## COVID-19 ISSUE (16)

### Outbreak Reports

Long Distance Transmission of SARS-CoV-2 from Contaminated Cold Chain Products to Humans — Qingdao City, Shandong Province, China, September 2020

<table>
<thead>
<tr>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Long Distance Transmission of SARS-CoV-2 from Contaminated Cold Chain Products to Humans — Qingdao City, Shandong Province, China, September 2020</td>
<td>637</td>
</tr>
</tbody>
</table>

### Preplanned Studies

Belief in Science and Attitudes Toward COVID-19: A Demographic Standardization Approach to China–US Comparison, 2020

<table>
<thead>
<tr>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
</table>

### Notes from the Field

An Imported Confirmed Case of COVID-19 Vaccinated in Brazil — Shanghai Municipality, China, March 17, 2021

<table>
<thead>
<tr>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>An Imported Confirmed Case of COVID-19 Vaccinated in Brazil — Shanghai Municipality, China, March 17, 2021</td>
<td>650</td>
</tr>
</tbody>
</table>


<table>
<thead>
<tr>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
</table>
Summary

What is already known about this topic? Though coronavirus disease 2019 (COVID-19) has largely been controlled in China, several outbreaks of COVID-19 have occurred from importation of cases or of suspected virus-contaminated products. Though several outbreaks have been traced to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) isolated on the outer packaging of cold chain products, live virus has not been obtained.

What is added by this report? In September 2020, two dock workers were detected as having asymptomatic SARS-CoV-2 infection using throat swabs during routine screening in Qingdao, China. Epidemiological information showed that the two dock workers were infected after contact with contaminated outer packaging, which was confirmed by genomic sequencing. Compared to the Wuhan reference strain, the sequences from the dock workers and the package materials differed by 12–14 nucleotides. Furthermore, infectious virus from the cold chain products was isolated by cell culture, and typical SARS-CoV-2 particles were observed under electron microscopy.

What are the implications for public health practice? The international community should pay close attention to SARS-CoV-2 transmission mode through cold chain, build international cooperative efforts in response, share relevant data, and call on all countries to take effective prevention and control measures to prevent virus contamination in cold-chain food production, marine fishing and processing, transportation, and other operations.

In December 2019, after the coronavirus disease 2019 (COVID-19) outbreak in China, the Chinese government implemented a series of strong measures including the introduction of COVID-19 into the mandatory reporting of infectious diseases, the lockdown of Wuhan, and the quarantine of all inbound passengers followed by isolation at designated sites for 14 days; under no circumstances were any foreign crewmembers of cargo ships allowed ashore. By the middle of April, China had successfully interrupted the virus’ transmission in the community. COVID-19 has since been largely controlled in China. However, several outbreaks or clusters of COVID-19 cases have occurred and have been linked to importation of cases or from suspected virus-contaminated imported products. Several outbreaks were suspected to have occurred due to the handling of cold chain seafood by the first infected case, especially with outbreaks in Beijing’s Xinfadi and Dalian City (1–3). After epidemiological investigation, the full-length viral genome in those outbreaks could be traced back to SARS-CoV-2 contamination of the outer packaging of cold chain products. However, the most important evidence, the isolation of the live virus, was not obtained.

Presently, there is still no consensus on whether the outer packaging of the cold chain products can carry live viruses and cause virus transmission. The World Health Organization (WHO) and Food and Agriculture Organization (FAO) of the United Nations believed that the outer packaging of cold chain products could not carry live viruses and cause virus transmission (4–5). However, China’s key ports of entry by air, land, and sea have faced outbreaks and challenges related to the COVID-19 epidemic. Qingdao, a major port in eastern Shandong Province...
and China’s second largest foreign trade port, started active monitoring using nucleic acid testing on 14-day intervals in August 2020 for the populations at high risk and those that process, sell, and handle frozen aquatic products. On September 22 and 24, 2 cold chain dock workers from the same company screened positive for SARS-CoV-2; these cases became the first reported in 151 consecutive days in Qingdao City. To identify the source of infection and evaluate the risk of virus transmission from the contaminated outer packaging of cold chain products, an in-depth field epidemiological investigation was conducted. Full-length viral genome sequencing, real-time reverse transcription polymerase-chain reaction (rtRT-PCR), and virus isolation were carried out.

