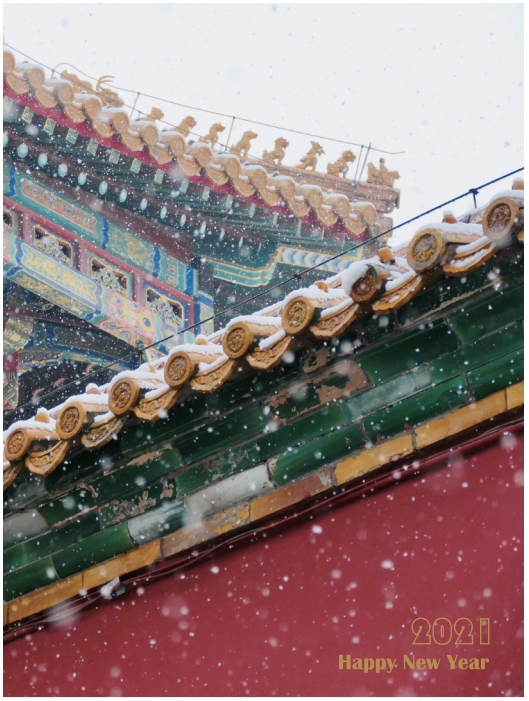
ISSN 2096-7071
CN 10-1629/R1

CHINA CDC WEEKLY

Vol. 3 No. 1 Jan. 1, 2021

CCDC weekly

中国疾病预防控制中心周报



ISSN 2096-7071
9 772096 707217 01>

Cover Photo: Adapted by Xin Zhang, Beijing Gloryway Medical Ltd., Co.

Notes from the Field

The First Case of New Variant COVID-19 Originating in the United Kingdom Detected in a Returning Student — Shanghai Municipality, China, December 14, 2020

Hongyou Chen[1,&]; Xiaoyan Huang[1,&]; Xiang Zhao[2]; Yang Song[2]; Peter Hao[3]; Hui Jiang[1]; Xi Zhang[1]; Chen Fu[1,#]

On December 14, 2020, a 23-year-old female returning from the United Kingdom (UK) via airplane was tested by the laboratory of Shanghai Customs using nose swab to test for coronavirus disease 2019 (COVID-19). At 20:30 on December 14, Shanghai CDC received notification from the Shanghai Customs that the patient tested positive for COVID-19. By 22:00, the patient was transported by ambulance from the isolation point to the fever clinic of Jiading District Central Hospital. Due to travel history from the UK and abnormalities in nucleic acid test results, the hospital organized a consultation with experts and formed a recommendation to transfer the patient to Fudan University's Public Health Clinical Center for further diagnosis and treatment, which was carried out the following day. On December 15, Jiading District CDC retested using a nasopharyngeal swab sample and the nucleic acid result was positive for COVID-19.

An epidemiological investigation revealed that the patient had a negative COVID-19 test result on December 12, 2020, two days before her flight to return to China. According to her statement, she had no exposure to symptomatic individuals and had not purchased or been exposed to frozen food products or raw meat. While remaining in the UK, the patient described running in a nearby park without wearing a mask and taking off her mask to eat and drink while waiting to board the plane. These are all potential situations for exposure, especially with 1.86 million confirmed cases of COVID-19 having been reported in the UK as of December 15, 2020. At the time of case report, the patient was diagnosed as a mild case according to the epidemiological investigation, symptoms and laboratory test.

On December 24, the sample of the COVID-19 patient was sequenced using MGI MGISEQ-200 platform (Sequence ID: NC20SCU2740-1). This strain was dissimilar with the previous Shanghai strain detected in the Shanghai outbreak in November, suggesting different route of transmission (*1*) (Figure 1). Compared with the Wuhan reference sequence (EPI_ISL_ 402119) (*2*), this new Shanghai strain showed 32 nucleotide variation sites, containing the single nucleotide polymorphisms (SNPs) that defined L-lineage European branch I. This Shanghai strain shared all 28 variation sites (C241T, C913T, C3037T, C3267T, C5388A, C5986T, T6954C, C14408T, C14676T, C15279T, T16176C, A23063T, C23271A, A23403G, C23604A, C23709T, T24506G, G24914C, C27972T, G28048T, A28111G, G28280C, A28281T, T28282A, G28881A, G28882A, G28883C, and C28977T) that were first detected in the VUI202012/01 (Pangolin lineage B.1.1.7) variant from the UK (*3*–*4*). It also had 2 specific variation sites (C3177T, A28271del), from which site C3177T was also detected in the VUI202012/01 variants that has been circulating since late October in the UK (Figure 1). Just like the other VUI202012/01 variants, the Shanghai strain also had 3 amino acid deletions (H69del, V70del and Y144del) and 7 amino acid mutations (N501Y, A570D, D614G, P681H, T716I, S982A and D1118H) in the spike protein. The Shanghai strain NC20SCU2740-1 is the first imported VUI202012/01 variant in China and poses a great potential threat to the prevention and control of COVID-19 in China.

Several control measures have been implemented in the response to this case. The patient has been transferred to the designated medical institution for isolation and treatment. Due to the closed-loop management upon passenger's arrival at the airport, close contact investigation has been initiated according to national and municipal work plans: 1) close contacts currently include passengers with seats in the same row, passengers within 3 rows of seats of the patient, and flight attendants providing cabin services to that section; 2) medical personnel at the point of isolation and at the central hospital are not deemed closed contacts due to the effective personal protective

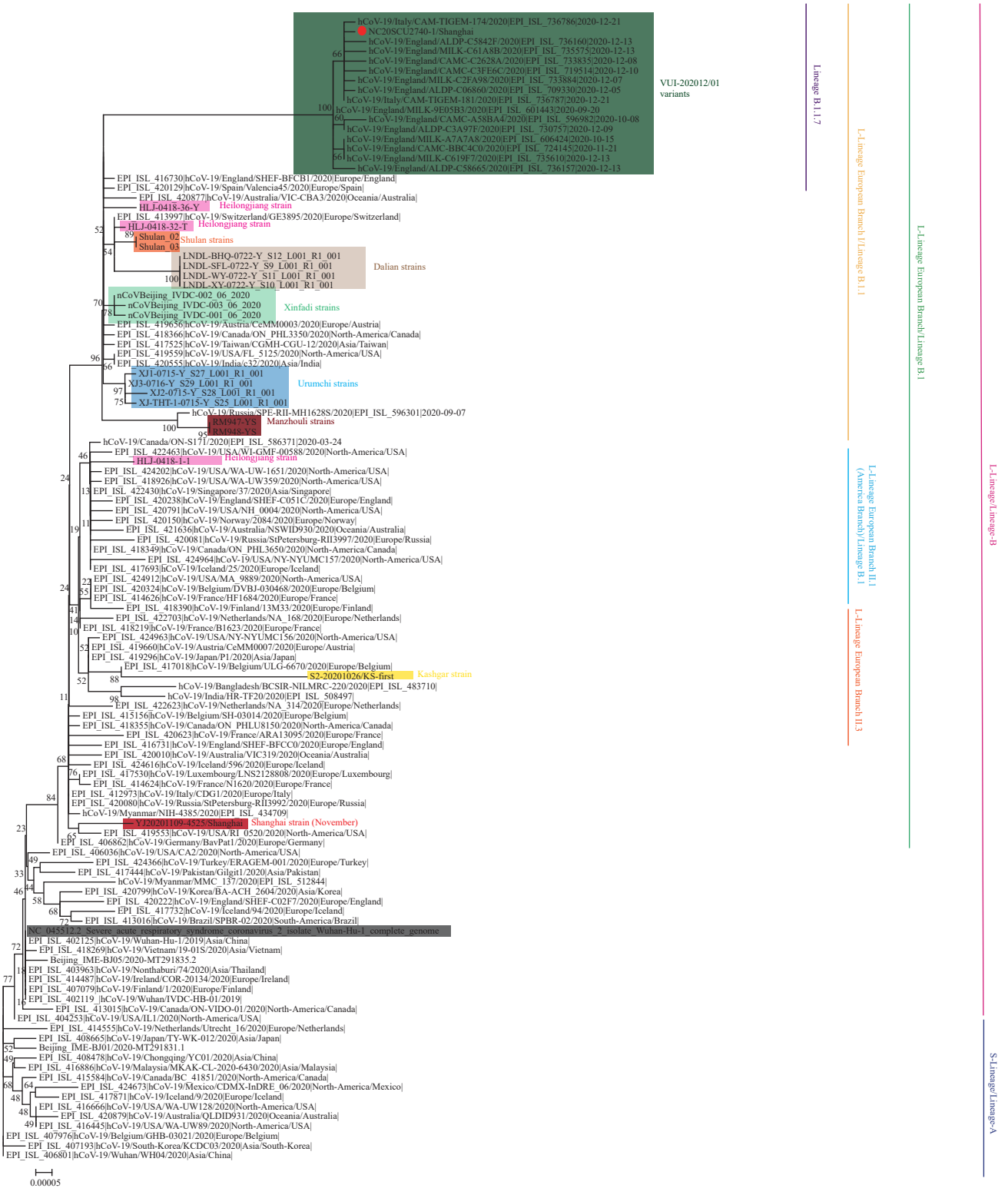


FIGURE 1. Phylogenetic tree based on the full-length genome sequences of the COVID-19 virus.
The VUI-202012/01 variants are highlighted in dark green and the first imported VUI-202012/01 variant of China detected in Shanghai is indicated by a red dot. The strains associated with specific outbreaks in China are as follows: Manzhouli City (burgundy/darker red); Shanghai Municipality in November (red); Kashgar Prefecture (yellow); Urumchi City (blue); Beijing Municipality Xinfadi Wholesale Market (light green); northeastern China including Heilongjiang Province (pink) and Shulan (orange) related to imported cases; Dalian City (brown); Wuhan City in December 2019 (dark gray). The S(A)- or L(B)-lineage and sublineages of the COVID-19 virus were marked and colored on the right.

measures; and 3) other possible close contacts are being investigated. Specific venues associated with the patient are being comprehensively disinfected. Experts have been assembled to supervise relevant work including disinfection, personal protection, and nosocomial infection control in areas in the medical facilities.

doi: 10.46234/ccdcw2020.270

[#] Corresponding author: Chen Fu, fuchen@scdc.sh.cn.

