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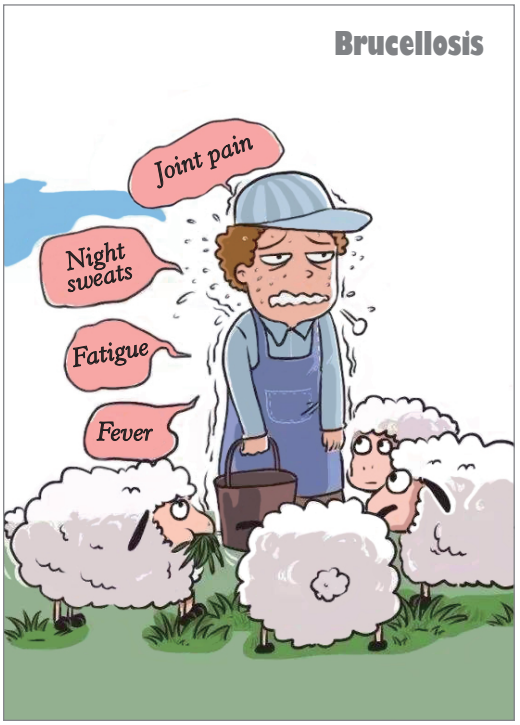

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Outbreak Reports

Brucellosis Outbreak Caused by *Brucella melitensis* — Jingyang County, Shaanxi Province, China, March–May, 2020

Wenhui Chang[1]; Yangxin Sun[1]; Suoping Fan[1]; Cuihong An[1]; Shoumin Nie[1]; Guozhong Tian[2]; Boyan Luo[1]; Hongxun Yang[3]; Xiaohua Zhai[3]; Haiying Tian[3]; Jia Zhang[4]; Hai Jiang[2,#]

Summary

What is already known about this topic?

Brucellosis is one of the world's most overlooked zoonotic diseases, and humans can easily acquire brucellosis from animals and their products. Reemerging brucellosis outbreaks are probably attributable to sociocultural factors and compounded by the lack of adequate control measures in sheep and goat rearing systems.

What is added by this report?

This is the first identified outbreak caused by *Brucella melitensis* bv.3 in Jingyang County, Xianyang City, Shaanxi Province. A total of 13 seropositve cases (7 acute patients and 6 asymptomatic persons) were identified from March to May, 2020, and the investigation indicated that sheep-to-canine-to-human was the likely transmission route.

What are the implications for public health practice?

Effective control of sheep brucellosis will significantly reduce the risk of human brucellosis. Priority should be given to building cooperation between all stakeholders, maintaining epidemiological surveillance to detect human brucellosis at medical centers, and making case reporting mandatory for both veterinary and public health services.

From April 29 to May 1, 2020, a brucellosis outbreak was reported in a village in Jingyang County, and as of May 7, 7 symptomatic cases and 6 asymptomatic cases were detected and reported. The investigation on this outbreak was conducted by the Jingyang County CDC and Livestock Center and revealed that Patient 1 and her eight relatives were exposed to their infected dogs, which might have been infected by the pathogen when they ate miscarried lambs that had been buried in the orchard of Patient 10. Patient 10 and the 3 individuals (Patient 11, 12 and 13) with positive test results were infected by contact with their sick sheep. In addition, four suspected *Brucella* strains (two from infected sheep and two from patients) were isolated and identified by a classical phenotyping method (*1*) and Abortus, Melitensis, Ovis, and Suis polymerase chain reaction (AMOS-PCR), as described elsewhere (*2*). MLVA-16 (multiple-locus variable-number tandem repeat analysis) was also performed for epidemiological tracing (*3*).

INVESTIGATION AND RESULTS

Suspected cases were defined as residents of the village and neighbouring villages who developed 2 or more of the following symptoms from March 1 to May 7, 2020: fever (≥37.5 ℃), fatigue, night sweats, and joint pain excluding patients with confirmed diagnosis for other diseases. Confirmed cases were defined as suspected cases with an antibody titer of ≥1∶100 (++) in serum agglutination test (SAT) or positive *Brucella* isolate according to the guidelines for the Diagnosis of Human Brucellosis (WS 269–2019).

So far, out of the 279 individuals who were tested, 13 met the criteria for diagnosis. The demographic and clinical data of individuals who tested positive during the brucellosis outbreak in the village were shown in Table 1. Among the 13 individuals with positive test results, there were 8 males and 5 females (male to female ratio, 1.6∶1). Their ages covered a wide range of 2 to 64 years. Interestingly, 9 of the individuals (Patients 1–9) were related to each other. Most of the cases were found in the family of Patient 1. Among the 3 asymptomatic individuals, 2 individuals were from the East Third Unit (Patients 11 and 12), and 1 was from the Z Group of the village (Patient 13). They were all sheep farmers and had a history of contact with a sheep that had a miscarriage. They did not live in the same village as the others who tested positive.

Patient 1 and her relatives (nine individuals in total) had no history of drinking cow and goat milk and no history of contact with any lamb. The family of Patient 1 currently had 2 dogs, which were sometimes tethered

TABLE 1. List of individuals who tested positive during the outbreak of brucellosis in Jingyang County, Shaanxi Province, China, 2020.

No.	Sex	Age (years old)	Occupation	Case relationship	Results of SAT	Date of onset	Time of diagnosis
1	Female	46	Beef cattle farmer	Initial case	1:800 (+++)	Mar 18	Apr 28
2	Male	15	Student	Nephew	≥1:800 (++++)	Apr 26	May 1
3	Male	24	Farmer	Son-in-law	1:200 (+++)	Apr 23	May 1
4	Female	2	Scattered child	Granddaughter	1:400 (+++)	Apr 26	May 1
5	Female	24	Farmer	Daughter	≥1:800 (++++)	May 1	May 1
6	Female	10	Student	Niece	1:800 (+++)	Apr 14	May 5
7	Female	20	Student	Niece	1:400 (++)	Apr 1	May 5
8	Male	47	Beef cattle farmer	Husband	1:800 (+++)	No symptom	–
9	Male	62	Farmer	Case 8's older brother	1:800 (++)	No symptom	–
10	Male	64	Sheep farmer	West No. 2	1:100 (++)	No symptom	–
11	Male	75	Sheep farmer	East No. 3	1:200 (++)	No symptom	–
12	Male	60	Sheep farmer	East No. 3	1:200 (+++)	No symptom	–
13	Male	67	Sheep farmer	Z Group	1:400 (+++)	No symptom	–