**INVESTIGATION AND RESULTS**

**Epidemiologic and Laboratory Information from the Dock Workers**

Since August 11, 2020, high-risk individuals in Qingdao city, including people working in frozen seafood processing, sales, and shipment chains, were routinely tested every 14 days for SARS-CoV-2 nucleic acids. By September 8, the 573,107 residents had tested negative 3 times for SARS-CoV-2 nucleic acid by rtRT-PCR. Throat swab samples that were collected from the identified 2 dock workers between September 22 and 24, 2020 tested positive with cycle threshold (Ct) values targeting the ORF1ab gene of 37 and 23 and the N-gene of 37 and 25, respectively; IgM/IgG OD value of Dock Worker 1 were <1/<1, 2.17/<1, and 8.26/3.54, and Dock Worker 2 were <1/<1, 2.55/<1, and 3.22/6.77 on September 25, October 2, and October 13, respectively. This revealed that the suspected exposure period was between September 8 and 23, 2020. Throat swabs from 232 close contacts of the two dock workers, including 69 dock workers who participated in the unloading of Transport Ship K (Ship K), as well as 2,019 residents who were placed under home quarantine tested negative for SARS-CoV-2 nucleic acid. The results of the serum antibody tests were all negative for all 71 dock workers who carried the cold chain products of Ship K were interviewed by telephone survey to investigate the crewmembers’ contact history and behavioral factors during loading of the frozen cod on Ship K. Although all 71 dock workers had habits of smoking, only 3 dock workers smoked during the loading and unloading of the frozen cod on Ship K. Among them, 2 dock workers who did not smoke during loading and unloading were infected. The difference between the two groups was statistically significant (P=0.001).

**Epidemiologic and Laboratory Results for Transport Ship K**

About 90 crewmembers boarded Fishing Trawler V (Trawler V) from July 2020. We reviewed the SARS-CoV-2 nucleic acid test results of the crewmembers of Trawler V. The 90 crewmembers were not tested for SARS-CoV-2 nucleic acids. The packaged frozen cod were transferred from Trawler V to Ship K on September 3, 2020. The crewmembers of Trawler V fetched the cod from their cold storage, transferred the cod to Ship K via cranes, and then froze (−18 °C) the cod on Ship K.
The 23 crewmembers of Ship K repeatedly tested negative for SARS-CoV-2 nucleic acids including before arrival in Qingdao (tested on August 18 and September 9, 2020), upon arrival in Qingdao (tested on September 16, 2020), and upon arrival in Busan, the Republic of Korea (tested on September 21, 2020). Furthermore, there was no contact history between the crew of Ship K and the frozen cod (Figure 1).

The 71 dock workers were interviewed individually. It was determined that the distance between the dock workers and the crew of Ship K was more than 10 meters. The dock workers did not have direct contact with the crew of Ship K during the cod handling process, and they all wore protective clothing, medical masks, and disposable gloves. Since the crews of Ship K did not have any evidence of SARS-CoV-2 infection, the origin of SARS-CoV-2 contamination of the packaging of frozen foods was highly likely from the crewmembers of Trawler V.

**Environmental Investigation and Sampling**

To assess contamination and increased viral load in the environment, a two-stage sampling method was used to sample the outer packaging of the cod from Ship K. All nucleic acid tests were completed within 24 hours after environmental sample collection. The rRT-PCR Ct value of ORF1ab and N gene target ≤40 was positive.

First-stage sampling was conducted on September 24, 2020 to determine which outer packaging was positive. In the cold storage of the frozen cod, 70 pallets (about 63 cartons of cod per pallet) were selected for sampling. The four surfaces of each pallet were sampled separately. Each smear sample that was pre-wetted with the viral transport medium (VTM) was smeared at five positions on each surface in one direction. A total of 420 smear samples were collected, and each swab was stored separately in a virus sampling tube containing 3 mL of VTM; the tail of the swab was then discarded, and the tube cap was screwed tightly for transportation in an ice box. Among the 420 smear samples, 51 were positive for SARS-CoV-2 nucleic acids.

To collect samples with high viral loads for virus gene sequencing and virus isolation, second-stage sampling was carried out on September 26, 2020 on the first SARS-CoV-2 nucleic acid positive 8 pallets. The 8 pallets were placed on the platform outside the cold storage by a forklift truck. Smear samples from all five outer surfaces of each carton of cod (for each of the five pre-wetted swabs) were placed in a virus sampling tube containing 3 mL of VTM (without virus inactivation), and the tube caps were screwed tightly.

FIGURE 1. Timeline of SARS-CoV-2 transmission from contaminated cold chain products to humans — Qingdao City, Shandong Province, China, September 2020.

Note: A timeline of Fishing Trawler V being at sea, Transport Ship K being at sea, the transfer of cod from Trawler V to Ship K, routine SARS-CoV-2 screening of transport Ship K’s crew, unloading at Qingdao port, positive tests being found among 2 dock workers, and testing of the cod packages.
for transportation in an ice box. A total of 499 smear samples were collected, and 51 were positive for SARS-CoV-2 nucleic acids.

**SARS-CoV-2 Detection and Genome Sequencing**

Overall, 2 case samples and 11 frozen cod samples with positive nucleic acid results (Ct value <32) were studied with whole genome sequencing. The viral RNAs were extracted directly from the swab samples with the QIAamp Viral RNA Mini Kit (QIAGEN, Germany), and rRT-PCR assay was used to detect SARS-CoV-2 nucleic acid. For genome sequencing, the libraries were prepared using the Nextera XT Library Prep Kit (Illumina, San Diego, CA, USA), and the resulting DNA libraries were sequenced on MiSeq platforms (Illumina, San Diego, CA, USA) using a 300-cycle reagent kit. Mapped assemblies were done using the SARS-CoV-2 genome (accession number NC_045512) as a reference. Variant calling, genome alignments, and sequence illustrations were generated with CLCBio software (QIAGEN, Germany).

