

COVID-19: China's Updates and Sharing

Chinese Center for Disease Control and Prevention



WHO Joint Mission in China (Feb. 16-24, 2020)



Epidemic of COVID-19 in China

Lab confirmed (as of April 13)

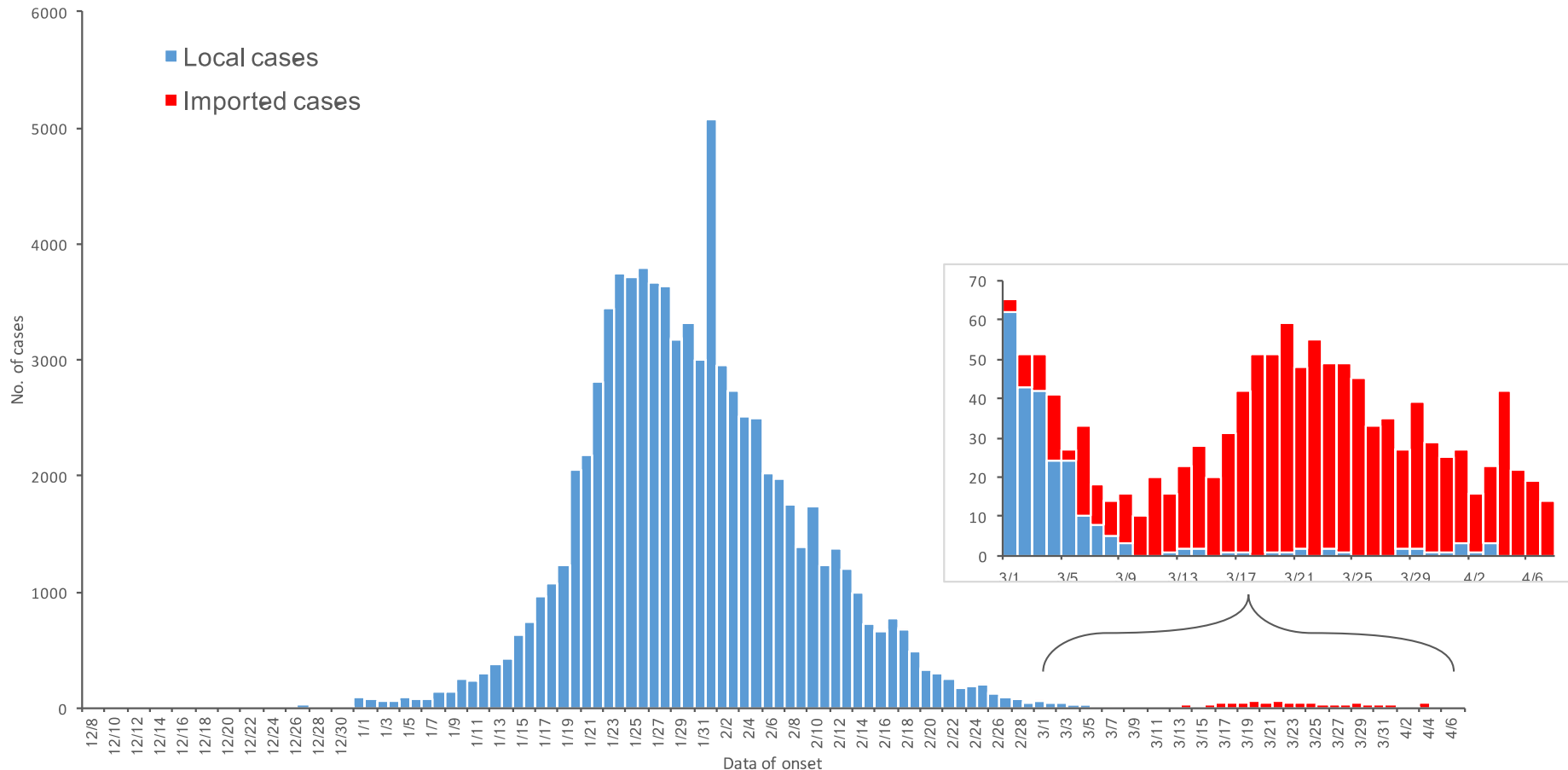
- Cumulative cases: 82249
- Cumulative recovered: 77738
- Cumulative deaths: 3341
- Crude CFR: 4.06%