Abreviation: SAT=serum agglutination test.

and sometimes let outside their cage, and Patient 1's husband once fed a stray dog. Starting in 2018, the family raised beef cattle in their backyard under poor sanitary conditions. Patient 1's husband was responsible for feeding the cattle, but he did not use any protective measures during the feeding process. Jingyang County's Livestock Center collected blood samples of 10 cattle that belonged to Patient 1, but the test results were negative for all cattle samples. All the individuals who visited Patient 1's family in her village were investigated, and the results showed that the visits were associated with disease onset. On May 5, the Livestock Center collected blood samples from the two dogs that belonged to Patient 1 and her family, and both tested positive for brucellosis. Given all cases had a suspected exposure to dogs, we concluded that contact with the dogs was a key risk factor of infection.

The family of Patient 10 had 2 long-term residents and live only 2 households away from Patient 1 and her family. Patient 10 had been raising sheep for 10 years by self-breeding and had not purchased any other sheep. By the end of 2019, they had 4 pregnant sheep, two of which miscarried, and the fetuses were buried in their own orchard. However, the miscarried fetuses later disappeared from the burial spot, and it was suspected that they had been taken away by an animal. The family of Patient 10 had 2 lambs in stock, and both tested positive in tests done by the Livestock Center on April 30 indicating that these 2 lambs were the source of infection.

On May 5, the Livestock Center collected samples from 70 sheep in stock at another possibly infected sheep farm in the village, and 4 sheep tested positive. On the same day, Jingyang County CDC collected samples from four employees of the sheep farm and all of them tested negative.

The results of epidemiological investigation and comprehensive analysis indicated that the brucellosis outbreak in Patient 1's family and the eight relatives was caused by exposure to their infected dogs that were likely exposed due to consuming miscarried lambs buried in Patient 10's family orchard. Patient 10 and 3 individuals with positive test results in the other groups were infected by contact with their sick sheep. All 4 isolates (2 isolates from sheep belonging to Patient 10 and 1 each from Patient 7 and Patient 11) were identified *B. melitensis* bv. 3 and showed an identical MLVA profile (1-5-3-13-2-2-3-2-4-40-8-6-4-3-4-5), suggesting the same exposure source.

PUBLIC HEALTH RESPONSE

During this investigation in May 2020, multiple emergency countermeasures were taken including case searching, diagnosis and treatment of patients, health education, tracing the sources, and disinfecting contaminated environments. Up to May 7, 252 blood samples were collected from sheep and 65 were collected from cattle by the Livestock Center, and only 25 blood samples from sheep tested positive. The Jingyang County CDC screened all high-risk populations, and a total of 279 individuals were tested.

A total of 7 patients were hospitalized in the Eastern Suburb Branch of Xianyang Central Hospital, and 6 asymptomatic persons were under medical observation at home. Based on this investigation, all stakeholders took long-term joint actions including promoting information dissemination and health education on brucellosis, cracking down on illegal activities related to aborted and sick animals, etc.

DISCUSSION

In this study, aborted sheep fetuses and close contact with infected dogs were found to be the key risk factors for human brucellosis, and aborted fetuses, placentas, and secretions were already known to be one of the most infective sources of *Brucella* species (*4*). However, although *Brucella* is easily transmitted among domesticated animals, such as cattle, goats, and sheep (*5*), the role of close contact with dogs is often ignored in the development and implementation of prevention and control strategies. Stray dogs are generally assumed to be able to contribute to the distribution and retention of *Brucella* spp. in dog populations (*6*). Literature considers the zoonotic potential of *B. canis* is low compared to *B. melitensis*, *B. suis*, and *B. abortus*, which are more frequently reported as the underlying cause of human brucellosis (*7*). Less attention has been paid to *B. canis* in China, although dogs usually live in close contact with their owners, and breeding for commercial purposes in poor housing conditions without veterinary care may constitute additional risks. Therefore, dogs should be prohibited from eating aborted sheep fetuses in rural areas, especially in endemic regions.

In case of an outbreak in the future, genome-based epidemiological tracing should be performed. Recently, whole-genome shotgun (WGS) for bacterial pathogens has become cheaper and faster, and bioinformatics analysis based on the WGS is crucial for both epidemic and outbreak investigations (*8*–*9*). In this study, the isolate from Patient 11 was of the same phenotype as that identified in Patient 7, but Patient 11 did not report any significant clinical symptoms. It is unclear whether the isolate had low virulence or the incubation period was longer.

Based on this outbreak investigation, infected animals should be promptly isolated, culled, and buried. Additionally, farmers should also receive guidance regarding performing daily disinfection of the family and livestock breeding environments. Importantly, regular screening of livestock farms and families must be undertaken. Local CDC's and Livestock Centers should conduct active surveillance of brucellosis among humans or animals, collect and analyze the epidemiological data on brucellosis, and carry out risk assessments to guide its prevention and treatment (*10*). Cooperative actions such as simultaneous monitoring, information exchange, complementary measures by various departments, and resource sharing should be included to formulate a practical monitoring and prevention strategy (*11*). Health education and consulting services should be provided to spread information about the prevention and treatment of brucellosis, to improve awareness regarding self-protection, and modify unhealthy production methods and lifestyles. Farmers should be actively guided to implement scientific feeding methods and strengthen personal protection by providing effective protective equipment.

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Corresponding author: Hai Jiang, jianghai@icdc.cn.

[1] Shaanxi Provincial Centre for Disease Control and Prevention, Xian, Shaanxi, China; [2] State Key Laboratory for Infectious Disease Prevention and Control, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China; [3] Jingyang County Centre for Disease Control and Prevention, Xianyang, Shaanxi, China; [4] Xianyang City Centre for Disease Control and Prevention, Xianyang, Shaanxi, China.