A total of 2 throat swabs samples from the 2 dock workers and 11 environmental samples tested positive for SARS-CoV-2 nucleic acids with Ct values <35. After high-throughput sequencing, a total of 9 SARS-CoV-2 genomes were obtained through high-throughput sequencing from the 2 infected dock workers, 7 outer packaging samples, 1 secondary sample taken from the outer packaging, and the isolated virus strains (the other 10 genomes all came from uncultured samples). Compared with the Wuhan reference strain (NC_045512) sequence, these 11 whole genomes had 12–14 nucleotide mutation sites and shared 12 nucleotide mutation sites. Among them, 7 shared mutation sites (C241T, C3037T, C14408T, A23403G, and GGG28881-28883AAC) were consistent with the characteristics of lineage B.1.1 (Figure 2) (6–7). The other 5 shared mutation sites (C3743T, C3773T, C5170T, A23299G, and G23755T) that were unique to SARS-CoV-2 were identified in Qingdao (Figure 3).

In addition to the 12 shared nucleotide mutation sites, the strain from dock worker 1 had 1 nucleotide mutation (C2523T) and that from dock worker 2 had 2 additional nucleotide substitutions (C1282T and C5144T); 5 outer packaging-related strains shared 1 unique nucleotide mutation (C1282T) with the strain from dock worker 2, and no additional nucleotide substitutions were found in the remaining 2 outer packaging strains (Figure 4). Therefore the viral genome sequence of dock worker 1 shared 12 mutations and added one specific mutation (C2523T) compared to the 2 viral genome sequences from Fish cluster 1, while the viral genome sequence of dock worker 2 shared 13 mutations and added one specific mutation (C5144T) compared to the 5 viral genome sequences from Fish cluster 2. It was preliminarily determined that the 2 dock workers were infected with SARS-CoV-2 by loading and unloading the frozen cod.

---

**FIGURE 2.** A multiple genome alignment of the SARS-CoV-2 genome sequences obtained from the two dock workers and from the environmental swab samples with reference strain (Strain Wuhan-Hu-1).
Isolation of SARS-CoV-2

During the second-stage sampling, 6 samples with high viral loads (Ct values 25, 28, 30, 31, 31, and 32) collected from Fish Cluster Pallet 1 were obtained for further viral isolation. The cell tube inoculated with specimen “Fish-27” with a Ct value of 25, showed obvious cytopathic effects after the second passage (Figure 4). Typical coronavirus-like particles were observed under cryoelectron microscope, which indicated live, infectious SARS-CoV-2 was isolated from specimen “Fish-27”. The sequencing results showed that the viral genomes from the specimen “Fish-27” and the corresponding strain shared 100% nucleic acid identity, and it showed that the viral sequence only had 12 nucleotide mutation sites, not including C1282T, C5144T, or C2523T. The sequencing match also suggested that the positive virus culture was not a result of contamination.

Data Availability

The 11 full-length genomic sequences detected in this study have been deposited to GISAID database under accession numbers EPI ISL 591270 to EPI ISL 591280.

Public Health Response

This study confirmed that imported cold chain products were contaminated with relatively high loads of SARS-CoV-2 through the excrement of Fishing Trawler workers infected with the SARS-CoV-2. After the contaminated cold chain products transported from Fishing Trawler to the transport ship, the SARS-CoV-2 can spread across countries and regions over long distances through the international marine fishery trade. This was similar to close contact transmission in families and medical institutions following SARS-CoV-2 contamination of external environments. This has brought about serious public health challenges to countries and regions that have successfully interrupted local SARS-CoV-2 transmission.

First, when contaminated packages have high viral load, the virus can survive for weeks to months (July to September being the longest recorded) at low temperatures, and the virus may still infect employees after being in cold storage for months or years, resulting in silent transmission of a “relatively old virus”. Second, it is strongly suggested that the management of the cold chain process should be strengthened globally to prevent SARS-CoV-2 contamination during fish and meat production. Regular screening for SARS-CoV-2 nucleic acids in high-risk population is necessary to identify infected
persons at an early stage. This will prevent both cold chain contamination by SARS-CoV-2 and potential silent transmission. Third, this study suggested that SARS-CoV-2 can survive in humid, low temperatures and high-salt environments, which is an important scientific issue. Thus, it is necessary to conduct further research on the influence of environmental factors, such as pH, salinity, temperature, and humidity, on the survival or transmission of the SARS-CoV-2. However, it is important to note that while further study and surveillance is possible, maintaining these efforts may be difficult given the infrequency of these outbreaks relative to the massive amount of trade in Chinese ports.