Imported cases

- Jan 31, the 1st imported case
- By April 13, 1464 confirmed, 72 possible

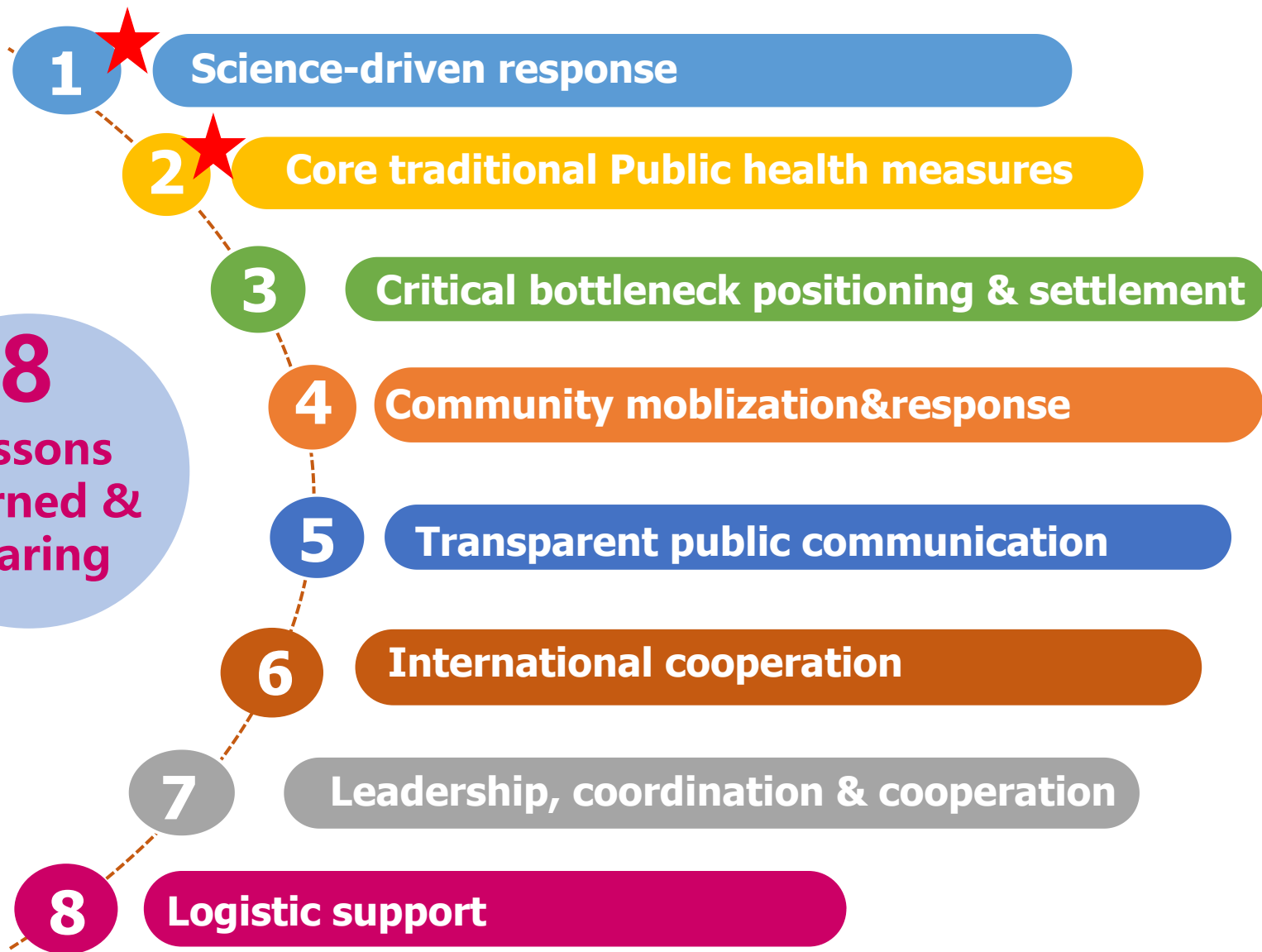
Asymptomatic infections

- By April 13, 1172 individuals, including 54 newly report, 1005 under medical observation





8
**Lessons
Learned &
Sharing**





Virus Discovery & Identification

Milestone scientific findings at the early stage

THE NEW ENGLAND JOURNAL OF MEDICINE

BRIEF REPORT

A Novel Coronavirus from Patients with Pneumonia in China, 2019

Na Zhu, Ph.D., Dingyu Zhang, M.D., Wenling Wang, Ph.D., Xingwang Li, M.D., Bo Yang, M.S., Jingdong Song, Ph.D., Xiang Zhao, Ph.D., Baoying Huang, Ph.D., Weifeng Shi, Ph.D., Roujian Lu, M.D., Peihua Niu, Ph.D., Faxian Zhan, Ph.D., Xuejun Ma, Ph.D., Dayan Wang, Ph.D., Wenbo Xu, M.D., Guizhen Wu, M.D., George F. Gao, D.Phil., and Wenjie Tan, M.D., Ph.D., for the China Novel Coronavirus Investigating and Research Team