[1] Shanghai Municipal Center for Disease Control and Prevention, Shanghai, China; [2] National Institute for Viral Disease Control and Prevention, China CDC, Beijing, China; [3] Chinese Center for Disease Control and Prevention, Beijing, China.
[&] Joint first authors.

Submitted: December 28, 2020; Accepted: December 29, 2020

REFERENCES

1. Fang FH, Song Y, Hao LP, Nie K, Sun XD. A case of COVID-19 detected in a cargo worker at Pudong Airport — Shanghai Municipality, China, November 8, 2020. China CDC Wkly 2020;2(47):910. http://dx.doi.org/10.46234/ccdcw2020.246.
2. Wu F, Zhao S, Yu B, Chen YM, Wang W, Song ZG, et al. A new coronavirus associated with human respiratory disease in China. Nature 2020;579(7798):265. http://dx.doi.org/10.1038/s41586-020-2008-3.
3. Rambaut A, Holmes EC, O'Toole Á, Hill V, McCrone JT, Ruis C, et al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assistgenomic epidemiology. Nat Microbiol 2020. http://dx.doi.org/10.1038/s41564-020-0770-5.2.
4. European Centre for Disease Prevention and Control, Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom– 20 December 2020. ECDC: Stockholm; 2020. https://www.ecdc.europa.eu/sites/default/files/documents/SARS-CoV-2-variant-multiple-spike-protein-mutations-United-Kingdom.pdf.

Methods and Applications

Establishment and Application of Heminested RT-PCR Assay for Detection of Mosquito-Borne Flavivirus — Guizhou Province, China, 2018

Zhijing Xue[1,2]; Ning Zhao[1]; Jun Wang[1]; Xiuping Song[1]; Fengxia Meng[1]; Wenqin Liang[3]; Jingzhu Zhou[3]; Dan Wang[3]; Zhong Zhang[4,5,#]; Qiyong Liu[1,#]

ABSTRACT

Introduction: Mosquito-borne flavivirus can lead to serious infectious diseases worldwide and cause high mortality and disability. In order to strengthen epidemiological investigation of flavivirus and meet the needs of early warning of diseases, a simple, rapid, and sensitive detection method needs to be established to prevent and control mosquito-borne diseases.

Methods: Using the NS5 gene of flavivirus in GenBank, 3 universal primers targeting the conserved regions were designed. The complementary DNAs (cDNAs) of Japanese encephalitis virus (JEV), dengue virus (DENV), West Nile virus (WNV), and yellow fever virus (YFV) were used as the template to optimize the reaction conditions. A heminested reverse-transcriptase polymerase chain reaction (hnRT-PCR) was established to verify the sensitivity and specificity of this method and to detect field-caught mosquitoes.

Results: Our results showed that this method exhibited better specificity, higher sensitivity, and the ability to detect multiple viruses simultaneously. The lowest detection limit of JEV, DENV-2, YFV, and WNV was 3×10^4, 3×10^6, 3×10^5, and 3×10^4 copies/μL, respectively. Mosquito-borne flavivirus was successfully detected in the field-caught mosquito samples using the method established in this study.

Discussion: The hnRT-PCR method established in this study can be employed for the rapid detection of flavivirus and provide technical support for early and rapid diagnosis of mosquito-borne flavivirus.

INTRODUCTION

Mosquito-borne viruses can be transmitted through mosquito bites on sensitive vertebrates and cause natural-focus infection diseases worldwide (*1*). Flavivirus is one of the most important mosquito-borne viruses, including Japanese encephalitis virus (JEV), dengue virus (DENV), West Nile virus (WNV), yellow fever virus (YFV), etc., which can lead to fever, headache, hemorrhagic fever, and encephalitis (*2*). Flaviviruses therefore are responsible for considerable morbidity and mortality and have become a serious public health problem worldwide (*3*).

It was reported that dengue fever was endemic in more than 100 countries worldwide, threatening the health of more than 2.5 billion people (*4*). JE had occurred everywhere in China except for Xinjiang, Tibet, and Qinghai, and it was the most harmful mosquito-borne infectious disease with high morbidity and mortality (*3*). WNV was imported into New York city in 1999 and spread widely in the neighboring states for 5 years (*5*). In recent years due to global warming, the rapid development of tourism, and continuous changes in the ecological environment, the incidence of mosquito-borne diseases has been on the rise, which brings new challenges to the prevention and control of mosquito-borne diseases (*6*). Therefore, efficient detection and diagnosis of mosquito-borne viruses is urgently needed to prevent and control mosquito-borne diseases. Currently, conventional flavivirus diagnostic methodologies include virus isolation and culturing methods, serological methods, and nucleic acid detection methods. However, virus culture is relatively laborious and time-consuming, and serological methods lack of specificity and are prone to cross-reactions between viruses (*7*–*8*). Compared with traditional virus isolation and serological methods, nucleic acid detection technology has unique advantages in early detection of mosquito-borne viruses.

METHODS

Primer Design

The complete genomic sequences of mosquito-borne flavivirus were downloaded from the GenBank

database and aligned using the Clustal W program (Table 1). A stretch of nucleotides conserved in the strains was identified and the primers were designed using the Primers Express software. The primer sequences and characteristics are shown in Table 2.

Viruses, Viral RNA Extraction, and Reverse Transcription

Viral strains, including JEV, DENV-2, YFV, WNV, Sindbis virus (SINV), and chikungunya virus (CHIKV), were provided by the National Institute for Viral Disease Control and Prevention of China CDC. Viral RNA was extracted using the Rneasy MiNi Kit (QIAGEN, Germany) and used directly for complementary DNA (cDNA) synthesis using QuantiNova^{TM} Reverse Transcription Kit (QIAGEN, Germany) according to the manufacturer's recommendations. Flaviviruses NS5 gene fragments were amplified from cDNA employing the oligonucleotide primers shown in Table 2. The amplicons were purified (TransGen, Beijing, China) and then each cDNA was cloned into the pEASYR-T1 Simple Cloning Vector (TransGen, Beijing, China) and transformed into *E. coli* Trans1-T1 cells. Plasmid DNAs were purified using the EasyPureR Plasmid MiniPrep Kit (TransGen, Beijing, China) according to the manufacturer's instructions. The DNAs were quantified by a NanoDrop-1000 spectrophotometry (Thermo Fisher Scientific, USA). The copy numbers of the DNA were calculated based on the concentration, and 10-fold serial dilutions of this DNA from 10^9 to 10^0 copies per reaction were used as a standard in all heminested reverse transcriptase polymerase chain reactions (hnRT-PCR).

Sensitivity and Specificity of the hnRT-PCR Assay

The analytical sensitivity of the hnRT-PCR assay was determined by quantification with external standards using serially diluted plasmids (10^9–10^0 copies/μL) containing JEV, DENV-2, WNV, and YFV. For specificity testing, we used cDNA of JEV, DENV-2, YFV, WNV, SINV, and CHIKV. We also used mosquito samples spiked with cDNA of JEV, DENV-2, YFV, and WNV, and the cDNA of mosquito samples was used as control.

Field-caught Mosquitoes

Mosquito samples were collected at different sites in Guizhou Province between July to August 2018. The collected mosquitoes were frozen and identified quickly and then pooled by species into groups of up 50 individuals. Viral RNAs were extracted and reverse transcribed into cDNA and the hnRT-PCR was performed using designed primers shown in Table 2.

RESULTS

In order to determine the sensitivity of the hnRT-PCR, we examined the lowest detection limits with external standards employing serial dilutions of quantified plasmid DNAs. The lowest detection limits in the first round PCR for JEV, YFV, and WNV were 3×10^7, 3×10^9, and 3×10^7 copies/μL. DENV-2 had never been detected. In the second round PCR, there was a substantial increase in sensitivity and the lowest detection limits of JEV, DENV-2, YFV, and WNV were 3×10^4, 3×10^6, 3×10^5, and 3×10^4 copies/μL, respectively (Figure 1). Therefore, through two rounds of amplification, the sensitivity of hnRT-PCR was increased 10,000 times, which greatly improved the sensitivity and made up for the possibility that conventional PCR could not be detected. For specificity testing, we used cDNA of JEV, DENV-2, YFV, WNV, SINV, and CHIKV. We also used mosquito samples spiked with cDNA of JEV, DENV-2, YFV, and WNV (JEV+mosquito cDNA, DENV-2+mosquito cDNA, YFV+mosquito cDNA, and WNV+mosquito cDNA), and cDNA of mosquito samples as control. The results showed that only the target bands appeared in the flavivirus and that no bands appeared in the control, suggesting that the test was 100% specific for the detection of flavivirus (Figure 2).