DISCUSSION

Since the outbreak of COVID-19, SARS-CoV-2 nucleic acids have been detected in the outer packaging of several cold-chain seafood products imported from abroad (8). It has long been suspected that SARS-CoV-2 contamination of the outer packaging of cold-chain seafood products could lead to infection among employees handling the outer packaging. This may be a hidden route of transmission due to the long-distance transportation of the cold-chain seafood products.

SARS-CoV-2 was found to be more stable on plastics and stainless steel than on copper and cardboard materials, and live virus was detected within

FIGURE 4. Schematic diagram of two transmission chains of SARS-CoV-2 from frozen product packaging to humans. (A) Person-to-cargo transmission of SARS-CoV-2 in Trawler V where the crew of Trawler V loaded the combined cargo. (B) Long distance transportation of cold chain seafood package contaminated with SARS-CoV-2 where the crew of Ship K had no contact with the cargo. (C) Cargo-to-person transmission of SARS-CoV-2 with new substitutions in Qingdao Port where the dock workers unloaded the combined cargo and then the 2 dock workers tested positive; the fish cargo was tested after it was unloaded. (D) Viral isolation and electron microscopic examination. Live virus was successfully isolated, full-length genome sequence of the live virus was 100% identical to the sequence from the swab smearing samples of cold-chain seafood packaging (Fish Cluster 1). The upper right picture shows the electron microscope image of the live virus. The orange triangle indicates 7 common mutation sites of lineages B.1.1 of SARS-CoV-2, including C241T, C3037T, C14408T, A23403G, and GGG28881-28883AAC. The red square indicates five unique mutation sites of SARS-CoV-2 identified in Qingdao, including C3743T, C3773T, C5170T, A23299G, and G23755T.
72 hours after application to these surfaces (9). Therefore, frequent exposure to contaminated surfaces in public places is a potential route of SARS-CoV-2 spread. Swabs were collected from the outer package of cold chain products, but the swabs collected from the seafood itself were negative, indicating that the products were likely not infected with SARS-CoV-2.

Furthermore, after the infected dock workers had been sent to Qingdao Chest Hospital for further investigation and treatment, an outbreak alarm was triggered on October 11, 2020 for an additional 12 cases, and initial epidemiological evidence suggested in a previous report that all 12 cases were linked to Qingdao Chest Hospital (10). They did not have contact with other people who were later found to be infected, but their chest computed tomography (CT) scans were done in the same CT suite that was visited by a hospital patient and a nursing assistant who later tested positive. After investigating the 12 cases and their close contacts, the 2 dock workers and their close contacts were not found to have any temporal and spatial links outside Qingdao Chest Hospital. The overseas frozen cod that caused the infection of two dock workers had also been sealed in the customs warehouse without entering the country. This evidence suggested the transmission in a ward of Qingdao Chest Hospital, forming a cluster epidemic. Fortunately, due to the timely discovery of the cases, this incident did not result in large-scale community transmission.

It should be emphasized that, so far, no cases of consumer infection due to exposure to contaminated cold chain seafood have been found, and the risk of consumer infection is, therefore, extremely low. In addition, the contamination of cold chain products by SARS-CoV-2 is an accidental event, and it is difficult to identify contaminated products by screening. Therefore, it is suggested that regular screening and detection should be strengthened (and testing should occur every 14 days). Monitoring of SARS-CoV-2 nucleic acid levels in employees of imported seafood cold chain products (especially workers engaged in port operations and seafood processing enterprises), should also be implemented for early detection of infected persons and early interruption of transmission.

We also noticed that the two dock workers infected with SARS-CoV-2 at the wharf took off their masks and smoked, while none of the other dock workers who had been wearing their masks were infected with SARS-CoV-2. This shows that SARS-CoV-2 can be transmitted from the outer packaging of the cold chain to the dock workers; however, infection can likely be avoided by using proper protection.

The major limitation of this study was that the symptoms and SARS-CoV-2 infection status of the crewmembers of Trawler V were unknown. If these crewmembers aboard Trawler V were indeed infected, then the transmission chain could be readily established.

It is particularly important that the international community should pay close attention to SARS-CoV-2 transmission by cold chain, build international cooperative efforts in response, share relevant data, and call on all countries to take effective prevention and control measures to prevent SARS-CoV-2 contamination in cold chain food production, marine fishing and processing, transportation, and other operations. At the same time, it is necessary to strengthen the health and epidemic prevention knowledge of employees and those in related occupations who are engaged in handling the outer packaging of imported seafood cold chain products. Formulation of standards for equipment and facilities related to the working environment of imported cold chain food and personal protection standards should be improved. It is also suggested that staff at the port should be included as a high-risk population for emergency vaccination.