SUMMARY

In December 2019, a cluster of patients with pneumonia of unknown cause was linked to a seafood wholesale market in Wuhan, China. A previously unknown betacoronavirus was discovered through the use of unbiased sequencing in samples from patients with pneumonia. Human airway epithelial cells were used to isolate a novel coronavirus, named 2019-nCoV, which formed a clade within the subgenus sarbecovirus, Orthocoronavirinae subfamily. Different from both MERS-CoV and SARS-CoV, 2019-nCoV is the seventh member of the family of coronaviruses that infect humans. Enhanced surveillance and further investigation are ongoing. (Funded by the National Key Research and Development Program of China and the National Major Project for Control and Prevention of Infectious Disease in China.)

EMERGING AND REEMERGING PATHOGENS ARE GLOBAL CHALLENGES FOR public health.¹ Coronaviruses are enveloped RNA viruses that are distributed broadly among humans, other mammals, and birds and that cause respiratory, enteric, hepatic, and neurologic diseases.^{2,3} Six coronavirus species are known to cause human disease.⁴ Four viruses — 229E, OC43, NL63, and HKU1 — are prevalent and typically cause common cold symptoms in immunocompetent individuals.⁴ The two other strains — severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) — are zoonotic in origin and have been linked to sometimes fatal illness.⁵ SARS-CoV was the causal agent of the severe acute respiratory syndrome outbreaks in 2002 and 2003 in Guangdong Province, China.⁶ MERS-CoV was the pathogen responsible for severe respiratory disease outbreaks in 2012 in the Middle East.⁷ Given the high prevalence and wide distribution of coronaviruses, the large genetic diversity and frequent recombination of their genomes, and increasing human-animal interface activities, novel coronaviruses are likely to emerge periodically in humans owing to frequent cross-species infections and occasional spillover events.^{5,8}

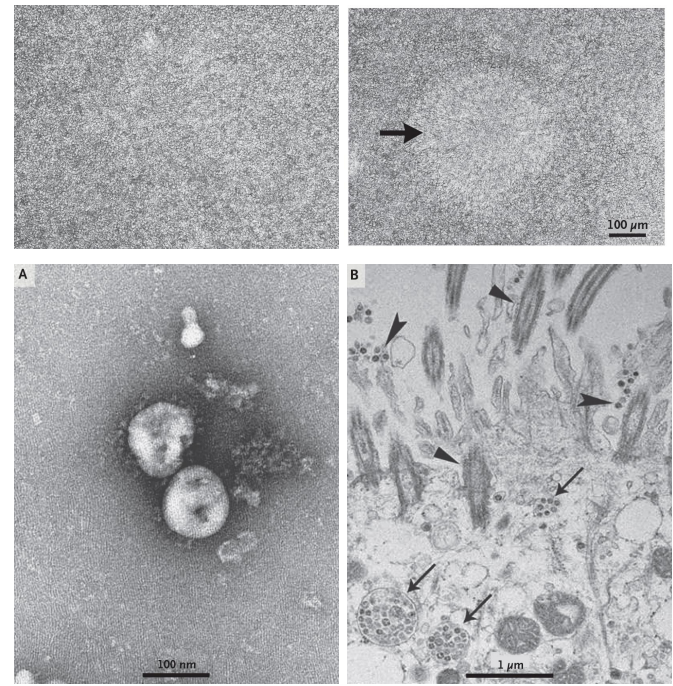
In late December 2019, several local health facilities reported clusters of patients with pneumonia of unknown cause that were epidemiologically linked to a seafood and wet animal wholesale market in Wuhan, Hubei Province, China.¹¹ On December 31, 2019, the Chinese Center for Disease Control and Prevention (China CDC) dispatched a rapid response team to accompany Hubei provincial and Wuhan city health authorities and to conduct an epidemiologic and etiologic investigation. We report the results of this investigation, identifying the source of the pneumonia