Overall, a total of 96 pools of mosquitoes belonging to 4 species of 3 genera were used to examine the sensitivity of the hnRT-PCR assay. Among all mosquitoes collected, 34% were *Culex tritaeniorhynchus*, 2.3% were *Culex pipiens pallens*, 24.7% were *Anopheles sinensis*, and 39% were *Armigeres subalbatus*. JEV was detected in 2 mosquito pools out of 96 from *Culex tritaeniorhynchus* and *Armigeres subalbatus*. One was identified as type JEV-Ⅰ isolated from *Culex tritaeniorhynchus*, and the other was identified as type JEV-Ⅲ isolated from *Armigeres subalbatus*.

DISCUSSION

Flaviviruses are single-stranded RNA viruses with

TABLE 1. Sequence alignment of oligonucleotide XF-F1, XF-F2, and XF-R with 36 flavivirus NS5 gene conserved regions.

	Sequence of oligonucleotide[*,†]		
Region	**XF-F1 (8916−8938)**	**XF-F2 (8964−8985)**	**XF-R (9153−9178)**
Primer	AACATGATGGGVAARMGWGARAA	AARGGMAGYMGNGCHATHTGGT	GTRTCCCANCCDGCDGTRTCATCNGC
Nakayama	AACATGATGGGAAAAAGAGAGAA	AAGGGAAGCAGGGCCATTTGGT	GCTGATGATACCGCCGGGTGGGACAC
SA(A)	- - - - - - - - - - - A- - AA-A- - G- -	- - A- - A- - CA- G- - C- - T- - - -	- - T- - - - - T- - C- - C- - G- - - - - C- -
Beijing-1	- - - - - - - - - - - A- - AA- A- - A- -	- - A- - A- - CA- G- - C- - T- - - -	- - T- - - - - T- - C- - T- - G- - - - - C- -
GP78	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - A- - CA- G- - C- - C- - - -	- - T- - - - - C- - C- - C- - G- - - - - C- -
HVI	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - A- - CA- G- - C- - T- - - -	- - T- - - - - T- - C- - C- - G- - - - - C- -
JaGAr01	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - A- - CA- G- - C- - T- - - -	- - T- - - - - T- - C- - C- - G- - - - - C- -
JaOArS982	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - A- - CA- G- - C- - T- - - -	- - T- - - - - C- - C- - C- - A- - - - - C- -
K94P05	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - A- - CA- G- - C- - T- - - -	- - C- - - - - C- - C- - C- - G- - - - - C- -
SA-14	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - A- - CA- G- - C- - T- - - -	- - T- - - - - T- - C- - C- - G- - - - - C- -
HawO3663	- - - - - - - - - - - A- - GA- A- - G- -	- - A- - A- - TC- C- - A- - A- - - -	- - A- - - - - C- - A- - C- - A- - - - - C- -
71/02GZ	- - - - - - - - - - - A- - GA- A- - G- -	- - A- - A- - TC- C- - A- - A- - - -	- - A- - - - - C- - A- - C- - A- - - - - C- -
Nauru Island	- - - - - - - - - - - A- - GA- A- - G- -	- - A- - A- - TC- C- - A- - A- - - -	- - A- - - - - C- - A- - C- - A- - - - - C- -
16681	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - C- - CA- A- - C- - A- - - -	- - C- - - - - C- - C- - A- - A- - - - - C- -
New Guinea C	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - C- - CA- A- - C- - A- - - -	- - C- - - - - C- - C- - A- - A- - - - - C- -
PUO-218	- - - - - - - - - - - A- - AA- A- - G- -	- - A- - C- - CA- A- - C- - A- - - -	- - C- - - - - C- - C- - A- - A- - - - - C- -
H87	- - - - - - - - - - - C- - GA- A- - G- -	- - A- - C- - TA- G- - T- - A- - - -	- - T- - - - - C- - A- - C- - T- - - - - C- -
80-2	- - - - - - - - - - - C- - GA- A- - G- -	- - A- - C- - TA- G- - T- - A- - - -	- - T- - - - - C- - A- - C- - T- - - - - C- -
P4	- - - - - - - - - - - A- - AC- T- - G- -	- - G- - A- - CC- A- - A- - C- - - -	- - T- - - - - C- - A- - A- - C- - - - - C- -
P75-215	- - - - - - - - - - - A- - AC- T- - G- -	- - A- - A- - CC- G- - A- - T- - - -	- - T- - - - - C- - A- - A- - T- - - - - C- -
11070	- - - - - - - - - - - A- - AC- T- - G- -	- - G- - A- - CC- A- - A- - C- - - -	- - T- - - - - C- - A- - A- - C- - - - - C- -
serum	- - - - - - - - - - - A- - GA- A- - G- -	- - G- - A- - CA- A- - C- - T- - - -	- - T- - - - - C- - A- - T- - C- - - - - C- -
FtC-3699	- - - - - - - - - - - A- - GA- A- - G- -	- - G- - A- - CA- A- - C- - T- - - -	- - T- - - - - C- - A- - T- - C- - - - - C- -
385-99	- - - - - - - - - - - A- - GA- A- - G- -	- - G- - A- - CA- A- - C- - T- - - -	- - T- - - - - C- - A- - T- - C- - - - - C- -
ARC13-12	- - - - - - - - - - - A- - GA- A- - G- -	- - G- - A- - CA- A- - C- - T- - - -	- - T- - - - - C- - A- - T- - C- - - - - C- -
Chin-01	- - - - - - - - - - - G- - GA- A- - A- -	- - G- - A- - CA- A- - C- - A- - - -	- - T- - - - - C- - A- - T- - C- - - - - C- -
33-G8	- - - - - - - - - - - A- - GA- A- - G- -	- - A- - C- - CA- A- - C- - C- - - -	- - T- - - - - T- - C- - A- - C- - - - - C- -
HNY1999	- - - - - - - - - - - A- - GA- A- - G- -	- - G- - A- - CA- A- - C- - T- - - -	- - T- - - - - C- - A- - T- - C- - - - - C- -
17D vaccine	- - - - - - - - - - - G- - AA- A- - G- -	- - G- - A- - CC- T- - C- - A- - - -	- - G- - - - - C- - C- - T- - A- - - - - C- -
French viscerotropic	- - - - - - - - - - - G- - AA- A- - G- -	- - G- - A- - CC- T- - C- - A- - - -	- - G- - - - - C- - C- - T- - A- - - - - C- -
17D vaccine	- - - - - - - - - - - G- - AA- A- - G- -	- - G- - A- - CC- T- - C- - A- - - -	- - G- - - - - C- - C- - T- - A- - - - - C- -
17DD	- - - - - - - - - - - G- - AA- A- - G- -	- - G- - A- - CC- T- - C- - A- - - -	- - G- - - - - C- - C- - T- - A- - - - - C- -
17D-213	- - - - - - - - - - - G- - AA- A- - G- -	- - G- - A- - CC- T- - C- - A- - - -	- - G- - - - - C- - C- - T- - A- - - - - C- -
85-82H	- - - - - - - - - - - G- - AA- A- - G- -	- - A- - A- - CC- T- - C- - C- - - -	- - G- - - - - T- - C- - T- - G- - - - - C- -
French viscerotropic	- - - - - - - - - - - G- - AA- A- - G- -	- - G- - A- - CC- T- - C- - A- - - -	- - G- - - - - C- - C- - T- - A- - - - - C- -
Trinidad 79A	- - - - - - - - - - - G- - AA- A- - G- -	- - G- - A- - CC- T- - C- - A- - - -	- - G- - - - - C- - C- - T- - A- - - - - C- -
French viscerotropic virus	- - - - - - - - - - - G- - AA- A- - G- -	- - G- - A- - CC- T- - C- - A- - - -	- - G- - - - - C- - C- - T- - A- - - - - C- -

[*] N=A+G+C+T, V=G+A+C, R=A+G, M=A+C, W=A+T, Y=C+T, H=A+T+C, D=G+A+T.

[†] DNA sequence were obtained from the GenBank databases. Accession numbers are as follows: Nakayama, EF571853.1; SA(A), D90195.1; Beijing-1, L48961.1; GP78, AF075723.1; HVI, AF098735.1; JaGAr01, AF069076.1; JaOArS982, M18370.1; K94P05, AF045551.2; SA-14, M55506.1; HawO3663, DQ672564.1; 71/02GZ, EF025110.1; Nauru Island, U88535.1; 16681, U87411.1; New Guinea C, AF038403.1; PUO-218, AF038402.1; H87, M93130.1; 80-2, AF317645.1; P4, AY648301.1; P75-215, EF457906.1; 11070, M14931.2; serum, AY646354.1; FtC-3699, KR868734.1; 385-99, AY842931.3; ARC13-12, KM012188.1; Chin-01, AY490240.2; 33-G8, M12294.2; HNY1999, AF202541.1; 17D vaccine, X03700.1; French viscerotropic, U21056.1; 17D vaccine, NC_002031.1; 17DD, U17066.1; 17D-213, U17067.1; 85-82H, U54798.1; French viscerotropic, U21055.1; Trinidad 79A, AF094612.1; French viscerotropic virus, U21056.1.