**Funding:** The SARS-CoV-2 emergency special project of the Chinese Government and National Key Research and Development Project (Project No. 2021YFC0863000); National Natural Science Foundation of China (No. 72042012); the National Key Technology R&D Program of China (Project No. 2017ZX10104001, 2018ZX10713002, 2018ZX10713001-003, and 2018ZX10711001).

doi: 10.46234/ccdcw2021.164

*Corresponding authors: Ruqin Gao, ruqingao123@sina.com; George F. Gao, gaofu@chinacdc.cn; Wenbo Xu, xuwb@ivdc.chinacdc.cn.

Preplanned Studies

Belief in Science and Attitudes Toward COVID-19: A Demographic Standardization Approach to China–US Comparison, 2020

Yue Qian; Yongai Jin; Yu Xie

Summary

What is already known about this topic?
Attitudes of disapproval toward public health measures led to behaviors that could increase vulnerability to contracting coronavirus disease 2019 (COVID-19).

What is added by this report?
Chinese citizens rated the necessity of mitigation measures for combating COVID-19 higher than did Americans (4.81 vs. 4.03 on a 1–5 scale). The China–US difference was attributable to 1) Chinese citizens having more confidence in scientists than Americans and 2) Chinese citizens almost invariably accepting the necessity of COVID-19 mitigation measures, regardless of their confidence in scientists.

What are the implications for public health practice?
Building public support for population health measures and public trust in science is crucial for handling epidemic crises.

Confirmed cases of coronavirus disease 2019 (COVID-19) have surpassed 175 million globally as of June 11, 2021. By then, the United States (US) has reported over 33 million infections, whereas China, the initial epicenter of the pandemic, has had 103,285 confirmed cases (1). Differences in the number of COVID-19 infections between China and the US might arise in part from different attitudes toward public health measures. Prior research suggested that Americans’ support for public health measures varied with their trust in science (2). This study examined the China–US difference in attitudes toward COVID-19 mitigation measures and evaluated the role of belief in science in the China–US difference in the attitudes.

During March–July 2020, comparable surveys were conducted in China and the US. The survey found that Chinese respondents rated higher the necessity of mitigation measures for combating COVID-19 than did Americans. The China–US difference was attributable to the following: 1) Chinese citizens had higher confidence in scientists than Americans; and 2) Chinese citizens rated the necessity of COVID-19 mitigation measures more highly than Americans did, regardless of their confidence in scientists. The research findings suggest that building public support for population health measures and public trust in science is crucial for handling epidemic crises, especially in individualistic societies where citizen consent to public policy is key for policy effectiveness.

Attitudes of disapproval toward public health measures led to behaviors that could increase vulnerability to contracting COVID-19 (3). Non-pharmaceutical interventions such as lockdowns played an important role in containing COVID-19 in China (4). Both city-wide lockdowns (e.g., the lockdown of Wuhan) and residential-compound lockdowns (i.e., residents not being allowed to leave their residential compound without authorization) were implemented in China, with a high degree of compliance from Chinese people (5). In the US, stay-at-home orders were implemented across states, but individuals’ behavioral responses varied greatly, with many Americans violating governmental directives (6).

The study conducted an online, opt-in survey of 9,014 Chinese adults in March–April 2020 and a follow-up survey with 5,403 (60%) of the first survey respondents who participated in June–July 2020. Respondents from 31 provincial-level administrative divisions (PLADs) in the mainland of China were recruited by a professional survey firm through various online and offline channels. The research oversampled people living in Hubei Province; within each stratum (Hubei versus other PLADs), we further set quota based on gender, age, and education to ensure sample diversity. Because only the second survey asked about one of our key variables (confidence in scientists), our analytic sample in China drew on the 5,403 subjects who responded to both surveys.

In May 2020, an online survey of 2,523 adults in the US was conducted through Ipsos KnowledgePanel,
The study applied a standard demographic standardization technique (8). The overall mean value of attitudes toward COVID-19 was calculated as follows:

\[
\text{Mean attitudes toward COVID-19} = \sum_{k=1}^{4} P_k \times m_k,
\]

where \(P_k\) denoted the proportion of the \(k\)th category of belief in science and \(m_k\) denoted the mean level of attitudes toward COVID-19 for the \(k\)th category of belief in science. We created counterfactual means of US attitudes toward COVID-19 in two ways: applying to the US either 1) China’s distribution of belief in science (\(P_k\)) or 2) China’s attitudes toward COVID-19 by belief in science (\(m_k\)). Stata (version 16.1; College Station, TX: StataCorp) was used to conduct all analyses.

On average, Chinese respondents rated the necessity of COVID-19 mitigation measures at a significantly higher level than US respondents (Panel A of Figure 1: 4.81 vs. 4.03). In addition, Chinese adults had greater confidence in scientists than did American adults (Panel B of Figure 1). For example, 50% of Chinese and 33% of Americans had a great deal of confidence in scientists. In contrast, 17% of Americans did not have much confidence in scientists and 5% had no confidence at all, compared to only 7% and 1% in China, respectively.