From the NHC Key Laboratory of Biosafety, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention (N.Z., W.W., J.S., X.Z., B.H., R.L., P.N., X.M., D.W., W.X., G.W., G.F.G., W.T.), and the Department of Infectious Diseases, Beijing Ditan Hospital, Capital Medical University (X.L.) — both in Beijing; Wuhan Jinyintan Hospital (D.Z.), the Division for Viral Disease Detection, Hubei Provincial Center for Disease Control and Prevention (B.Y., F.Z.), and the Center for Biosafety Mega-Science, Chinese Academy of Sciences (W.T.) — all in Wuhan; and the Shandong First Medical University and Shandong Academy of Medical Sciences, Jinan, China (W.S.). Address reprint requests to Dr. Tan at the NHC Key Laboratory of Biosafety, National Institute for Viral Disease Control and Prevention, China CDC, 155 Changbai Road, Changping District, Beijing 102206, China; or at tanwj@ivdc.chinacdc.cn. Dr. Gao at the National Institute for Viral Disease Control and Prevention, China CDC, 155 Changbai Road, Changping District, Beijing 102206, China, or at gaozf@im.ac.cn, or Dr. Wu at the NHC Key Laboratory of Biosafety, National Institute for Viral Disease Control and Prevention, China CDC, Beijing 102206, China, or at wuzgz@ivdc.chinacdc.cn.

Dr. Zhu, Zhang, W. Wang, Li, and Yang contributed equally to this article.

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Cytopathic Effects in HAE cell & Visualization of 2019-nCoV with Transmission Electron Microscopy. Negative-stained 2019-nCoV particles are shown in Panel A, and 2019-nCoV particles in the human airway epithelial cell ultrathin sections are shown in Panel B. Arrowheads indicate extracellular virus particles, arrows indicate inclusion bodies formed by virus components, and triangles indicate cilia.



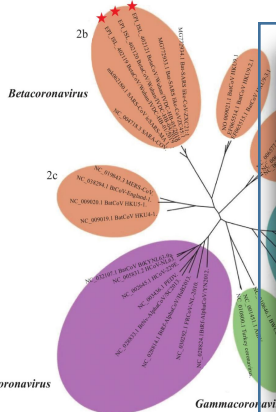
Information & Sequence Sharing

CHINA CDC WEEKLY

CCDC weekly

中国疾病预防控制中心周报

Notes from the Field: A Novel Coronavirus Genome Identified in a Cluster of Pneumonia Cases — Wuhan, China



GISAID

About us EpiFlu™ Features

In Focus

China releases genetic sequence of newly discovered coronavirus from Wuhan

The Chinese Center for Disease Control and Prevention, the Chinese Academy of Science and the Chinese Academy of Medical Science released through the GISAID Initiative the genome sequence of a newly discovered coronavirus. The virus was identified during an outbreak in the city of Wuhan, where patients were suffering from respiratory illnesses such as pneumonia since late December 2019.

The genome sequence of this betacoronavirus is crucial to develop specific diagnostic tests and to identify potential intervention options.

[► read more and access the data](#)



Courtesy: IV

国家微生物科学数据中心 National Microbiology Data Center

国家病原微生物资源库 National Pathogen Resource Center

新型冠状病毒国家科技资源服务系统

病毒名称: 2019-nCoV (NC_0230833), NCoV_2019_0001
 中文名称: 新型冠状病毒2019-nCoV
 英文名称: C-Tan-nCoV Wuhan strain 1
 缩写: 2019-nCoV, 新型冠状病毒
 病毒科: 冠状病毒科
 病毒属: 冠状病毒属
 病毒种: 新型冠状病毒
 来源: 国家微生物科学数据中心 (国家病原微生物资源库)
 病毒来源: 国家微生物科学数据中心 (国家病原微生物资源库)
 病毒来源: 国家微生物科学数据中心 (国家病原微生物资源库)

TABLE 1. Basic information for the first strain of 2019-nCoV.

Descriptors	Description
Code	CHPC2020.00001, NPIRC2020.00001
Name in Chinese	新型冠状病毒武汉株01
Name in English	C-Tan-nCoV Wuhan Strain
Taxonomy	novel β genus coronavirus
Source of the Specimen	Clinical Patients
Source of Collection	Wuhan, Hubei Province, China
Isolation Date	Jan 6, 2020
Risk Level	BSL-3
Contact Info	info@nrc.chinacdc.cn, zhao@nrc.chinacdc.cn
Note	Note: CHPC refers to the Center for Human Pathogen Collection of China CDC, and NPIRC refers to the National Pathogen Resource Center of China.

TABLE 2. Real-time RT-PCR primers and probes targeting the nucleocapsid gene region (nucleoprotein N) was used.