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Outbreak Reports

First Outbreak of Occupational Brucellosis Involving Multiple Clusters — Hubei Province, China, 2019

Zhong Zhang[1,2,&]; Yeqing Tong[3,&]; Xinjun Lei[4,&]; Li Liu[3]; Zhiqiang Deng[2,5]; Fei Sun[6]; Huilai Ma[2]; Zhaorui Chang[7]; Lijie Zhang[2]; Huihui Liu[2]; Qi Chen[3]; Jianzhong Zheng[8]; Haibing Chen[9]; Ximei Sun[9]; Yang Wu[3,#]; Xuhua Guan[3,#]

Summary

What is already known on this topic?

Human brucellosis, a neglected zoonotic disease, causes more than 500,000 new cases each year globally. The disease is of major public health concern in China, and northern provinces are traditionally endemic areas.

What is added by this report?

This is the first published outbreak of occupational brucellosis involving multiple clusters in Hubei Province. This investigation characterizes the transmission chain of the outbreak and reveals that provinces south of the Yangtze River are faced with a series of challenges and hurdles to overcome including, but not limited to, health education, law enforcement, and occupational protection.

What are the implications for public health practice?

In addition to measures aimed at this outbreak, the local agricultural department has issued special notices based on this investigation to adjust and strengthen local eradication program of brucellosis.

The incidence of human brucellosis is surging dramatically in southern provinces of China (*1*–*3*), including provincial-level administrative divisions (PLADs) along and to the south of the Yangtze River*, and no brucellosis outbreaks were reported in southern Hubei Province before this investigation (*4*–*5*). An eradication program of brucellosis has been put into action in Hubei since 2017.

On June 3, 2019, 2 clusters of brucellosis involving 5 cases in Xianning, a prefecture-level city in southern Hubei, were reported to the National Public Health Emergency Reporting Information System (NPHERIS), and 1 cluster involved 3 employees of L mutton restaurant in Chongyang County, Xianning with the other involving 2 goat keepers of J goat farm in Jiayu County, Xianning. A field investigation was initiated to identify the infection source and risk factors.

INVESTIGATION AND RESULTS

Suspected cases were defined as residents of Chongyang County and suppliers of the L mutton restaurant who developed two or more of the following symptoms from January 1 to June 31, 2019: fever (≥ 37.5 ℃), fatigue, night sweats, and joint pain excluding patients with confirmed diagnosis for other diseases. Confirmed cases were defined as suspected cases with positive 1∶100 (+ +) or above serum agglutination test (SAT) for *Brucella*.

Case finding was carried out by interviewing cases, doctors, restaurant managers, and others employees, reviewing Infectious Disease Reporting Management Information System and medical records, and implementing symptom surveillance in local major hospitals.

Serum samples of all suspect cases were collected and tested. If the Rose Bengal plate agglutination test (RBPT) or SAT was positive, detailed demographic information, clinical information, eating habits, occupational history, preventive measures, and sources of animal products were collected. A field investigation was also initiated to ascertain possible polluted environments which these patients were exposed to.

A total of 8 cases (including 5 initial cases mentioned above) of brucellosis were identified with 6 patients experiencing onset of illness in April and 2 patients in May. All cases were confirmed. The most commonly reported symptoms were fever (88%), joint pain (75%), and fatigue (75%), and they were all

* These include Jiangsu, Anhui, Shanghai, Hubei, Sichuan, Zhejiang, Chongqing, Jiangxi, Hunan, Guizhou, Fujian, Yunnan, Guangdong, Guangxi, and Hainan of the mainland of China.

discharged after a treatment of doxycycline and rifampin (42 d). Of these patients, 6 came from Chongyang County, and 2 from Jiayu County, and their ages ranged from 26 to 57 years old with a median age of 49 years. Their suspected exposures included goat-slaughtering, abortive ewes, and environmental exposure. Time intervals between onset of symptoms and diagnosis varied from 6 to 43 days, and the onset-to-diagnosis intervals of 6 cases exceeded 1 month.

The trade relationship among the work sites was further investigated. In Hubei, mutton consumption peaks between October and February of the next year, and L mutton restaurant mainly engaged in mutton hot pots and mutton noodles. During the off-season, the restaurant bought frozen mutton from B wholesale market in Wuhan, whose mutton originated from a market in Huanghua, Hebei Province of Northern China. During the peak months, it bought live goats from J goat farm and then slaughtered them in a back room of the restaurant. J goat farm bought live goats from M live goat market in Fang County, Shiyan City, northern Hubei Province (Figure 1).

During the investigation, a total of 19 serum samples were collected and 8 of them tested positive for RBPT and SAT. A strain of *Brucella melitensis* was isolated (Table 1).

Given that most cases had a suspected exposure to goat-slaughtering, we hypothesized that slaughtering was a key risk factor of infection. Subsequently, we investigated the exposure histories of 21 individuals, including all employees of L mutton restaurant, J goat farm, and D butcher's. No employees wore any personal protective equipment at work, and no patients had a history of consuming unpasteurized contaminated animal products or a history of travelling to endemic areas beforehand. The results showed that slaughtering without protective measures was a risk factor (RR=11.38, 95%CI: 1.70–76.14) (Table 2), and 6 of the 8 patients had not heard of brucellosis before and no patients had an awareness of clinical signs and symptoms of human brucellosis.

Further field investigation revealed that the slaughterhouse of L mutton restaurant was a low-

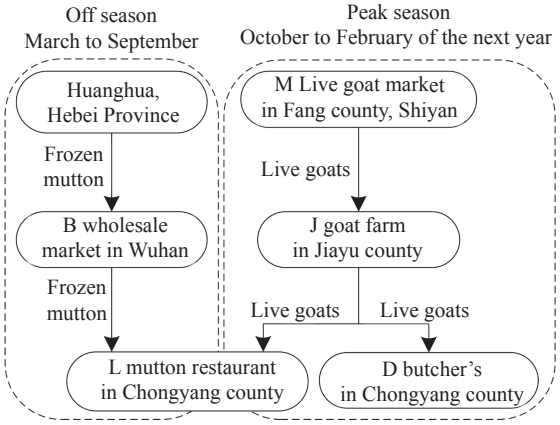

FIGURE 1. Transaction flow charts of an outbreak of brucellosis in Hubei Province, China, 2019.

TABLE 1. Laboratory results of an outbreak of brucellosis in Hubei Province, China, 2019.