In terms of attitudes toward COVID-19 by belief in science (Figure 2), Chinese respondents without confidence in scientists gave lower ratings to the necessity of COVID-19 mitigation measures (4.17),...
but all other Chinese respondents rated the necessity very high (4.77–4.83). By contrast, there was a clearer relationship among American respondents, such that greater confidence in scientists was strongly and positively associated with support for mitigation measures. The average scores rating the necessity of COVID-19 mitigation measures (in parentheses) corresponded to confidence in scientists as follows: no confidence at all in scientists (2.79), not too much confidence (3.24), a fair amount of confidence (4.02), and a great deal of confidence (4.65).

The results of demographic standardization were shown in Figure 3. The observed means indicated Chinese respondents’ higher average rating of the necessity of mitigation measures when compared to Americans (4.81 vs. 4.03), with a difference of 0.78. When China’s distribution of belief in science ($P_k$) was applied to that of the US and Americans’ attitudes toward COVID-19 by belief in science ($m_k$) was kept as observed, the counterfactual mean for the US was 4.27, resulting in a China–US difference of 0.54, a 30% reduction from the observed gap. When China’s $m_k$ was applied to the US and America’s $P_k$ was kept as observed, the counterfactual mean for the US

![FIGURE 2. Mean of attitudes toward COVID-19, by belief in science and country, 2020.](image)

![FIGURE 3. Observed and counterfactual mean values of attitudes toward COVID-19, 2020.](image)
was 4.78, reducing the China–US difference to practically nil (only 0.03). That is, if Americans held the same attitudes as Chinese for each category of confidence in scientists, the China–US difference in attitudes toward COVID-19 would have been almost entirely explained.

**DISCUSSION**

This study drew on original survey data from China and the US to compare attitudes toward COVID-19 and their associations with belief in science in the two countries. This research measured attitudes toward COVID-19 with survey questions about the necessity of mitigation measures (lockdowns or stay-at-home orders) for combating COVID-19. This research assessed belief in science through respondents’ level of confidence in scientists to act in the public interest. We showed that Chinese respondents rated higher the necessity of mitigation measures for combating COVID-19 than did American respondents. The China–US difference could be decomposed into two components: (1) Chinese people had higher confidence in scientists than did Americans, and (2) Chinese rated the necessity of COVID-19 mitigation measures more highly than Americans did, regardless of level of confidence in scientists.

The US is unique among Western developed nations in having a large portion of its citizenry who does not trust science (9). Previous research showed that over 30% of Americans thought that evolution was “absolutely false,” compared to 7%–15% in European countries (9). Distrust in science may diminish individuals’ confidence in scientists and government policies recommended by scientists. Chinese people, however, largely trust scientists, and over 90% of the Chinese public regarded scientists as role models (10). We demonstrated that belief in science played a role in accounting for the China–US difference in attitudes toward COVID-19.

This study was subject to some limitations. Although our China and US data were collected during similar time periods, the two countries were at different stages of the pandemic: the COVID-19 outbreak was under control in China, whereas in the US, daily new cases were rising. Given the cross-sectional survey design, we were unable to establish causality or capture changes over time in individuals’ attitudes toward COVID-19 and belief in science. Additionally, as we lacked data on individuals’ COVID-19 infection histories, we cannot ascertain the potential impact of COVID-19-related experiences on attitudes toward COVID-19. Finally, it was possible that confidence in scientists was associated with trust in other authorities such as the government, which in turn was related to support for and conformity with the government’s COVID-19 mitigation measures (2). However, we did not have data to test this alternative explanation.

In conclusion, Chinese people’s overall confidence in scientists and invariably high levels of support for COVID-19 mitigation policies have allowed China to contain COVID-19 with strong government interventions that were well supported by the public. By contrast, a large number of Americans’ distrust in scientists may have undermined their acceptance of science-based government policies (2). Individuals’ approving attitudes toward public health measures have been shown to promote adoption of behaviors that help reduce infection risk and slow COVID-19 transmission (3). Thus, the China–US difference in the severity of the COVID-19 outbreak may be partly attributable to differences in attitudes towards COVID-19 mitigation measures between China and the US. Taken together, our findings underscore that public trust in science and public support for population health measures are crucial for controlling the spread of COVID-19, especially in individualistic societies where citizen consent to public policy strongly influences policy effectiveness.

**Funding:** The Canadian Institutes of Health Research (OV7-170372); Fundamental Research Funds for the Central Universities, the Research Funds of Renmin University of China; the financial support for data collection from Princeton University.


* Corresponding author: Yongai Jin, jinyongai0416@ruc.edu.cn.

1. Department of Sociology, University of British Columbia, Vancouver, Canada; 2 Center for Population and Development Studies, Renmin University of China, Beijing, China; 3 Department of Sociology, Princeton University, New Jersey, USA; 4 Center for Social Research, Peking University, Beijing, China.

