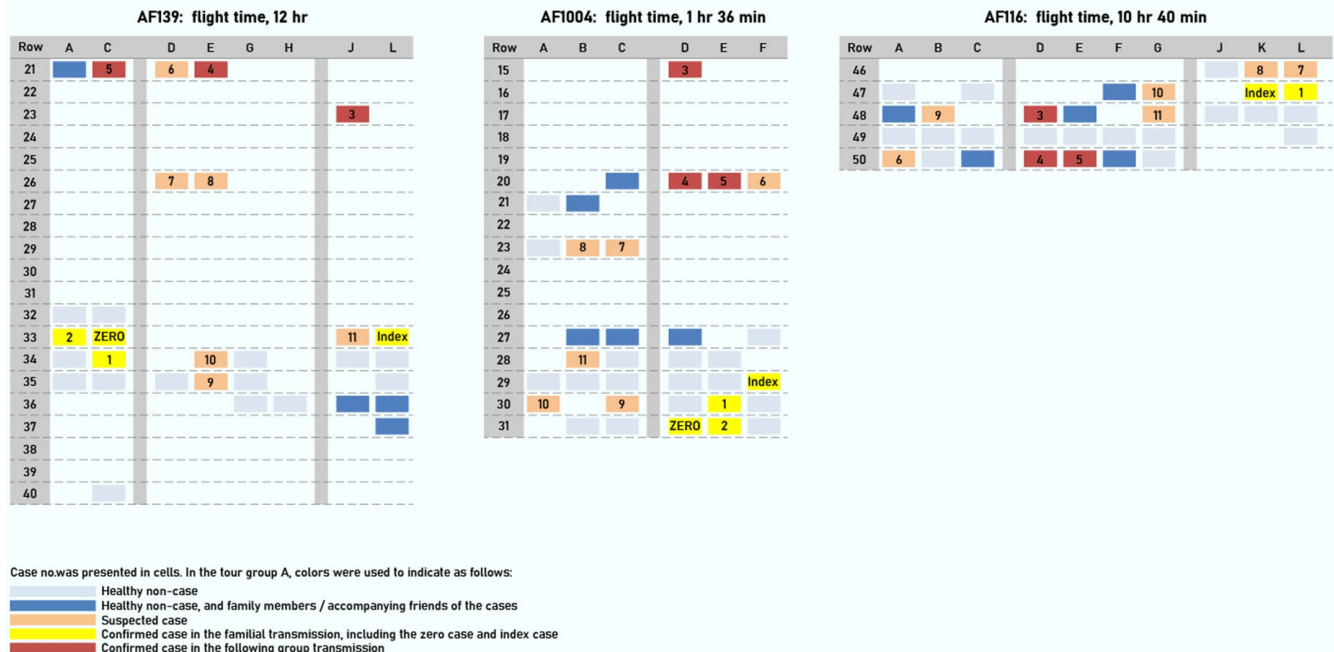
<sup>b</sup>Case 18 was kept in quarantine for 10 days after her arrival in China and then diagnosed another 9 days later, due to a stay-home notice sent by Shanghai Municipal Center for Disease Control and Prevention; thus, we did not obtain detailed clinical examination and virological testing results.

Furthermore, we supposed that group C had a connection to group A and could not exclude a connection between groups B and A. These connections suggest potential transmission on the plane. Recent studies have documented conflicting findings, including possible transmission on planes (Liu, Liao, Chang, Chou, & Lin, 2020) or in cars (Pongpirul et al., 2020), but also no observed transmission in vehicles (Phan et al., 2020). Previous studies have shown that planes have high-efficiency particulate air filters that may avoid airborne

transmission of pathogens, whereas buses have about 70% recirculated inside air (Han et al., 2009). We did not precisely examine the seats in tour bus. The confirmed and suspected cases had an obvious cluster of seats on the inbound flight, suggesting the infection was very likely to occur on plane, which may be associated with high affinity of SARS-CoV-2 spike glycoprotein binding ACE2 (Wrapp et al., 2020). However, we also identified healthy members after taking seats close to the family cases on board. Thus, we hypothesized that



## Seats



**FIGURE 3** Seat map of three flights containing cases of novel coronavirus disease (COVID-19)

disabling the efficient transmission of SARS-CoV-2 may depend on social distance and personal protection, in addition to air conditioning system and air filters.

The tour groups included in our study had visited France, Italy, Switzerland, Spain, Portugal, Germany and Morocco, which has raised a public health concern of spreading the virus internationally. Currently, China is the number 3 sender of tourists globally and is estimated to be 1 by 2030 (Arcibal, 2018). However, the entry–exit quarantine in airports has limited capability in detecting cases whose course of infection is in the incubation period. This problem of detection has been documented in the influenza A/H1N1 (Priest, Duncan, Jennings, & Baker, 2011) and current COVID-19 pandemic (Gostic, Gomez, Mumma, Kucharski, & Lloyd-Smith, 2020). The spread of SARS-CoV-2 into South Korea, Italy and Iran has increased attention towards those tourists (Gostic et al., 2020; Pongpirul et al., 2020; Tuite et al., 2020). However, it is possible that the typical activities undertaken by tourists make them less likely to infect compared with other members of the tour group. The zero case in group A was diagnosed in France. However, we did not identify any local cases epidemiologically linked to the tour group members in the above-mentioned countries. This lack of transmission may be attributed to the absence of sustained contact in a confined space between local people and Chinese tourists. There of course could be existing cases with mild or no obvious symptoms. Since February 22, COVID-19 cases have increased dramatically in Italy, Iran and South Korea, which have been retrospectively traced to some locals who reported no known exposure history (World Health Organization, 2020b, 2020c). They might have been exposed to asymptomatic carriers of SARS-CoV-2. Thus,

improvement in the continuous surveillance on international tourists remains crucial.

The study has several limitations. The sensitivity of the PCR assays could be low and result in a large number of false-negative results in the diagnosis of COVID-19 (Sheridan, 2020; Wang et al., 2020). All of the suspected cases reported in this study were finally excluded from the diagnosis of COVID-19 due to a negative RT-PCR test, though some of them had pulmonary inflammation according to chest CT examination. Because our diagnostic methods may have underestimated the incidence of disease in the study population, we combined suspected cases with confirmed cases to explore potential transmission dynamics. Another limitation was recall bias and concealment in the investigation. We checked the activities with each case, cross-checked activities between cases, illustrated the transmission chains and then determined the potential connections between cases and groups. We also may have missed asymptomatic carriers on the passenger flights.

In conclusion, we reported a cluster of 13 COVID-19 cases, which was initiated by within-family transmission followed by propagative transmission into tour groups travelling in European countries. The study findings show that clustered cases in tour groups may be more propagative than simple familial transmission. Currently, the COVID-19 pandemic is spreading to increased numbers of countries and regions worldwide. If we consider each country as a group, such as China, South Korea, Iran and Italy, we could understand the pandemic of the COVID-19 as a propagative transmission within a 'group' and then between 'groups'. Thus, the government should improve screening at airports and consider increased surveillance of tour groups—particularly those with older tour members.

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## CONFLICT OF INTEREST

All authors declare no competing interests.

## ETHICAL APPROVAL

This study involved the use of existing, routinely collected data from a public health outbreak investigation, under the National Health Commission of the People's Republic of China. All data included in the study were kept confidential without person identifiers. No additional interviews were conducted, and no data were collected independently for this study. Thus, this study is exempt from ethical review and there was no need of obtaining informed consent.

## DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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