TABLE 2. Nucleotide sequences and positions of primers used in the heminested RT-PCR (hnRT-PCR) assay for detection of mosquito-borne flavivirus.

	Primer	Sequence (5′–3′)*	Nucleotide position	Annealing temperature (℃)	Length (bp)
1st round PCR	XF-F1	AACATGATGGGVAARMGWGARAA	8916–8938	52	263
	XF-R	GTRTCCCANCCDGCDGTRTCATCNGC	9153–9178		
2nd round PCR	XF-F2	AARGGMAGYMGNGCHATHTGGT	8964–8985	54	215
	XF-R	GTRTCCCANCCDGCDGTRTCATCNGC	9153–9178		

*N=A+G+C+T, V=G+A+C, R=A+G, M=A+C, W=A+T, Y=C+T, H=A+T+C, D=G+A+T.

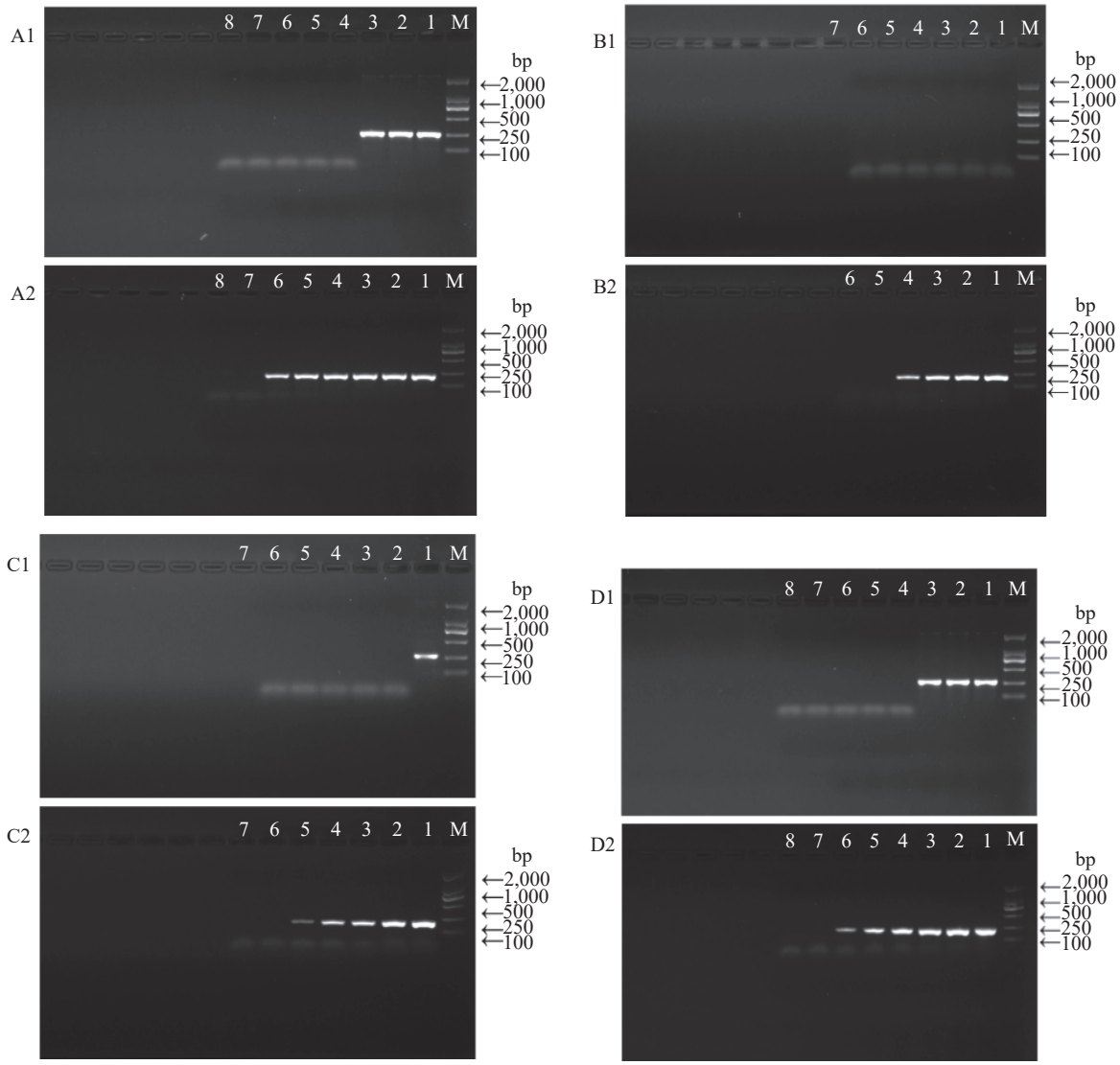


FIGURE 1. Sensitivity of heminested RT-PCR (hnRT-PCR) for detection of mosquito-borne flavivirus.
A, B, C, and D show the lowest limit for JEV, DENV-2, YFV, and WNV, respectively; 1 and 2 denote the lowest limit for the first and second round PCR, respectively. The numbering 1–8 refers to 10^9–10^3 copies/μL and negative control, respectively. M: DL2000 DNA markerr.

various species and are widely distributed worldwide. Most flaviviruses are pathogens causing natural infectious diseases, which can lead to fever, hemorrhage, and encephalitis with a high mortality rate (*9*). In this study, four flaviviruses were screened based on the epidemic situation, pathogenicity, and risk of disease, including JEV, DENV-2, WNV, and YFV. Among them, JEV and DENV-2 are the

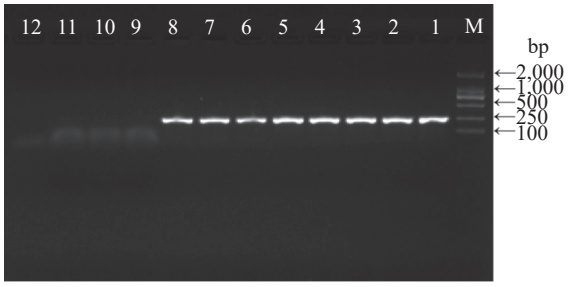


FIGURE 2. Specificity of heminested RT-PCR (hnRT-PCR) for detection of mosquito-borne flavivirus.
The numbering 1−12 refers to JEV, DENV-2, YFV, WNV, JEV + mosquito cDNA, DENV-2 + mosquito cDNA, YFV + mosquito cDNA, WNV + mosquito cDNA, mosquito cDNA, SINV, CHIKV, and negative control, respectively. M: DL2000 DNA marker.

common mosquito-borne viruses, and associated outbreaks occur almost every year in China. Therefore, the rapid and accurate high-throughput detection method for flavivirus is of great significance for the prevention and control of mosquito-borne diseases.

The traditional methods for detecting mosquito-borne viruses are isolation and culturing method, but virus culturing is relatively time-consuming and cannot be used for early diagnosis of disease. Serological detection is a classical virus detection method, which is mainly used to detect specific antibodies or antigens in specimens, and it is indispensable in the diagnosis and identification of virus infection. But serological methods lack of specificity and are prone to cross-reactions between viruses. Traditional species-specific RT-PCR and real-time RT-PCR based on Taq-Man Probe are rapid and sensitive, but only detect single pathogens.

Wu et al. (*10*) established a method for screening samples by multiplex real-time RT-PCR and the lower limit of detection of this method was 11 copies/μL. However, compared with singleplex real-time PCR, multiplex real-time PCR requires multiple pairs of primers and probes in a single reaction tube and, therefore, will have to account for competition between reactants resulting in significantly increased difficulty of primer design. Gao et al. (*11*) used the established RT-PCR method to detect JEV, and the lower limit of detection was 10 pg/μl but could only detect a single flavivirus.

In this study, a new hnRT-PCR method for the simultaneous detection of various flaviviruses was established. The performance of the new hnRT-PCR method was evaluated including specificity and sensitivity. In the specificity testing, only the target bands appeared in the flavivirus, and no bands appeared in control, which indicated high specificity in detecting mosquito-borne flavivirus. In the sensitivity testing, the lowest detection limits of JEV, DENV-2, YFV, and WNV were 3×10^4, 3×10^6, 3×10^5, and 3×10^4 copies/μL, respectively. When testing field-caught mosquito samples, 2 strains of JEV were detected by the method established in this study. Other flaviviruses had not been detected, which may be related to the species and quantity of mosquitoes collected, and the epidemic situation of the virus. However, considering that the variety and high genetic diversity of flavivirus, whether the hnRT-PCR method established in this study had a good detection effect for all flavivirus viruses needs to be further validated by other flavivirus viruses. In summary, the hnRT-PCR established in this study possessed both high specificity and sensitivity and could simultaneously be used for detection of multiple flaviviruses. This can be effectively used to detect the pathogen of flavivirus and provide technical support for early and rapid diagnosis of mosquito-borne flavivirus.

Acknowledgment: Guizhou Province CDC.

Funding: the National Important Scientific & Technology Project (2018ZX10101002-002) and China Prosperity Strategic Programme Fund (SPF) 2015-16 (15LCI1).

doi: 10.46234/ccdcw2021.001

[#] Corresponding authors: Zhong Zhang, nasonia@163.com; Qiyong Liu, liuqiyong@icdc.cn.