Source of samples	Samples collected	RBPT positive	SAT positive	Brucella strain isolated
L mutton restaurant	9	5	5	1
J goat farm	2	2	2	–
D butcher's	2	1	1	–
M live goat market	1	0	0	–
Relatives	5	0	0	–
Total	19	8	8	1

Abbreviations: RBPT=Rose Bengal plate agglutination test, SAT=Serum agglutination test.

TABLE 2. A cohort study of an outbreak of brucellosis in Hubei Province, China, 2019.

Factors	Exposed		Unexposed		Attack rate (%)		RR (95%CI)
	Total	Cases	Total	Cases	Exposed	Unexposed	
Slaughtering without precautions	8	7	13	1	87.50	7.69	11.38 (1.70–76.14)
In slaughterhouse without precautions	5	1	16	7	20.00	43.75	0.46 (0.07–2.88)
Processing frozen mutton without precautions	8	0	13	8	0	61.54	0*

Abbreviations: RR=Relative Risk.
* p=0.007.

roofed room of nine square meters with a door connecting the lobby of the restaurant. There were no windows, ventilation, or disinfection facilities, and the conditions in D butcher's were similar.

J goat farm is located beside the Yangtze River and separated from residential areas. In the off season, the farm kept about 200 self-bred goats. In November 2018, the farm bought about 100 goats from M live goat market and kept them with self-bred goats, which might have led to cross-infection. Several pregnant ewes were aborted between December 2018 and January 2019 but were still sold. There were no inspections or quarantine measures while in transit since these goats were transported through a rural road. All the goats in the farm were sold for the first time in nearly a decade in January 2019 without any inspection measure.

PUBLIC HEALTH RESPONSE

The routine control measures, including daily inspection of livestock transport on highways and annual random testing of the goats for brucella in farms during spring and autumn, failed to detect the outbreak in January 2019 when the infections were spreading so no emergency measures were taken then. During this investigation in June 2019, multiple emergency countermeasures were taken including case searching, diagnosis and treatment of patients, health education, tracing the sources of goats and mutton, and disinfecting contaminated environments. Based on this investigation, local agricultural departments and health departments took long-term joint actions including promoting health education, general surveying of goat breeding across Xianning, cracking down on illegal activities related to sick animals and animal products, etc. In addition, a special notice was issued to strengthen and adjust the eradication program of brucellosis.

DISCUSSION

This is the first outbreak of occupational brucellosis involving multiple clusters in Hubei. The investigation indicates that 2 clusters involving 5 initial cases were part of an outbreak and presented a transmission chain for a brucellosis outbreak. This report revealed that southern provinces are faced with a series of challenges and hurdles to overcome. Trans-regional goat trading and lax inspection measures might result in importation of infected goats, which were fed in the same sheepfold with local goats, and then led to cases of human brucellosis in those who slaughtered or raised these goats without protection in the process of slaughtering in January 2019. Seven cases were engaged in slaughtering and one case might have been infected by inhaling aerosols. J goat farm, L mutton restaurant and D butcher's all fell victims of this outbreak.

Brucellosis is spreading in humans and animals in Asian countries, and Northern China has been more heavily impacted traditionally by brucellosis than Southern China (*2*–*3*,*6*). Many brucellosis infections in southern provinces resulted from imported infected animals or products from Northern China (*7*–*8*), so northern provinces should strengthen brucellosis control at the source.

Neither imported goats nor the self-bred goats were found to be vaccinated, and both types of goats were all mixed together, which resulted in the spread of brucellosis among these goats. We also found that the transportation of goats was not strictly inspected. When an outbreak of animal disease occurs, the farm owners often sell all their livestock in a short time without realizing the infectiveness (*4*). The phenomenon of emptying stock is worthy of attention. Comprehensive control strategies should be adopted including isolated feeding of imported goats from local ones, vaccination, and inspection measures, all of which can reduce the incidence of brucellosis as evidenced by Italy (*9*).

Awareness and knowledge of brucellosis among occupational workers are commonly regarded as a vital aspect of human brucellosis control (*10*). This investigation found that local occupational workers had a low awareness of brucellosis and personal protective measures, so health education should be promoted among relevant occupational groups.

Due to the swelling demand of fresh mutton, the influx of live goats from northern provinces to the south is becoming increasingly frequent. This report reveals a series of challenges in the current eradication program of brucellosis and provides a useful reference for strengthening and adjusting the action in southern provinces.

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[#] Corresponding authors: Yang Wu, 6021975@qq.com; Xuhua Guan, 552371433@qq.com.

[1] Nanjing Municipal Center for Disease Control and Prevention, Nanjing, China; [2] Chinese Field Epidemiology Training Program (CFETP), Beijing, China; [3] Hubei Provincial Center for Disease Control and Prevention, Wuhan, China; [4] Chongyang Center for Disease Control and Prevention, Xianning, China; [5] Nanchang Municipal Center for Disease Control and Prevention, Nanchang, China; [6] Yiling Center for Disease Control and Prevention, Yichang, China; [7] Division of Infectious Disease, Key Laboratory of Surveillance and Early Warning on Infectious Disease, Chinese Center for Disease Control and Prevention, Beijing, China; [8] Xianning Municipal Center for Disease Control and Prevention, Xianning, China; [9] Jiayu Center for Disease Control and Prevention, Xianning, China.
[&] Joint first authors.

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Notes from the Field

Reemergent Cases of COVID-19 — Xinjiang Uygur Autonomous Region, China, July 16, 2020

Cao Chen[1,2,&]; Hemuti Ma[3,&]; Zhiyuan Jia[1]; Xiang Zhao[1]; Dayan Wang[1,2]; Jun Zhao[3]; Zhenguo Gao[3]; Peipei Liu[1]; Yang Song[1]; Zhixiao Chen[1]; Yuchao Wu[1]; Yao Meng[1]; Guizhen Wu[1,2]; Wenbo Xu[1,2]; Xucheng Fan[4,#]; Yong Zhang[1,2,#]

Before the coronavirus disease 2019 (COVID-19) outbreak on July 16, 2020, no new COVID-19 cases were reported in Urumqi City of Xinjiang for 150 consecutive days. During this outbreak, 826 confirmed COVID-19 cases have been reported in Urumqi. The phylogenetic characteristics of COVID-19 virus from clinical specimens of the initial 4 cases in the Urumqi outbreak were sequenced.