Submitted: June 18, 2021; Accepted: June 26, 2021

**REFERENCES**


On March 17, 2021, a 42-year-old male returning from Brazil tested positive by Qingpu CDC for coronavirus disease 2019 (COVID-19) during medical observation at a designated isolation point. He was then sent to the Shanghai Public Health Clinical Center (SHPHCC) and confirmed again, and because he demonstrated no abnormal clinical signs (until the infection was controlled), he was diagnosed as an asymptomatic infection.

According to an epidemiological investigation of this patient, the timeline of this patient’s relevant history, from COVID-19 vaccination to release from medical observation, was shown in Figure 1. The patient had completed two doses of COVID-19 vaccination (Beijing Institute of Biological Products Co. LTD) in Brazil on September 7, 2020, and October 3, 2020. In addition, he had self-tested using an antibody kit on October 24, while the test results were negative. The patient maintained his normal work and living conditions during his stay in Brazil until January 4, 2021, when his test results of IgM and IgG of COVID-19 both returned positive. Since the conditions for returning to China were not met, the patient self-isolated at home until March 9, 2021. Because administration of the inactivated vaccine is followed by the production of IgM and IgG in the body, the policy on returning to China has since been adjusted.

On March 10, 2021 (GMT-3), the patient departed from Sao Paulo International Airport in Brazil and arrived at Shanghai Pudong International Airport on March 12 (GMT+8). The patient was sent to the corresponding isolation hotel. From January 4 to March 15, 2021, all tests [including nucleic acid tests and computed tomography (CT) tests] were normal, except for the results monitoring IgM and IgG, which were all positive. Subsequently, on March 16, due to two confirmed patients being on the same flight, he was considered a potential close contact and was sent to a designated isolation point for close contacts to receive medical isolation and observation. However, the nucleic acid test results of the nasopharyngeal swab of the patient were then positive on March 17 and were further confirmed at the SHPHCC. The patient recovered on March 28 and was then sent to a medical isolation point for another 14-day quarantine observation. With no abnormalities during the quarantine period, the patient was finally discharged from isolation on April 11.

Though the self-test results of the patient conducted on October 24, 2020 were negative, these results may be related to differences in the vaccines (J). This would likely be reflected in the patient still having a risk of COVID-19 infection during this period. In addition, the possibility of false negatives in the self-test could not be excluded. However, during the home isolation period of the patient in Brazil, the patient’s serum antibody test results returned positive. IgM maintained a high titer for a long time, while the IgG titer gradually decreased, as shown in Figure 2 (according to

the data provided by the patient and part of the test report). Moreover, the antibody level of IgM from February to early March was about 2–3 times higher than that of IgG in each test result. As an asymptomatic infection, the changes of antibodies of the patient were different from those in related studies (2–3), so it is uncertain whether the antibody changes in this patient were caused by vaccination. Future research may yield clarification for this issue.

The patient in this investigation was vaccinated but still became infected with COVID-19. This implies that those receiving vaccines are still at a potential risk of infection under certain conditions. In addition, according to the official website of the US CDC, there are 9,425 people who have been vaccinated in the US that have become infected with COVID-19 (4), which demonstrates the continued, albeit diminished, risk of infection post-vaccination. However, vaccination is a process of stimulating the production of protective antibodies in the body. Usually there is no vaccine that can achieve 100% protection (5), meaning that the possibility of breakthrough infections still exists even after vaccination. Individual differences, vaccine failure during the vaccination process, COVID-19 mutant variants, and high-risk exposure behaviors may all contribute to breakthrough vaccine immunity (6). Therefore, the secondary infection post-vaccination is unsurprising. In the epidemiological investigation of this patient, we found that after COVID-19 vaccination, he had a history of suspected exposure to COVID-19 during his work in Brazil and during his journey returning to China. This may be the way that the patient was infected with COVID-19. Individual differences and other factors cannot be ruled out.

People who have completed a full course of vaccination are highly recommended to remain cautious and take personal protective measures such as wearing masks and maintaining appropriate social distance to protect themselves and others (7), regardless of whether vaccination has been completed or not. Before achieving herd immunity, these continued measures are essential to protect the health of individuals and the public.

doi: 10.46234/ccdcw2021.140

1. Corresponding authors: Hongrang Zhou, hrzhou0223@foxmail.com; Ning Xiao, xiaoning@nipd.chinacdc.cn.

3. Qingpu District Center for Disease Control and Prevention, Shanghai, China; 2 National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention; Chinese Center for Tropical Diseases Research; WHO Collaborating Centre for Tropical Diseases; National Center for International Research on Tropical Diseases, Ministry of Science and Technology; Key Laboratory of Parasitic and Vector Biology, National Health Commission of China; The School of Global Health, Chinese Center for Tropical Diseases Research, Shanghai Jiao Tong University School of Medicine; Huangpu, Shanghai, China; 3 Program in Public Health, College of Health Sciences, University of California at Irvine, Irvine, USA.

* Joint first authors.

Submitted: May 10, 2021; Accepted: June 11, 2021

REFERENCES


A 47-year-old male (Patient A) passenger from Vietnam whose nucleic acid results for coronavirus disease 2019 (COVID-19), also known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), were positive at Pingxiang Customs on April 29, 2021, and subsequently confirmed by Guangxi CDC laboratories on April 30.