[1] National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China; [2] School of Basic Medical Sciences, Shandong First Medical University, Taian, Shandong, China; [3] Guizhou Province Center for Disease Control and Prevention, Guiyang, Guizhou, China; [4] School of Life Sciences, Shandong First Medical University, Taian, Shandong, China; [5] Collaborative Innovation Center for the Origin and Control of Emerging Infectious Diseases, Taian, Shandong, China.

Submitted: September 07, 2020; Accepted: December 28, 2020

REFERENCES

1. Weaver SC, Reisen WK. Present and future arboviral threats. Antiviral Res 2010;85(2):328 – 45. http://dx.doi.org/10.1016/j.antiviral.2009.10.008.
2. Erlanger TE, Weiss S, Keiser J, Utzinger J, Wiedenmayer K. Past, present, and future of Japanese encephalitis. Emerg Infect Dis 2009;15(1):1 – 7. http://dx.doi.org/10.3201/eid1501.080311.
3. Gould E, Pettersson J, Higgs S, Charrel R, de Lamballerie X. Emerging arboviruses: why today? One Health 2017;4:1 – 13. http://dx.doi.org/10.1016/j.onehlt.2017.06.001.
4. Tang KF, Ooi EE. Diagnosis of dengue: an update. Expert Rev Anti-Infect Ther 2012;10(8):895 – 907. http://dx.doi.org/10.1586/eri.12.76.
5. Asnis DS, Conetta R, Teixeira AA, Waldman G, Sampson BA. The west Nile virus outbreak of 1999 in New York: the flushing hospital

experience. Clin Infect Dis 2000;30(3):413 – 8. http://dx.doi.org/10.1086/313737.
6. Franca RFO, Neves MHL, Ayres CFJ, Melo-Neto OP, Filho SPB. First international workshop on Zika virus held by Oswaldo Cruz foundation FIOCRUZ in Northeast Brazil March 2016-a meeting report. PLoS Negl Trop Dis 2016;10(6):e0004760. http://dx.doi.org/10.1371/journal.pntd.0004760.
7. Jarman RG, Nisalak A, Anderson KB, Klungthong C, Thaisomboonsuk B, Kaneechit W, et al. Factors influencing dengue virus isolation by C6/36 cell culture and mosquito inoculation of nested PCR-positive clinical samples. Am J Trop Med Hyg 2011;84(2):218 – 23. http://dx.doi.org/10.4269/ajtmh.2011.09-0798.
8. Lu Z, Lu XJ, Fu SH, Zhang S, Li ZX, Yao XH, et al. Tahyna virus and human infection, China. Emerg Infect Dis 2009;15(2):306 – 9. http://dx.doi.org/10.3201/eid1502.080722.
9. Yang CF, Chen CF, Su CL, Teng HJ, Lu LC, Lin C, et al. Screening of mosquitoes using SYBR Green I-based real-time RT-PCR with group-specific primers for detection of Flaviviruses and Alphaviruses in Taiwan. J Virol Methods 2010;168(1 – 2):147 – 51. http://dx.doi.org/10.1016/j.jviromet.2010.05.006.
10. Wu WH, Wang J, Yu N, Yan JY, Zhuo ZH, Chen MY, et al. Development of multiplex real-time reverse-transcriptase polymerase chain reaction assay for simultaneous detection of Zika, dengue, Yellow fever, and chikungunya viruses in a single tube. J Med Virol 2018;90(11):1681 – 86. http://dx.doi.org/10.1002/jmv.25253.
11. Gao ZQ, Yue BF, He ZM. Development and application of RT-PCR assay of *Japanese encephalitis* virus. Chin J Pharm Anal 2010;30(10):1928-31. http://d.wanfangdata.com.cn/periodical/ChlQZXJpb2RpY2FsQ0hJTmV3UzIwMjAxMjI4Eg95d2Z4enoyMDEwMTAwMjgaCDF6Y2tsem9t. (In Chinese).

Recollection

Water Supply Improvement and Health Promotion Campaigns in Rural Areas — China, 1949–2020

Hongxing Li[1,#]; Alasdair Cohen[2]; Lin Lin[3]; Xiaoxiao Zhang[1]; Rong Zhang[1,#]

In the 1950s, shortly after the founding of the People's Republic of China (PRC), the central government created the Patriotic Health Campaign (PHC) in order to standardize and disseminate health-focused educational materials intended to control and prevent infectious diseases (*1*). "Water improvement", meaning measures aimed at providing safe drinking water for households in China, was an important part of the PHC. After 60 years of water improvement policies, programs, and investments, the rural water supply sanitation and hygiene in China has improved dramatically, and water-related diseases no longer negatively impact the rural population as they once did. In addition to improvements related to the quantity and quality of the rural water supply, water improvement programs also promoted improved hygiene, sanitation, and other health-related behaviors among rural households. Together, such initiatives have improved the quality of life and the health of hundreds of millions of rural residents, while also contributing to economic and social advancement across rural China (*2*). The purpose of this article is to describe how the PHC served as a foundation for the expansion and improvement of drinking water supply in rural China, and to summarize the key programs, projects, and initiatives that followed over the last 60 years.

BACKGROUND

China is a large, still developing country with a total rural population of 564 million, accounting for 40.4% of the country's total population as of 2018/2019 (*3*). At the time of the country's founding in 1949, nearly all rural residents collected their drinking water from rivers, lakes, ponds, and relatively shallow hand-dug wells, as they had done for generations before. Not surprisingly then, early surveillance studies revealed a relatively high incidence of various gastrointestinal infections and other water-related endemic diseases (*4*). The associated burden of disease threatened people's health and hindered socioeconomic development in rural areas. This dynamic wherein "poverty begets disease, and disease begets poverty" was widespread prior to the implementation of China's water improvement programs and other health-focused campaigns in rural areas.

Central to the PHC was an emphasis on health-focused education and the construction of health-related infrastructure. Importantly, the PHC also fostered improved collaboration among government agencies at different levels of governance (e.g., national, provincial, county levels) and between agencies with overlapping or complementary mandates to improve the well-being and health of rural households. As a result, PHC initiatives were successful in reaching the rural population and encouraging them to adopt improved health-related attitudes and behaviors (*1*).

RURAL WATER IMPROVEMENT IN PRACTICE

Since the founding of the PRC, China's government recognized the importance of rural water supply and sanitation and sought to promote the development of improved water and sanitation infrastructure and management (*5*). Water improvement actions were specifically embedded in China's National Social and Economic Five-Year Development Plans as early as 1986.

Water Quality Improvement

In broad terms, China's rural water supply development evolved over the course of four stages as summarized in Table 1. As a consequence of these decades of deliberate and planned efforts — especially the implementation of the Rural Water Supply Five Year Plans starting in 2005 — more than 520 million rural residents, including more than 47 million rural schoolteachers and students, now have access to some form of piped water supply. By 2019, the proportion of the rural population covered by centralized

TABLE 1. The four primary stages of rural water supply, time period, and primary water improvement programs in China, 1949–2020.

Stage	Period	Primary water improvement programs	Additional Details
Initial development and improvement of decentralized water supply	1949 to early 1980s	Basic water improvement measures (e.g., building well protection platforms and/or covers, separating drinking water sources used for people and livestock)	Most measures were improvements to existing water supply systems; reservoirs, irrigation infrastructure, and some new drinking water facilities were also constructed during this period.
Construction of centralized water supply infrastructure	Early 1980s to early 2000s.	● International Drinking Water Supply and Sanitation Decade (*7*) ● The Rural People/Livestock Drinking Water Program ● China Rural Water and Sanitation Program (supported by the World Bank and Asian Development Bank).	The central government creates long-term strategies and plans for rural water supply, including the establishment of national water standards, and collaborates with international agencies.
Rapid development of drinking water supply in rural areas	2000 to 2015	● Rural Drinking Water Emergency Project Plan ●Rural Drinking Water 11th Five-Year Plan ● Rural Drinking Water 12th Five-Year Plan	Government agencies at all levels emphasize the importance of rural water supply, which is also incorporated into the National Socioeconomic Development Plan. These efforts are accompanied by a focus on sustainable development goals.
The consolidation, improvement, and promotion of rural water supply	2015 to present	● Rural Drinking Water Supply Consolidation and Improvement Plan	Focus on upgrading existing rural water supply projects and improving management and operation systems to further expand piped water supply in rural areas, with an emphasis on consistent compliance with national water supply and quality standards.

drinking water treatment and distribution had reached 82% (*6*).

Establishment and Improvement of the National Rural Drinking Water Quality Monitoring Network

Furthermore, the National Rural Drinking Water Quality Monitoring Network (NRDWMN) was created in the 1990s and included Rural Drinking Water Projects from Five-Year Plans through 2003 (*8*). From 2004 to 2007, the NRDWMN was incorporated into the National Health Risk Factor Monitoring System, an internet-based information system which covers all provincial-level administrative divisions (PLADs), cities, and counties. By the end of 2019, data collected for the NRDWMN covered >98% of the townships in China. As one of China's largest public health monitoring systems, NRDWMN provides information related to water and sanitation management and serves to help safeguard drinking water safety around the country.