The full-length genome sequencing of COVID-19 virus was performed on the Illumina MiSeq platform, and 4 full-length COVID-19 virus genome sequences were obtained from clinical specimens of the initial 4 cases in this outbreak. Compared with the reference sequence EPI_ISL_402119 (*1*), which was isolated from Wuhan City in Hubei Province on January 7, 2020. A total of 13 nucleotide variations were determined, among which 7 nucleotide variations (C241T, C3037T, C14408T, A23403G, G28881A, G28882A, and G28883C) were identified in each full-length genome of the 4 Xinjiang strains, which were consistent with the characteristics of the L-lineage European branch 1/B.1.1 according to the latest classification principle (*2*) (Figure 1). The Xinjiang strains were different from the previous hCoV-19/Wuhan/IVDC-HB-01/2019 hCoV-19/Wuhan/IVDC-HB-03/2019 hCoV-19/Wuhan/IVDC-HB-05/2019 (belonging to S-lineage/A) strains in Wuhan in December 2019, indicating that they were not continuous transmission of indigenous COVID-19 virus strains. Other nucleotide substitutions were also identified in these Xinjiang strains, including C12789T and G14118T substitutions in all 4 genomes of the viruses, C2197T in specimen 1, C12809T in specimen 2, and C19718T and C23481T in specimen 3.

Since no Xinjiang strains contained the characteristic substitutions of Beijing Xinfadi strains (C6024T) (*3*) and Dalian strains (C2091T, A5128G, A8360G, C13860T, T19839C, G19999T, and C28905T) (*4*) and because the Beijing Xinfadi strains and Dalian strains also did not contain the characteristic substitutions of Xinjiang strains (C12789T and G14118T), the correlation between Xinjiang strains, Beijing Xinfadi strains, and Dalian strains were preliminarily excluded. The Xinjiang strains had high nucleotide similarity with several genomes of the COVID-19 virus (Shulan strains, Harbin strains) from the recently imported COVID-19 cases in northeastern China from April to May that also belonged to L-lineage European branch 1 (*5*–*6*). However, because of the interval (more than 2 months) and epidemiological evidence (no epidemiological link of the cases and contacts from Shulan and Harbin with the Xinjiang outbreak), the possibility of Harbin strains and Shulan strains spreading in Xinjiang was also ruled out. In addition, the full-length genome sequence analysis of the Xinjiang strains further confirmed that the virus source of the outbreak was not transmitted from natural animal hosts or intermediate animal hosts to human beings.

Although the source of COVID-19 virus of the Urumqi outbreak has not been determined, the possibility of transmission of the COVID-19 virus through importing contaminated products could not be excluded according to the characteristics of the recent COVID-19 outbreaks. Therefore, the COVID-19 virus detection in imported products should be further strengthened. Meanwhile, entry control at ports in Xinjiang and among key populations from Central Asia should be strengthened. A comprehensive analysis of epidemiology, serology, and etiology is needed to determine the source of the virus.

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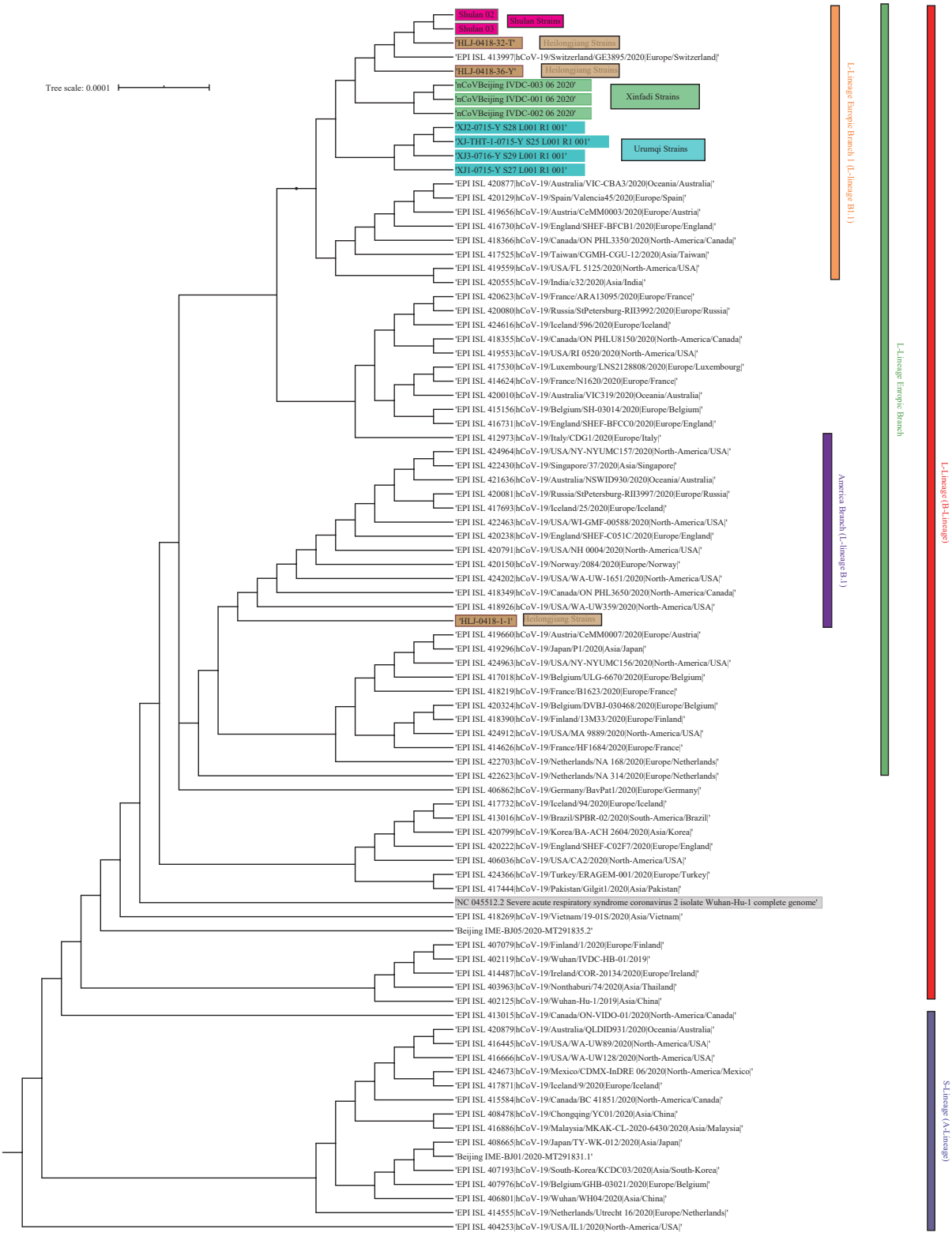