Item	Sequence
Target 1 (ORF1ab)	
Forward primer (F)	CCGCTCTGGGTTTACACTTAA
Reverse primer (R)	AGCAGTTGTGCAGCACTG
Fluorescent probes (P)	5'-FAM-CGGTCTGGCGGTATGTGGAAAGGTTATGG-BHQ1-3'
Target 2 (N)	
Forward primer (F)	GGGGAACCTCTCTGCTGAAGAT
Reverse primer (R)	CAGACATTTCTGCTGCAAGCTG
Fluorescent probes (P)	5'-FAM-TTCTGCTCTGCTTACAGAAATT-TAMRA-3'

Note: Results meeting magnitude 10 C_t value or C_t value < 37, considered positive, and suspicious of C_t value is between 37 and 40, repeat testing is recommended. If C_t value is 40, in repeat testing and distinctive peaks are observed in the amplification curve, the sample is considered positive; otherwise, the sample is considered negative.

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SUMMARY

In December 2019, a cluster of patients with pneumonia of unknown cause was linked to a seafood wholesale market in Wuhan, China. A novel coronavirus, named 2019-nCoV, was discovered through the use of unbiased screening of respiratory specimens. The virus caused pneumonia and mild to severe respiratory disease. Human airway epithelial cells and two primary mouse airway epithelial cell lines permissive for virus entry were infected by 2019-nCoV. This novel coronavirus represents a new member of the coronavirus family. The virus has a genome similar to that of group 1B betacoronaviruses, which are known to cause common colds in humans and other mammals, and is distinct from group 2A and 2B betacoronaviruses, which cause severe acute respiratory syndrome (SARS) in humans and other mammals. The virus is genetically distinct from the 2002 SARS coronavirus and the 2012 Middle East respiratory syndrome coronavirus. The virus is genetically distinct from the 2002 SARS coronavirus and the 2012 Middle East respiratory syndrome coronavirus. The virus is genetically distinct from the 2002 SARS coronavirus and the 2012 Middle East respiratory syndrome coronavirus.

From the NHC Key Laboratory of Biosafety, National Institute for Viral Disease Control and Prevention, Beijing, China.

The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia

Qun Li, M.Med., Xuhua Guan, Ph.D., Peng Wu, Ph.D., Xiaoye Wang, M.P.H., Lei Zhou, M.Med., Yeqing Tong, Ph.D., Ruiqi Ren, M.Med., Kathy S.M. Leung, Ph.D., Eric H.Y. Lau, Ph.D., Jessica Y. Wong, Ph.D., Xuesen Xing, Ph.D., Nijuan Xiang, M.Med., Yang Wu, M.Sc., Chao Li, M.P.H., Qi Chen, M.Sc., Dan Li, M.P.H., Tian Liu, B.Med., Jing Zhao, M.Sc., Man Liu, M.Sc., Wenzuo Tu, M.Med., Chudong Chen, M.Sc., Lianmei Jin, M.Med., Rui Yang, M.Med., Qi Wang, M.P.H., Suhua Zhou, M.Med., Rui Wang, M.D., Hui Liu, M.Med., Yinbo Luo, M.Sc., Yuan Liu, M.Med., Ge Shao, B.Med., Huan Li, M.P.H., Zhongfa Tao, M.P.H., Yang Yang, M.Med., Zhiqiang Deng, M.Med., Boxi Liu, M.P.H., Zhitao Ma, M.Med., Yanping Zhang, M.Med., Guoqing Shi, M.P.H., Tommy T.Y. Lam, Ph.D., Joseph T. Wu, Ph.D., George F. Gao, D.Phil., Benjamin J. Cowling, Ph.D., Bo Yang, M.Sc., Gabriel M. Leung, M.D., and Zijian Feng, M.Med.

ABSTRACT

BACKGROUND

The initial cases of novel coronavirus (2019-nCoV)-infected pneumonia (NCIP) occurred in Wuhan, Hubei Province, China, in December 2019 and January 2020. We analyzed data on the first 425 confirmed cases in Wuhan to determine the epidemiologic characteristics of NCIP.

METHODS

We collected information on demographic characteristics, exposure history, and illness timelines of laboratory-confirmed cases of NCIP that had been reported by January 22, 2020. We described characteristics of the cases and estimated the key epidemiologic time-delay distributions. In the early period of exponential growth, we estimated the epidemic doubling time and the basic reproductive number.

RESULTS

Among the first 425 patients with confirmed NCIP, the median age was 59 years and 50% were male. The majority of cases (59%) was onset before January 1, 2020, were linked to the Huanan Seafood Wholesale Market, as compared with 8.0% of the subsequent cases. The mean incubation period was 5.2 days (95% confidence interval [CI], 4.1 to 7.0), with the 95th percentile of the distribution at 12.5 days. In its early stages, the epidemic doubled in size every 7.4 days. With a mean serial interval of 7.5 days (95% CI, 5.3 to 19), the basic reproductive number was estimated to be 2.2 (95% CI, 1.4 to 3.9).