From Water Quality Monitoring to Water Quality Management

To improve the management and quality of rural drinking water supply, China has expanded from a focus on water quality testing to a more holistic water quality management model based on strengthening preventive measures across the water supply process. In recent years, several PLADs have started to use Water Safety Plans (WSP), a drinking water quality management approach and toolset promoted by the World Health Organization's (WHO) Guidelines for Drinking Water Quality (*9*). The WSP is a comprehensive drinking water management framework which encompasses all steps of water supply from source to consumer. Although the implementation of WSPs in China is not yet widespread, the Ministry of Health (now called the National Health Commission, NHC) proposed Technical Rules for Sanitary Evaluation (TRSE) (for rural drinking water safety) in 2008 which were in developed in part based on WSP principles (*10*). Much like the WSPs rationale, the TRSE was designed to support the systematic identification of potential water quality risks in water systems and to help establish control measures to responsibly manage such risks (*11*).

EXPANDING ACCESS TO SAFE WATER AND IMPROVING HEALTH IN RURAL AREAS

From 1990 to 2012, close to 500 million people in China received access to improved sources of drinking water (*12*). Over the same period (1990 to 2013), the age-standardized death rate from (mostly water-related) diarrheal disease decreased by 95% (*13*). Alongside the rapid expansion of piped water access in rural China,

the incidence of reportable water-associated infectious diseases also decreased dramatically. For example, typhoid and paratyphoid dropped from a rate of 10.32/100,000 population in 1990 to 0.66/100,000 in 2019, the incidence of dysentery decreased from 127.44/100,000 in 1990 to 5.81/100,000 in 2019, and the incidence of viral hepatitis A decreased from 7.37/100,000 in 2003 to 1.38/100,000 in 2019 (Figure 1).

Since 2005, the central government has implemented the 2005–2006 Plan for Rural Drinking Water Safety Emergency Projects, the 11th and 12th Five-Year National Plans for Rural Drinking Water Safety Projects, and the 13th Five-Year Plan for National Rural Drinking Water Safety Consolidation and Promotion Projects—all of which also prioritized efforts to address areas with endemic fluorine and arsenic exposures. These projects adopted a variety of technical and management approaches, including fluorine and arsenic remediation, which in turn improved the drinking water quality dramatically in areas historically suffering from arsenicosis and fluorosis. Consequently, the number of patients with dental fluorosis decreased from 21.0 million in 2003 to 1.3 million in 2018, a decrease of 93.8%. The number of patients with skeletal fluorosis decreased from 1.3 million in 2003 to 0.09 million in 2018, a decrease of 93.1%.

The main experiences of rural water supply development in China could be summarized as the following: 1) The government attached great importance to rural water supply development in addition to the wide participation of the pubic; 2) The '3-in-1' concept combining rural water improvement, sanitation, and health education had promoted the improvement of water and sanitation infrastructure, as well as popularization of health knowledge.

CHALLENGES AND PROSPECTS

Water improvement programs in China have evolved considerably over the last 60 or so years and rural water supply infrastructure has been improved significantly. However, considering China's vast size, varied topography, regional disparities in the distribution of natural water resources, and other constraints, the challenge of addressing all of China's drinking water related problems remains a long-term and dynamic one.

During the 13th Five-Year Plan period, enormous effort will be made to boost capacity for further expanding safe drinking water access in rural China. The country will strive to move towards the equalization of rural-urban water supply by supplementing, upgrading, and establishing new rural networks alongside existing drinking water projects. At

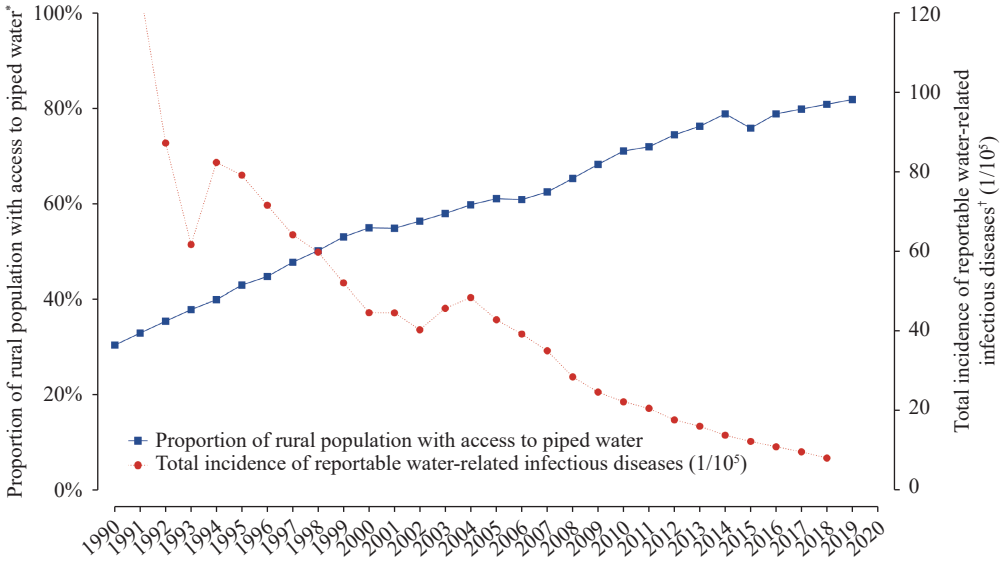


FIGURE 1. Proportion of rural population with access to piped water and mean incidence of reportable water-related infectious diseases in china: 1990 to 2020.
* Data source: National Health and Family Statistical Yearbook; Water Conservancy Development Bulletin.
† Data source: National Health and Family Statistical Yearbook; including typhoid fever, paratyphoid fever, dysentery, hepatitis A.

the time of writing of this article (towards the end of 2020), the coverage ratio of centralized water supply projects in rural areas is estimated to be 87%, and the proportion of the country's rural population with access to piped water supply is estimated to exceed 82% (*6*).

Looking to the years ahead, in addition to infrastructure construction, the management of water supply quality needs to be strengthened further. Comprehensive and routine evaluation of rural drinking water supply management via the use of WSPs should be expanded to more rural water supply systems (*11*). In addition to continued progress in water supply infrastructure and management, health education and health behavior promotion programs remain a crucial element of water improvement, just as they were during the early years of the PHC.

doi: 10.46234/ccdcw2021.002

[#] Corresponding authors: Hongxing Li, lihx@ncrwstg.chinacdc.cn; Rong Zhang, zhangrong@chinacdc.cn.

[1] National Center for Rural Water Supply Technical Guidance, Chinese Center for Disease Control and Prevention, Beijing, China; [2] Department of Population Health Sciences & the Public Health Program, Virginia Polytechnic Institute & State University (Virginia Tech), Blacksburg, VA, USA; [3] Office for public health management, Chinese Center for Disease Control and Prevention, Beijing, China.

Submitted: November 18, 2020; Accepted: December 29, 2020

REFERENCES

1. Li ZD. Review of patriotic health campaign. Beijing Dangshi 2010(3): 25 – 30. http://www.cnki.com.cn/Article/CJFDTotal-BJDY201003009.htm. (In Chinese).
2. Ministry of Water Resources, People's Republic of China. Rural water supply in China. Beijing (China): Ministry of Water Resources, People's Republic of China. http://www.mwr.gov.cn/english/. [2020-12-29].
3. National Bureau of Statistics. China statistical yearbook 2019. Beijing: China Statistics Press. 2019. http://www.stats.gov.cn/tjsj/ndsj/2019/indexch.htm. (In Chinese).
4. Wei CY. Basic situation and prevention countermeasures of intestinal infectious diseases in China. J Chin Phys 2001;29(6):6 – 8. http://dx.doi.org/10.3969/j.issn.1008-1089.2001.06.004. (In Chinese).
5. Li HX, Zhang Q, Li WW, Luo Q, Liu KT, Tao Y. Spatial analysis of rural drinking water supply in China. Water Policy 2015;17(3):441 – 53. http://dx.doi.org/10.2166/wp.2014.193.
6. Zhang YL. The rate of centralized water supply reached 87% and the penetration rate of tap water reached 82% in rural areas, China. China.org.cn, 2020 Apr 14. http://news.china.com.cn/txt/2020-04/14/content_75931127.htm. [2020-12-29]. (In Chinese).
7. World Health Organization. Community Water Supply and Sanitation Unit. International drinking water supply and sanitation decade: project and programme information system. Rev. ed. Geneva: World Health Organization. 1983. https://apps.who.int/iris/handle/10665/61592.
8. Zhang R. Current situation and countermeasures of rural drinking water quality monitoring in China. In: Proceedings of Paper Collection of Annual Meeting of China Science and Technology Association 2017. Wuhan, China: China Association for Science and Technology, China Instrument Society, China Electronics Society, China Society of Electrical Engineering, China Railway Society. 2017. http://d.wanfangdata.com.cn/conference/6441774. (In Chinese).
9. WHO. Guidelines for Drinking-Water Quality. 3th ed. Geneva: World Health Organization. 2004. https://www.who.int/water_sanitation_health/publications/gdwq3/en/. [2020-12-29].
10. Office of the National Patriotic Health Campaign Committee. Notice on printing and distributing the technical rules for hygienic evaluation of rural drinking water safety projects (for trial Implementation). Beijing (China): Government of the People's Republic of China; 2008. http://www.gov.cn/gzdt/2008-05/10/content_966400.htm. [2020-12-29]. (In Chinese).
11. Li HX, Smith CD, Cohen A, Wang L, Li Z, Zhang R, et al. Implementation of water safety plans in China: 2004-2018. Int J Hyg Environ Health 2020;223(1):106 – 15. http://dx.doi.org/10.1016/j.ijheh.2019.10.001.
12. UNICEF, WHO. Progress on drinking water and sanitation: 2014 update. New York: UNICEF, WHO. 2014: 74. https://www.unicef.org/publications/index_73448.html.
13. Zhou MG, Wang HD, Zhu J, Chen WQ, Wang LH, Liu SW, et al. Cause-specific mortality for 240 causes in China during 1990-2013: a systematic subnational analysis for the Global Burden of Disease Study 2013. Lancet 2016;387(10015):251 – 72. http://dx.doi.org/10.1016/S0140-6736(15)00551-6.