FIGURE 1. Phylogenetic tree based on the full-length genome sequences of the COVID-19 virus. The genomes of COVID-19 virus from Xinjiang were highlighted in blue. The genomes of reference COVID-19 virus from Wuhan in December 2019 were highlighted in grey. The recent reemergence of COVID-19 virus in Beijing Xinfadi were highlighted in green, and the recent reemergence of COVID-19 virus in northeastern China (Shulan and Heilongjiang) that related to imported cases were highlighted in pink and brown, respectively. S(A)- or L(B)-lineage of the COVID-19 virus were marked and colored on the right.

[#] Corresponding authors: Xucheng Fan, 27980310@qq.com; Yong Zhang, zhangyong8@ivdc.chinacdc.cn.

[1] National Health Commission Key Laboratory for Medical Virology and Viral Diseases, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China; [2] Center for Biosafety Mega-Science, Chinese Academy of Sciences, Wuhan, China; [3] Xinjiang Uygur Autonomous Region Center for Disease Control and Prevention, Xinjiang, China; [4] Urumqi Center For Disease Control And Prevention, Xinjiang, China.
[&] Joint first authors.

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Commentary

Ending the Global HIV Epidemic Begins at the Individual National Level: An Update from the United States

Robert W. Eisinger[1]; Anthony S. Fauci[1,#]

The pathway to achieving an end to the HIV pandemic begins with innovative and sustainable initiatives that optimize for each individual nation the implementation of evidence-based tools in the HIV prevention and treatment toolboxes. This article provides an update on the current global HIV epidemic and describes the current activities associated with the recently announced plan to end the HIV epidemic in the United States.

The latest global statistics on HIV/AIDS showed that in 2019 there were an estimated 38.0 million people living with HIV, 1.7 million new HIV infections, 690,000 deaths from AIDS-related illnesses, and 25.4 million individuals receiving antiretroviral therapy (ART). UNAIDS estimates that in 2019, 81% of people living with HIV knew their HIV status with 67% receiving ART, while only 59% of those individuals receiving ART had undetectable levels of virus (*1*). In 2014, the UNAIDS issued 3 global targets for achieving HIV treatment scale-up by 2020 that would enable the end of the AIDS epidemic by 2030. These targets included: 90% of all people living with HIV infection will know their HIV status; 90% of all people diagnosed with HIV infection will receive sustained ART; and 90 % of all people receiving ART will have viral suppression (*2*). However, the 2019 epidemiologic global statistics clearly show that the 90-90-90 targets will not be met by the end of 2020. The coronavirus disease 2019 (COVID-19) pandemic further endangers achieving the 90-90-90 targets and may in fact seriously endanger the progress made to date (*3*). Novel strategies to increase scale up are essential if we are going to successfully achieve the end of HIV/AIDS on a global scale.

Research sponsored and/or conducted by the United States National Institutes of Health (NIH) has and continues to provide much of the essential HIV prevention and treatment tools that need to be implemented to end the HIV pandemic. Landmark prospective clinical studies, including HPTN 052 (*4*–*5*), Partners of People on ART—A New Evaluation of the Risks (PARTNER) 1 and 2 (*6*–*7*), and Opposites Attract (*8*), have demonstrated treatment as prevention (TasP) as a critical tool in the prevention toolbox along with voluntary medical male circumcision, condoms, HIV testing/counseling, screening of the blood supply, and syringe exchange services. A significant tool in preventing HIV infection with ART is pre-exposure prophylaxis (PrEP), with optimal/consistent use of PrEP being about 99% effective in preventing sexual acquisition of HIV (*9*). The HIV treatment toolbox includes more than 30 antiretroviral drugs currently approved by the US Food and Drug Administration for treating HIV infection. There are 13 single-drug combinations of 2 or more antiretroviral drugs which can be administered, with limited toxicity, in one-tablet simplified regimens. The consistent use of ART has resulted in near-normal life expectancies for individuals newly diagnosed with HIV (*10*). While providing ART to everyone living with HIV and providing PrEP to all individuals at-risk of HIV acquisition could theoretically end the epidemic, there is a significant gap that must be bridged in the implementation of the existing HIV prevention and treatment tools (*11*). There is an underlying need for programs at both a national and global level to optimize the integration of these tools into real-world settings reflecting locally relevant social, cultural, and structural norms.

Transformative programs including the President's Emergency Plan for AIDS Relief (PEPFAR) and the Global Fund to Fight AIDS, Tuberculosis and Malaria continue to maximally implement the existing HIV treatment regimens and prevention strategies throughout the developing world. These efforts are having a significant impact in preventing new HIV infections, providing ART to persons with HIV and achieving viral suppression, and building the health system infrastructure in many countries severely impacted by the HIV pandemic. However, there remains a global HIV treatment gap of roughly 12.4 million persons with HIV who are not receiving ART in 2019 (*1*), as well as an HIV prevention gap with only an estimated 575,000–580,000 PrEP users

worldwide—representing a significant underutilization of this effective prevention strategy (*12*). This latter figure is far below the 2020 UNAIDS target of 3 million PrEP users globally (*13*). The challenge is to scale-up the uptake of PrEP for at-risk uninfected individuals and provide ART and achieve viral suppression in individuals with HIV. Recent modeling analyses indicate that the COVID-19 pandemic could significantly impact HIV prevention services and disrupt the supply chain of ART resulting in a significant increase in HIV incidence and HIV-associated deaths, especially in high-burden, low- and middle-income nations (*3*, *14*). More must be done at the local, regional, and national levels to successfully meet these challenges.