CONCLUSIONS

On the basis of this information, there is evidence that human-to-human transmission has occurred among close contacts since the middle of December 2019. Considerable efforts to reduce transmission will be required to control outbreaks if similar dynamics apply elsewhere. Measures to prevent or reduce transmission should be implemented in populations at risk. (Funded by the Ministry of Science and Technology of China and others.)

The authors' affiliations are listed in the Appendix. Address reprint requests to Dr. Feng at the Chinese Center for Disease Control and Prevention, No. 155 Changbai Rd., Changping District, Beijing, China, or at fenggj@chinacdc.cn to Dr. G.M. Leung or Dr. Cowling at the School of Public Health, Li Ka Shing Faculty of Medicine, University of Hong Kong, 21 Sassoon Rd., Pokfulam, Hong Kong, China, or at gmkung@hku.hk or bowling@hku.hk, respectively, or to Dr. B. Yang at the Hubei Center for Disease Control and Prevention, No. 35 Zhongshan North Rd., Hongshan District, Wuhan, Hubei, China, or at 4920595@qq.com.

Dr. Q. Li, X. Guan, P. Wu, and X. Wang and Drs. B. Cowling, B. Yang, M. Leung, and Z. Feng contributed equally to this article.

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The New England Journal of Medicine



Timely Risk-based Precise Strategy

Science-driven timely adjustment

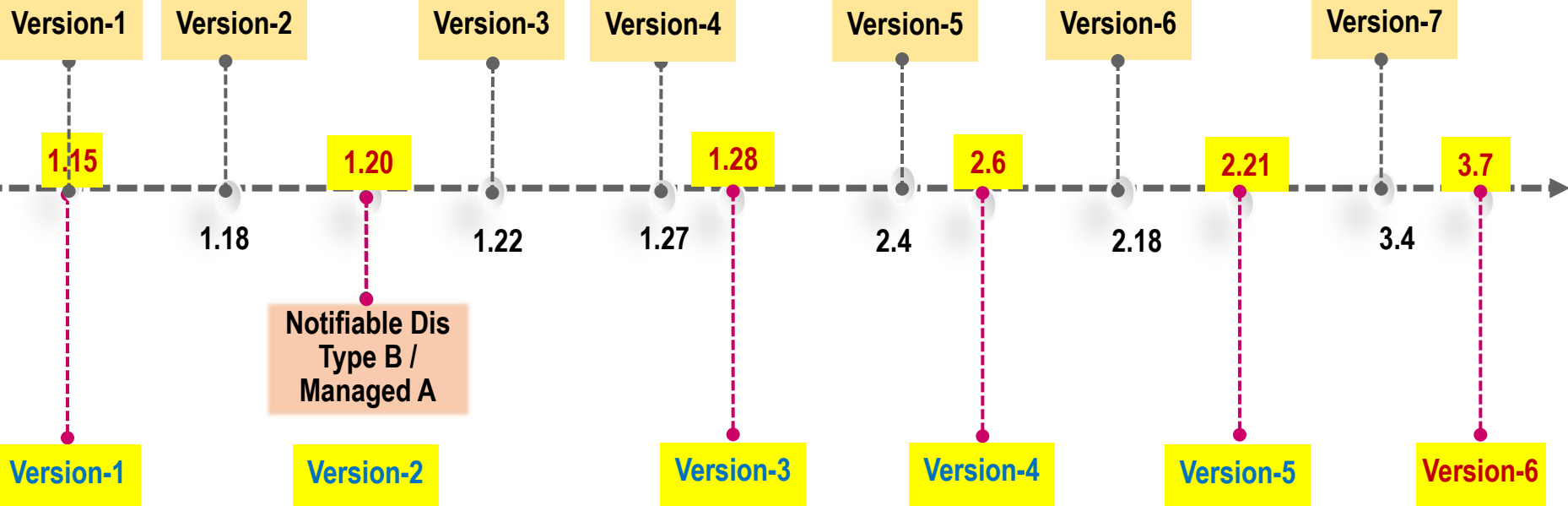
- **Low-risk areas -- strictly prevent importation**
 - No confirmed cases were reported, or no new confirmed cases were reported for 14 consecutive days.
- **Middle-risk areas -- prevent importation, stop local transmission**
 - Cumulative number of confirmed cases does not exceed 50, and there are new confirmed cases reported within 14 days; Or
 - Cumulative number of confirmed cases exceeds 50, and there are new confirmed cases reported within 14 days but without clustering outbreaks.
- **High-risk areas -- stop local transmission, prevent exportation, implement strict measures**
 - There are more than 50 confirmed cases with a clustered outbreak within 14 days.