Healthy China

Construction and Implementation of Big Data in Healthcare in Yichang City, Hubei Province

Fangfang Lu[1]; Chengzhong Xu[1]; Pei Zhang[1]; Yong Xu[1,#]; Jianhua Liu[1,#]

Summary

Environmental pollution, aging, emerging infectious diseases, and unhealthy lifestyles are affecting human health and resulting in serious social and economic burdens. The government-led healthcare big data platform in Yichang has continuously worked towards exploring the use of comprehensive health-related information through top-level design and scientific planning. The platform is based on the following principle: "Openness, inclusiveness, and win-win cooperation." So far, by relying on one-to-one verification, comparison, correlation, and correction with the source, the platform has succeeded in establishing a unique foundation to benefit the people, government, medical care, and health service. Its successes can hopefully act as a positive case for exploring domestic healthcare big data.

To solve challenges brought forth by economic development, social transformation, environmental pollution, aging, and poor lifestyles on population health and disease burdens, Healthy China 2030 Plan proposed promoting the application of healthcare and medical big data (*1*). The Chinese government also lists the application and development of healthcare big data as an important national task (*2*). The Alibaba Health Strategy Platform (*3*), Tencent Smart Medical Platform, and regional healthcare big data centers (*4*) such as Shanghai, Ningbo, Fujian, and Jiangsu have emerged to explore how big data can help solve problems people encounter in their everyday lives.

Lying in the western part of China's Hubei Province, Yichang City is located at the conjunction of the middle and upper reaches of the Yangtze River. Yichang has five districts, three county-level townships, five counties and one national-level high-tech zone. It covers an area of 21,000 square kilometers and has a population of 4.1379 million, including a registered population of 3.9094 million. As one of the first National Pilot City and Healthy City Using Information to Benefit the People, Yichang began to explore the construction of a big data platform from 2014, formed the current platform in 2016, and consistently improved it over the last 3 years.

The government-led Yichang Healthcare Big Data Center adopts the cloud model under an urban framework that breaks barrier of information sharing among different sectors (Figure 1) in China for the first time (*5*–*6*). There are over 4 billion pieces of stored data in Yichang Healthcare Big Data Center and more than 1.8 million pieces of data being generated daily covering all 13 counties and districts and the 4.1 million residents. The Yichang regional public health information platform passed the Assessment of Standardization Maturity of National Medical and Health Information Interconnection and achieved the highest grades. After nearly four years of practice and exploration, disease discovery and reporting and health management and delivery has changed dramatically.

Based on one-to-one sources and information sharing, new technologies such as artificial intelligence were used to monitor and report specified infectious diseases, tumors, cardiovascular and cerebrovascular events, hypertension, and diabetes in real time (Figure 2).

Figure 3 shows the in-patient and out-patient admission among total and special populations (children under 5 years old, middle school students, and people older than 65 years old), number of vaccinations, 4 categories of disease event reports (cardiovascular and cerebrovascular diseases, tumors, causes of death, and infectious diseases), daily births and deaths, and other medically related events (for example, first-aid, blood donation and transfusion). It also outlines the follow-up of hypertension and diabetes required by Basic Public Health Services.

Yichang's healthcare big data platform has transformed the city's data collection, integration, sharing, and analysis of population health and health-related information, which contains medical and environmental indicators, birth and death registrations, insurance claims, and other important health indicators. Successful information sharing among different departments is meaningful for policymaking

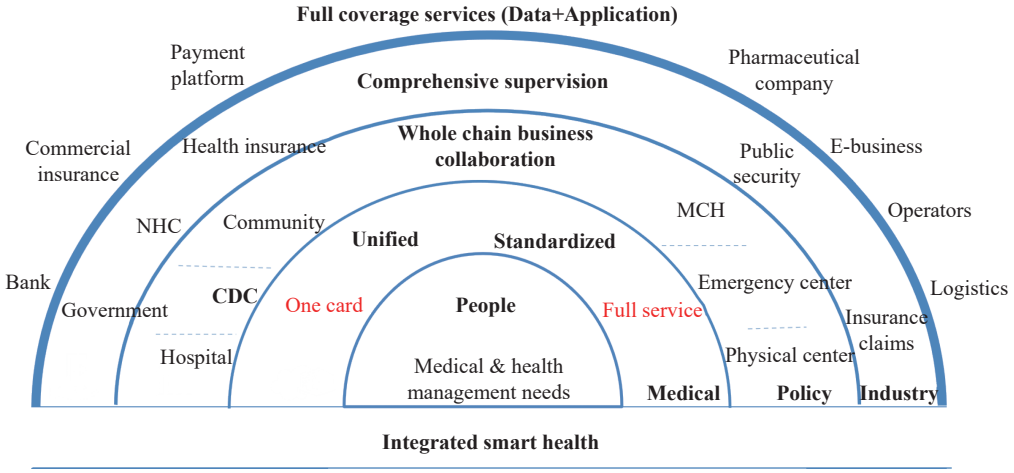


FIGURE 1. The regionally integrated smart healthcare big data platform in Yichang, Hubei province, 2020.

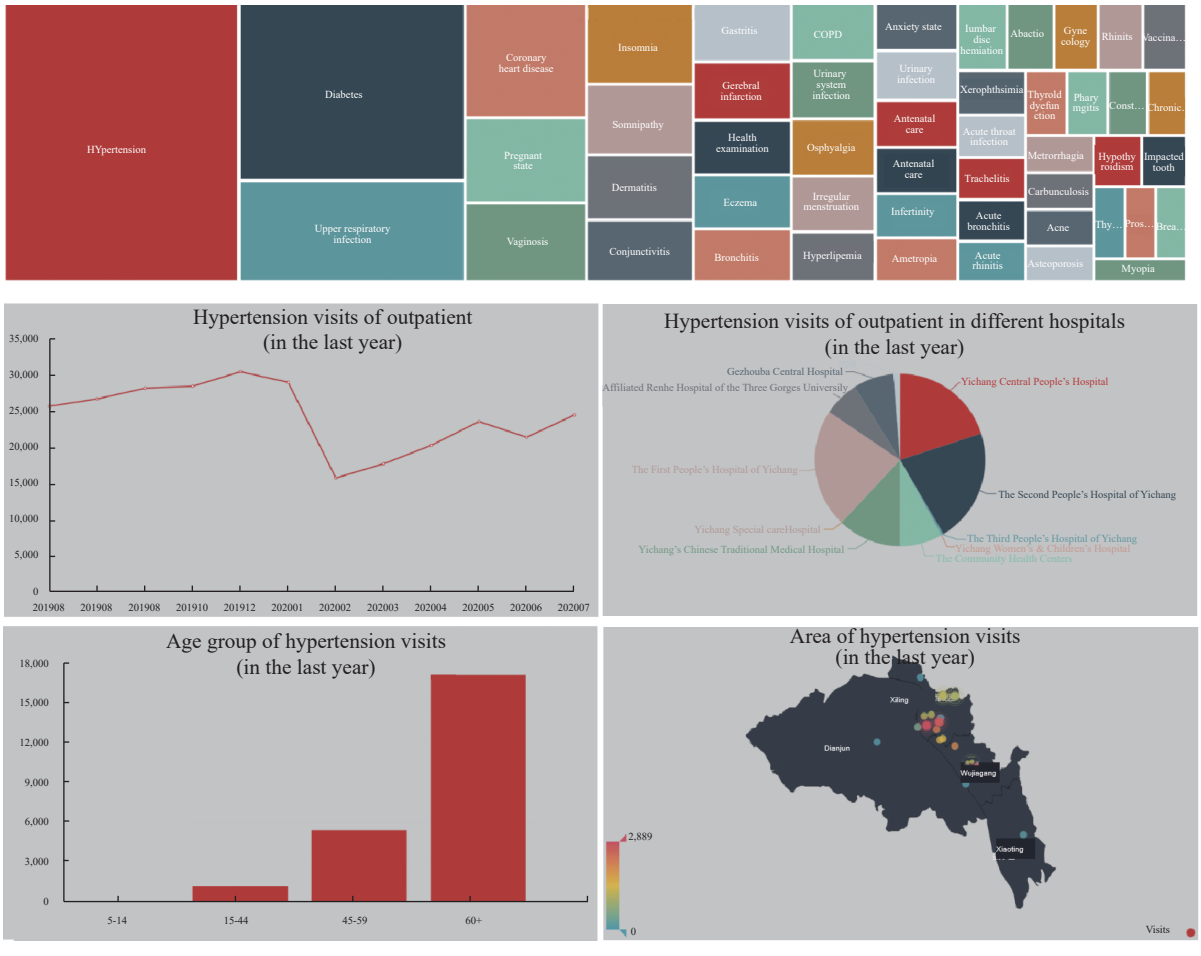


FIGURE 2. The monthly out-patient admissions of Yichang City displayed in real-time on the Healthcare Big Data Platform, Hubei Province, 2020.