On a national level, the latest statistics from the United States Centers for Disease Control and Prevention (US CDC) indicated that in 2018 there were 1.2 million individuals with HIV, of whom about 14% were unaware of their HIV infection; 37,968 newly diagnosed HIV infections, with 21% of these among youths 13–24 years of age and 26% among adults 25–34 years of age; and the greatest burden of HIV among men who have sex with men (MSM), Blacks/African Americans (*15*). CDC also reports that in that same year there were 1.2 million individuals in the United States who were at substantial risk for HIV and should be offered PrEP; however, only 219,700 individuals were prescribed PrEP, resulting in a PrEP gap of approximately 900,000 individuals (*16*).

Facing these daunting statistics, the Trump Administration and key government health officials developed a nationwide initiative entitled, "Ending the HIV Epidemic: A Plan for the United States". This plan was launched in 2019. The goal of this multifaceted "Ending the HIV Epidemic" (EHE) program is to decrease the number of incident HIV infections by 75% in 5 years and by 90% by 2030. The plan is focused on 4 key strategies: 1) diagnose all people with HIV as early as possible; 2) treat people rapidly after diagnosis and effectively reach sustained viral suppression; 3) prevent new HIV transmissions using evidence-based interventions, including PrEP and syringe services programs; and 4) respond quickly to potential outbreaks and emerging clusters of infection (*17*). The scientific basis for this initiative leverages the significant scientific advances during the past 4 decades that have and continue to provide new and improved HIV diagnostics, therapeutics, and vaccine candidates in the HIV prevention and treatment toolboxes.

The EHE initiative is based on an HIV vulnerability profile including both demographic populations and geographic hotspots. In the United States, demographically 13% of the population is Blacks/African Americans. CDC reports that 43% of all new HIV diagnoses are among Blacks/African Americans with 60% of new HIV infections among MSM in this population and 75% of new HIV infections in individuals under 35 years of age (*15*). There also is a geographic concentration as the majority (>50%) of new HIV cases reported in 2016 and 2017 were in 48 of the 3007 counties in the United States, Washington D.C., and Puerto Rico, as well as in 7 states with a disproportionate occurrence of HIV in rural areas (*17*).

Multiple agencies of the United States Department of Health and Human Services (HHS) are cooperating in this initiative including the NIH, US CDC, Health Resources and Services Administration (HRSA), Indian Health Service (IHS), and Substance Abuse and Mental Health Services Administration (SAMHSA). This effort is coordinated by the HHS Office of the Assistant Secretary of Health. Each agency plays a vital role in this multi-HHS agency initiative with CDC intensifying its existing programs in cooperation with local and state health departments for HIV testing, diagnosis, and epidemiologic surveillance and providing rapid linkage to HRSA Ryan White HIV/AIDS Program centers for comprehensive health care. HRSA also accelerates these program centers for HIV treatment and care, as well as providing PrEP for at-risk individuals through its Health Centers Program. The IHS focuses its activities on urban and rural tribal communities. SAMHSA expands use of its Minority AIDS Program and Substance Abuse Prevention and Treatment grants for HIV prevention among individuals with substance abuse or mental illness (*17*).

The NIH Centers for AIDS Research (CFAR) and AIDS Research Centers (ARCs) serve a critical role in the EHE initiative by informing HHS partners of the best evidence-based state-of-the-art practices resulting from implementation science studies, as well as compiling and disseminating data on the effectiveness of prevention and treatment practices. The 19 CFARs and 7 ARCs are co-located in many of the jurisdictions included in this phase of the initiative (*17*). These CFAR projects build on close collaborations with local health officials and community groups to design and test implementation strategies reflecting demographic and geographic challenges unique to the local jurisdictions. These studies focus on planning optimal

delivery of evidence-based HIV prevention interventions, including PrEP for individuals at-risk for HIV, and rapid linkage/relinkage to treatment and health care services for those individuals with HIV (*18*).

The successful achievement of the EHE initiative in the United States and those in other countries will require optimal implementation of the existing tools in the HIV prevention and treatment toolboxes, as well as the development of new and improved strategies including a safe and effective vaccine and an HIV cure. The ultimate goal of ending the HIV pandemic will require cooperation across the spectrum of the scientific community, industry partners, funders, and civil society at the individual, national, and ultimately, the global levels.

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[#] Corresponding author: Anthony S. Fauci, afauci@niaid.nih.gov.

[1] United States National Institutes of Health, Chicago, USA.

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Anthony S. Fauci, M.D.
Director
National Institute of Allergy and Infectious Diseases (NIAID)
United States National Institutes of Health (NIH)

Robert W. Eisinger, Ph.D.
Former Acting Director
Office of AIDS Research (OAR)
United States National Institutes of Health (NIH)

Profiles

Wenhua Zhao, China CDC's Chief Expert of Nutrition

Peter Hao[1,&]; Nankun Liu[1,&]; Zhenjun Li[1]; Jingjing Xi[1,#]; Feng Tan[1,#]

Wenhua Zhao is the China CDC's Chief Expert of Nutrition and the Chairwoman of the Society for Noncommunicable Diseases (NCDs) Control and Prevention, Chinese Preventive Medicine Association (CPMA). She has been working in public health for almost four decades and has expertise in nutrition, epidemiology, and NCD control and prevention.

Zhao received her Bachelor of Medicine degree from Beijing Medical College in 1983 majoring in public health. She was then assigned to the Shunyi District CDC in Beijing as a Food Hygiene Inspector. She became the Deputy Director of this district-level CDC at age twenty-nine. In 1995, she received her Master of Nutrition degree from the University of the Philippines and later in 2003, a Ph.D. in Nutrition from Kagawa Nutrition University of Japan.

Zhao moved to China CDC (formally known as Chinese Academy of Preventive Medicine, CAPM) in 1996 and since then has made significant contributions to China's public health, particularly in the areas of nutrition epidemiology and dietary assessment methods; national nutrition and NCDs surveillance; obesity and the intervention strategies in China; diabetes and related risk factors; and policy research, health promotion, and education on balanced diet and active lifestyle.

Zhao frequently overcame challenges in adapting international standards to local Chinese settings. For example, differences in food cultures made the Food Frequency Questionnaire (FFQ), a well-established method based on western dietary habits, incapable of being directly applied in China in the 1990s. By 1996, Zhao addressed this problem by leading the establishment of the Chinese Food Frequency Questionnaire (CFFQ) for adults, and the reproducibility and validity of CFFQ was assessed and available by 2000. The CFFQ was successfully applied as the first large-scale epidemiological survey on nutrition and NCDs, which was named the China National Nutritional and Health Survey (CNHS) in 2002 and continued in 2012 and 2015, and was included in the National NCDs Surveillance since 2010.