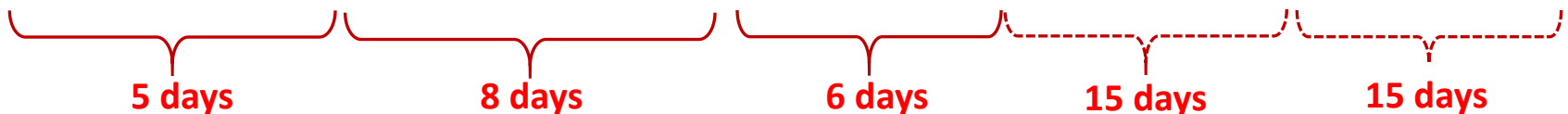
Development and Revisions of Technical Documents

Science-driven timely adjustment

Diagnostic and Treatment Protocols

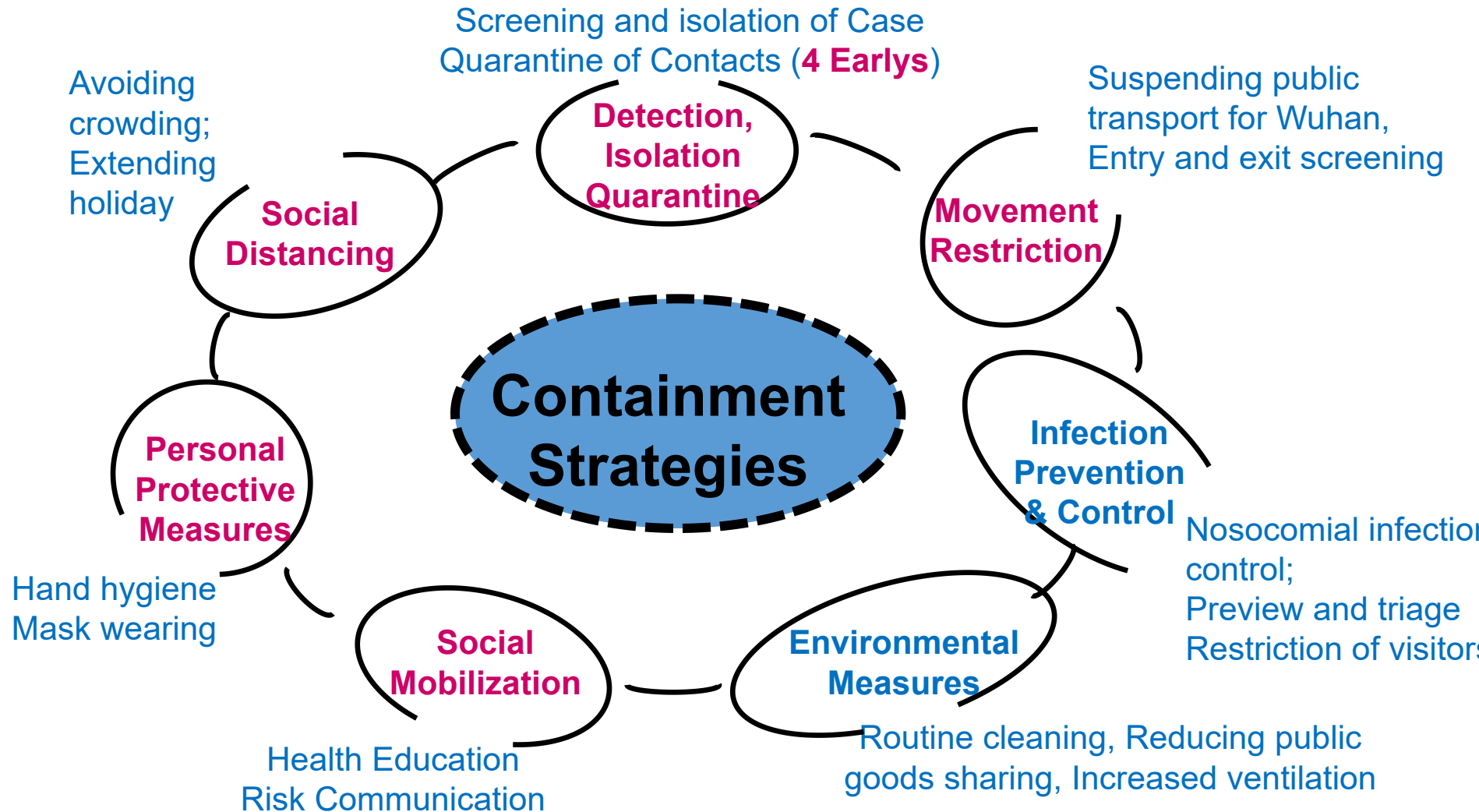


Prevention and Control Protocols





Traditional Containment Measures





Early and Active Case Detection

1 Healthcare facilities at all levels

2 Existing surveillance networks for PUE, ILI and SARI

3 Health status monitoring of close contacts

4 Port health quarantine for the imported cases detection

5 Primary level organizations or employers



Chinese Web-based Reporting System

- Notifiable Individual Case Information System
- Public Health Event Information Management System
- Epidemiological Investigation Information System
- Close Contacts Tracing and Management System
- Death Monitoring System