and resource allocation. Many innovations have been made, especially in disease monitoring, health management, and "healthy city" construction. First, intelligent discovery and reporting systems of notifiable infectious diseases, hypertension, diabetes, tumors, cardiovascular and cerebrovascular events have been developed. Similar systems can lay a solid foundation for the full coverage of disease monitoring on health

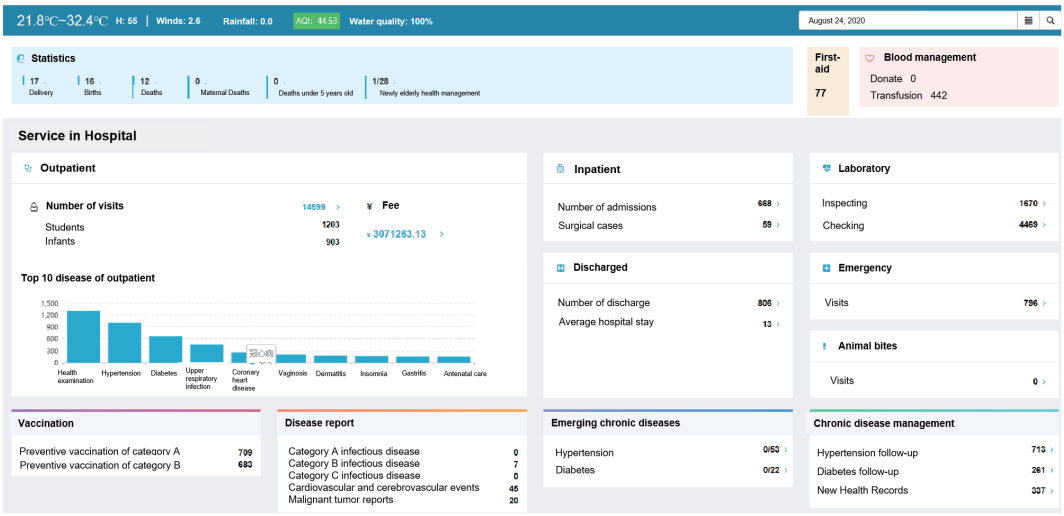


FIGURE 3. Healthcare big data information integration display platform in Yichang City, Hubei Province, 2020.

risk factors, diagnosis, treatment, etc. and allow for deep exploration of disease occurrence and development. Second, combined with personal electronic health records and mobile applications, a full lifecycle and full chain of healthcare information application platform can be built for all permanent residents. Third, integrated department data will also benefit "healthy city" construction by allowing for enhanced urban construction planning and city health evaluation. Functions and advantages of healthcare big data on emergent events of public health such as the coronavirus disease 2019 (COVID-19) pandemic, which emerged in Hubei Province, were also crucial to the response.

One of the most efficient ways to prevent the spread and prevalence of disease is to carry out a detailed and thorough epidemiological investigation to uncover the characteristics of outbreaks. The onset time, symptoms, diagnosis, treatment, laboratory testing, results, underlying diseases of the patient, the departments and doctors involved, and other helpful information can be obtained from the healthcare big data platform to help quickly ascertain the index case, disease characteristics, susceptible populations, and other important evidence. Using big data to assist epidemiological investigations efficiently and accurately has also protected investigators and provided an important basis for government decisions in Yichang.

Another application related to COVID-19 is the Grid Management Information System for joint prevention and control of major epidemics, which was developed by integrating the information data of multiple channels such as the national temperature detection platform, short message reporting platform, and the grid agent reporting system to collect information including dynamic temperature data and information of key prevention and control personnel including those returning or coming to Yichang, members of these families, close contacts, and pyrexia patients. Intelligent prevention and control programs were set up for different personnel and automatically distributed to each township and urban neighborhood office for isolation management and medical observation. The dynamic supervision applied in urban areas in Yichang has avoided heavy and complicated reports, provided strong evidence for emergency management and early warnings, and allowed for closed-loop management of all personnel.

By using the aspects of the big data platform for patient data, improvements in timeliness, accuracy, and integrity of data can be tracked and displayed. Missing, delayed, and repeated reports can be prevented. The medical records of patients who were diagnosed as COVID-19 in the big data platform were also useful for doctors to make more informed treatment plans.

In the big data era, accurate, comprehensive, and available data will be the source of high-quality developments of healthcare in the future and the basis and key to decision making (*7*). To construct a "smart and healthy city," Yichang's Healthcare Big Data Center has carried out some beneficial practices and explorations in data standardization, interconnection, and sharing. However, further effort should be taken to guarantee long-term, stable, high-quality data sources. In addition, deeper and broader explorations

are needed to use big data for monitoring diseases and health, allocating public resources, supporting government decisions, and serving people's health.

doi: 10.46234/ccdcw2020.254

[#] Corresponding authors: Yong Xu, hbycxy2007@163.com; Jianhua Liu, amour_1114@163.com.

[1] Yichang Center for Disease Control and Prevention,Yichang, Hubei, China.

Submitted: August 28, 2020; Accepted: November 12, 2020

REFERENCES

1. Central Committee of Chinese Communist Party. State Council. The Plan for Healthy China 2030. Beijing: Government of the People's Republic of China, 2016. http://www.gov.cn/xinwen/2016-10/25/content_5124174.htm. [2020-11-11]. (In Chinese).
2. General Office of the State Council, Guiding opinions of the general office of the State Council on promoting and standardizing the application and development of health and medical big data. Beijing: Government of the People's Republic of China, 2016. http://www.gov.cn/zhengce/content/2016-06/24/content_5085091.htm. [2020-11-11]. (In Chinese).
3. Huang YT. Full analysis of Alibaba health platform strategy. High-Technol Ind 2017;(4): 52-6. http://www.wanfangdata.com.cn/details/detail.do?_type=perio&idgkjycyh201704010. (In Chinese).
4. Zhang LX, Wang HB, Li QZ, Zhao MH, Zhan QM. Big data and medical research in China. BMJ 2018;36:j5910. http://dx.doi.org/10.1136/bmj.j5910.
5. Chen GJ. Breaking the information island to release the dividend of medical big data. Cap Med 2017(5):38 – 9. http://dx.doi.org/10.3969/j.issn.1005-8257.2017.05.016. (In Chinese).
6. Wang J. From e-government, smart city to smart society--analysis on the practice of smart Yichang integration. E-Government 2018(5):52 – 63. http://dx.doi.org/10.16582/j.cnki.dzzw.2018.05.006. (In Chinese).
7. Baillie J. How 'Big data' will drive future innovation. Health Estate 2016;70(3): 59-64. https://pubmed.ncbi.nlm.nih.gov/27132307/.

Notifiable Infectious Diseases Reports

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

Diseases	Cases	Deaths
Plague	0	0
Cholera	0	0
SARS-CoV	0	0
Acquired immune deficiency syndrome	5,824	1,738
Hepatitis	125,059	55
Hepatitis A	1,243	0
Hepatitis B	100,561	37
Hepatitis C	20,801	16
Hepatitis D	22	0
Hepatitis E	1,639	1
Other hepatitis	793	1
Poliomyelitis	0	0
Human infection with H5N1 virus	0	0
Measles	118	0
Epidemic hemorrhagic fever	1,796	14
Rabies[§]	12	20
Japanese encephalitis	10	0
Dengue	63	0
Anthrax	22	0
Dysentery	3,568	0
Tuberculosis	69,640	126
Typhoid fever and paratyphoid fever	517	2
Meningococcal meningitis	5	0
Pertussis	291	0
Diphtheria	0	0
Neonatal tetanus	2	0
Scarlet fever	1,925	0
Brucellosis	3,611	0
Gonorrhea	11,260	0
Syphilis	45,305	7
Leptospirosis	31	1
Schistosomiasis	6	0
Malaria	63	0
Human infection with H7N9 virus	0	0
COVID-19[*]	545	0
Influenza	22,783	1
Mumps	15,211	0

Continued

Diseases	Cases	Deaths
Rubella	276	0
Acute hemorrhagic conjunctivitis	2,538	0
Leprosy	35	0
Typhus	131	0
Kala azar	10	1
Echinococcosis	403	1
Filariasis	0	0
Infectious diarrhea[†]	83,209	1
Hand, foot, and mouth disease	189,017	1
Total	**583,286**	**1,968**

[*] The data were extracted 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.
[§] Of the 20 reported death cases of rabies, there were 7 reported in November, the others were reported previously.
The number of cases and cause-specific deaths referred to data recorded in National Notifiable Disease Reporting System (NNDRS) in China, which include both clinically-diagnosed cases and laboratory-confirmed cases. Only reported cases in 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, China are not included. Monthly statistics were calculated without annual verification, which is 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 NNDRS according to information verification or field investigations by local CDCs.

doi: 10.46234/ccdcw2021.003

The inauguration of *China CDC Weekly* is in part supported by Project for Enhancing International Impact of China STM Journals Category D (PIIJ2-D-04-(2018)) of China Association for Science and Technology (CAST).

CCDC weekly

Vol. 3 No. 1 Jan. 1, 2021

Responsible Authority
National Health Commission of the People's Republic of China

Sponsor
Chinese Center for Disease Control and Prevention

Editing and Publishing
China CDC Weekly Editorial Office
No.155 Changbai Road, Changping District, Beijing, China
Tel: 86-10-63150501, 63150701
Email: weekly@chinacdc.cn

CSSN
ISSN 2096-7071
CN 10-1629/R1