On April 30, four accompanying persons (Patient B–E) of Patient A returned from Vietnam. After being tested by the laboratory of Pingxiang Customs using nasopharyngeal swab tests for COVID-19, the results for patients showed COVID-19 positive. All five patients were transported to the Pingxiang Emergency Medical Center for isolated treatment by ambulance. Clinical conditions of the five patients included normal body temperature, blood tests, and liver-kidney functions. Abnormalities in chest computed tomography (CT) suggested infectious lesions, four patients (A/B/D/E) classified as mild type of COVID-19, and one (patient C) was classified as severe type.

Preliminary epidemiological investigation revealed those patients were on a business trip from April 9, when they came to Yen Bai Province, Vietnam, and were isolated in a designated isolation hotel until April 22. From April 23 to 28, all five patients performed their business and travel in Vietnam. The latest negative results for Patients A, B, and C were on April 22 and were on April 27 for Patients D and E, respectively.

Further investigations demonstrated a group of Indian nationals who were isolated in the hotel on April 18, and four of these individuals eventually tested positive for COVID-19 on April 19. In addition, guests of the hotel had activity unrestricted in the hotel during the quarantine, and there was only one attendant who took no relevant precautionary measures against COVID-19 when on duty. The attendant was later confirmed positive for COVID-19 on April 26.

The specimens of the confirmed patients were sent to Guangxi CDC and sequenced by Illumina MiSeq Sequencing platform using a 500-cycles MiSeq v2 Reagent Kit between April 30 to May 4. On May 3, one patient’s whole genome sequence was obtained, and on May 7, the other four patients’ sequences were obtained. In comparison with the COVID-19 reference strain (Gene Bank Accession: NC_045512), these isolates possessed 28–34 variation sites in nucleic acids, including 11 variations in the spike protein (T19R, G142D, A222V, L452R, T478K, D614G, P681R, D950N, E156del, F157del, and R158del). Notably, eight variation sites of amino acid residues (T19R, L452R, T478K, D614G, P681R, D950N, F157del, and R158del), which were identical to those in Indian B.1.617.2 variants, were observed in all five isolates. Phylogenetic analysis of genome sequence indicated these isolates belonged to the PANGO lineage (1) B.1.617.2 (Figure 1), an emerging variant first identified in India in October 2020 and has recently been designated as a variant of concern (VOC) which labeled as Delta by the World Health Organization (WHO) (2–3). The COVID-19 infection in these five patients probably occurred when they were staying in the designated isolation hotel in Vietnam and sharing space with the Indian nationals that were confirmed positive for COVID-19. Furthermore, the hotel attendant was confirmed as COVID-19 positive on April 26. The B.1.617 variant had been detected in Chongqing (4) and had been identified in dozens of countries worldwide, posing a serious challenge to the global pandemic. Among the sub-variants of B.1.617, the B.1.617.3 shares the L452R and E484Q mutations found in B.1.617.1 (VOI, Kappa), whereas B.1.617.2 does not have the mutation E484Q but has the T478K mutation not found in B.1.617.1 and B.1.617.3. Since most of B.1.617 variants reported in 17 countries contained 2 key mutations, L452R and E484Q, these imported
FIGURE 1. Neighbor-joining phylogenetic tree based on the whole genome sequences of COVID-19 representative strains. Note: The five Guangxi strains are indicated by dots; the Wuhan reference strain is indicated by triangle. The PANGOLIN lineages were marked on the right. The tree was rooted using strain WH04 (EPI_ISL_406801) in accord with the root of PANGOLIN tree.
cases in Guangxi were excluded from such double-mutant variants.

Guangxi Zhuang Autonomous Region is adjacent to Association of Southeast Asian Nation (ASEAN) countries by land and sea and is an important provincial-level administrative division for China open to ASEAN. During the 13th Five-Year Plan period, the import and export trade of Guangxi to ASEAN accounted for 48.9% of the total foreign trade value. However, over the past year, cases of COVID-19 rose 40-fold to 162 million globally, while the number of deaths has increased 11-fold to more than 3.3 million. To prevent COVID-19 cases from entering, Guangxi has taken strict restrictions on all entry-exit personnel. The five patients were found among returning Chinese nationals from Vietnam at a border port for the first time, suggesting that the COVID-19 (B.1.617.2 variants) still poses a risk of transmission in some ASEAN countries. Therefore, constant surveillance of genome sequences in imported cases is required to track the transmission and evolution of the COVID-19 virus during the ongoing COVID-19 pandemic. The pathogenicity and transmissibility of these mutant variants urgently need further study (5–6).

Funding: Guangxi Key Technologies Research and Development Program (Grant No. AB20149001).

Funding: Guangxi Key Technologies Research and Development Program (Grant No. AB20149001).
doi: 10.46234/ccdcw2021.147