Zhao has been involved in several national nutrition and NCDs surveillance systems since 2002. For instance, as the Field Director in the 2002 CNHS, she led completion of protocol development, the training of local research teams, quality control, data analysis, project management and coordination, and the completion of the final report issued by The Information Office of the State Council of China.

Based on the 2002 CNHS, Zhao published the first monograph of blood lipid profiles, "*Blood Lipid Profile and Prevalence of Dyslipidemia in Chinese Adults*". The monograph also promoted the publication of the first edition of *Chinese Guidelines for the Management of Dyslipidemia in Adults* in 2007.

Zhao has also focused on obesity since 1996, which became one of her key research areas. Her related work provided significant information, such as using waist circumference (WC) as a simpler indicator to predict the risk of central-obesity-related hypertension and diabetes in 2000. For an intervention of childhood obesity, she established the "Nutrition School" pilot program in Shunyi District, Beijing in 2016, and the program subsequently expanded rapidly to 8 provinces by 2017.

Zhao also focused on a community-based study on maintaining healthy body weight by multisectoral collaboration to promote physical activities for the public. She was the Chief Editor of the *Physical Activity Guidelines for Chinese Adults*, issued by the Bureau for Disease Control and Prevention of China's Ministry of Health (now the National Health Commission) in 2011. She was also the co-author of a national standard: the Criteria of Weight for Adults in China (WS/T 428-2013).

In 2010, as the Director of National Working Group of the 2010 China Chronic Disease and Behavior Risk Factors Surveillance, Zhao collaborated with Dr. Guang Ning and his team in Shanghai Ruijin Hospital to jointly complete the Diabetes Epidemiology Study, which covered 162 counties in 31 provincial-level administrative divisions (PLADs) and involved almost 100,000 adults in China. This surveillance led to a publication in JAMA in

2013. It was a remarkable exploration of the collaboration between China CDC and a hospital in the medical system. The research had provided fundamental techniques and experiences for the establishment of the China NCDs Control and Prevention Plan and Healthy China 2030 strategies. Zhao also published the first monograph on the national population distribution of body-mass index (BMI), prevalence of obesity, and 10 years changes among different age groups in China: *Present Status of Overweight and Obesity and 10 Years Changes in China*.

Zhao also contributed to international public health community. In 2003 and 2004, as a short-term consultant to the World Health Organization (WHO), she provided technical support to the National Food Consumption Survey in Papua New Guinea. She now is a member of WHO and United Nations Children's Fund (UNICEF) Technical Expert Advisory group on nutrition Monitoring (TEAM).

Zhao has extensive experience in policy research, health promotion, and education on balanced diet and active lifestyles nationally and internationally. She has supported national policymaking on NCDs control and prevention, e.g. in the "Health Lifestyle for All" program initiated in 2007 and a joint program by Shandong Province and the Ministry of Health of China on "Salt Reduction" in 2011. In 2020, as the China CDC's Chief Expert of Nutrition, Zhao emphasized the importance of a balanced diet in response to the coronavirus disease 2019 (COVID-19) pandemic in the Press Conference of the Joint Prevention and Control Mechanism of the State Council. Her livestreamed lectures were viewed over 10 million times.

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[#] Corresponding authors: Jingjing Xi, xijj@chinacdc.cn; Feng Tan, tanfeng@chinacdc.cn.

[1] Chinese Center for Disease Control and Prevention, Beijing, China.
[&] Joint first authors.

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Notifiable Infectious Diseases Reports

Reported Cases and Deaths of National Notifiable Infectious Diseases — China, August, 2020

Diseases	Cases	Deaths
Plague	2	2
Cholera	5	0
SARS-CoV	0	0
Acquired immune deficiency syndrome	5,166	1,560
Hepatitis	126,950	42
Hepatitis A	1,401	0
Hepatitis B	102,304	30
Hepatitis C	20,520	11
Hepatitis D	19	0
Hepatitis E	1,759	0
Other hepatitis	947	1
Poliomyelitis	0	0
Human infection with H5N1 virus	0	0
Measles	119	0
Epidemic hemorrhagic fever	313	2
Rabies	23	15
Japanese encephalitis	69	2
Dengue	55	0
Anthrax	39	0
Dysentery	7,270	0
Tuberculosis	76,423	131
Typhoid fever and paratyphoid fever	830	0
Meningococcal meningitis	4	0
Pertussis	142	0
Diphtheria	1	0
Neonatal tetanus	3	0
Scarlet fever	763	0
Brucellosis	4,972	0
Gonorrhea	10,724	0
Syphilis	46,838	9
Leptospirosis	51	0
Schistosomiasis	10	0
Malaria	57	0
Human infection with H7N9 virus	0	0
COVID-19*	721	0
Influenza	12,833	0
Mumps	9,008	0

Continued

Diseases	Cases	Deaths
Rubella	96	0
Acute hemorrhagic conjunctivitis	2,561	0
Leprosy	39	0
Typhus	138	0
Kala azar	18	0
Echinococcosis	283	0
Filariasis	0	0
Infectious diarrhea[†]	109,407	2
Hand, foot and mouth disease	59,143	1
Total	**475,076**	**1,766**

[*] The data were from the website of the National Health Commission of the People's Republic of China.
[†] Infectious diarrhea excludes cholera, dysentery, typhoid fever and paratyphoid fever.
The number of cases and cause-specific deaths refer to data recorded in National Notifiable Disease Reporting System in China, which includes both clinically-diagnosed cases and laboratory-confirmed cases. Only reported cases of the 31 provincial-level administrative divisions in the mainland of China are included in the table, whereas data of Hong Kong Special Administrative Region, Macau Special Administrative Region, and Taiwan are not included. Monthly statistics are calculated without annual verification, which were usually conducted in February of the next year for de-duplication and verification of reported cases in annual statistics. Therefore, 12-month cases could not be added together directly to calculate the cumulative cases because the individual information might be verified via National Notifiable Disease Reporting System according to information verification or field investigations by local CDCs.

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