Case Reporting Requirement

Case reporting

- Suspected cases, confirmed cases, or asymptomatic infected individuals were required to report
- Web-based reporting system within 2h after diagnosis
- Information checking by CDCs within 2h after receiving the report

Updating reports

- When suspected cases confirmed or excluded
- When clinical severity changed with the progression of illness
- When status of asymptomatic infected individuals changed
- when died of COVID-19, date of death need to be updated

Reporting public health events

- The first COVID-19 confirmed case or cluster in a county/district
- Web-based emergency events reporting system within 2h
- The emergency level should be updated based on investigation findings and assessments



Measures for Asymptomatic Infection

- Isolation and medical observation for 14 days
- Be discharged only after their nucleic acid testing are negative for respiratory pathogen twice consecutively (sampling interval being at 24h)
- Close contact of asymptomatic infection
 - Any person who had contact (within 1 meter) with an asymptomatic infection within 2 days before sampling
 - Medical observation at designated places



Contact Management

- Quarantine either at home or at designated places (i.e. hotel)
- Duration: **14 days** from the last contact with a case or an asymptomatic individual
- Temperature and symptoms are monitored, **twice a day**, by individuals themselves, and report to a supervisor
- No outdoor activity is allowed, daily living allowance and supplies are provided by local community



Mask Wearing

Protect yourself, Protect others

Wearing a mask based on risk assessment

- **For general public**

- No need in general, e.g., at home, in open areas.
- Wearing a surgical mask when gathering, in an elevator or public vehicle, face-to-face interact, high risk area (hospital, clinics)

- **For Occupational exposure**

- Settings: Health care settings; airplane, public vehicle (e.g., train, bus), supermarket, restaurant, etc.
- KN95/N95 for health professionals, surgical mask for others



Key Experiences

FOUR Defense Lines

- 1st Line-Wuhan and Hubei
- 2nd Line-Beijing
- 3rd Line-Hubei's surrounding regions
- 4th Line-nationwide

FOUR Earlys

- Early Detection
- Early Reporting
- Early Isolation
- Early Treatment

For the People, By the People

- Community engagement
- Community health education
- Communities hygiene & Disinfection

C Coordination C Cooperation C Communication

- Resources allocation (HCW, PPE, etc)
- Logistic support
- Public understanding & Infodemic response



Proactive Defense Strategy

“Dance” with the virus

Strictly prevent importation and community resurgence

- **Control strategy for imported cases**
- **Tailored control measures at varied risk levels**
- **Four early measures in new situation**
 - **Strengthen case reporting and surveillance**
 - **Enhance laboratory test capability in county level**
 - **Maintain gridded community prevention and control measures**
- **Resuming production and work**
- **Prevention and control protocols at varied risk levels**



Control Strategy for Imported Cases

- **Whole chain management from border to community to home**
- **Entry Screening**
 - 14-day history and health status reporting
 - Temperature screening
 - **Four categories of persons**: confirmed case, suspicious case, person with fever, close contacts
 - Medical examination for suspected symptoms
 - Transfer
 - Suspected cases to designated hospitals
 - Close contacts to designated hotels for quarantine
- **Quarantine policy for travelers**
 - 2 weeks' quarantine in the designated hotels
 - Depending on the risk evaluation and local policy
 - Regardless of domestic or foreigners



Resuming Measures

- **Health code and travel cards**

- Jointly promote travel card service; provide different colors of "health codes" for the accurate management of people with different risk score results to provide support for the orderly flow of personnel

- **"point-to-point" labor cooperation**

- Organize migrant workers to return to work in an orderly manner through cross-regional **"point-to-point" labor cooperation**; implement "point-to-point" one-stop direct chartered car (railway and highway) transportation services;
- Carry out the mode of “delivering labor to the door” in the labor export place and “returning to the factory” in the labor input place

- **Prevention & control guidance for work resumption in enterprises**

- Health monitoring & reporting; workplace and individual precautions



Effectiveness of Resuming by Province

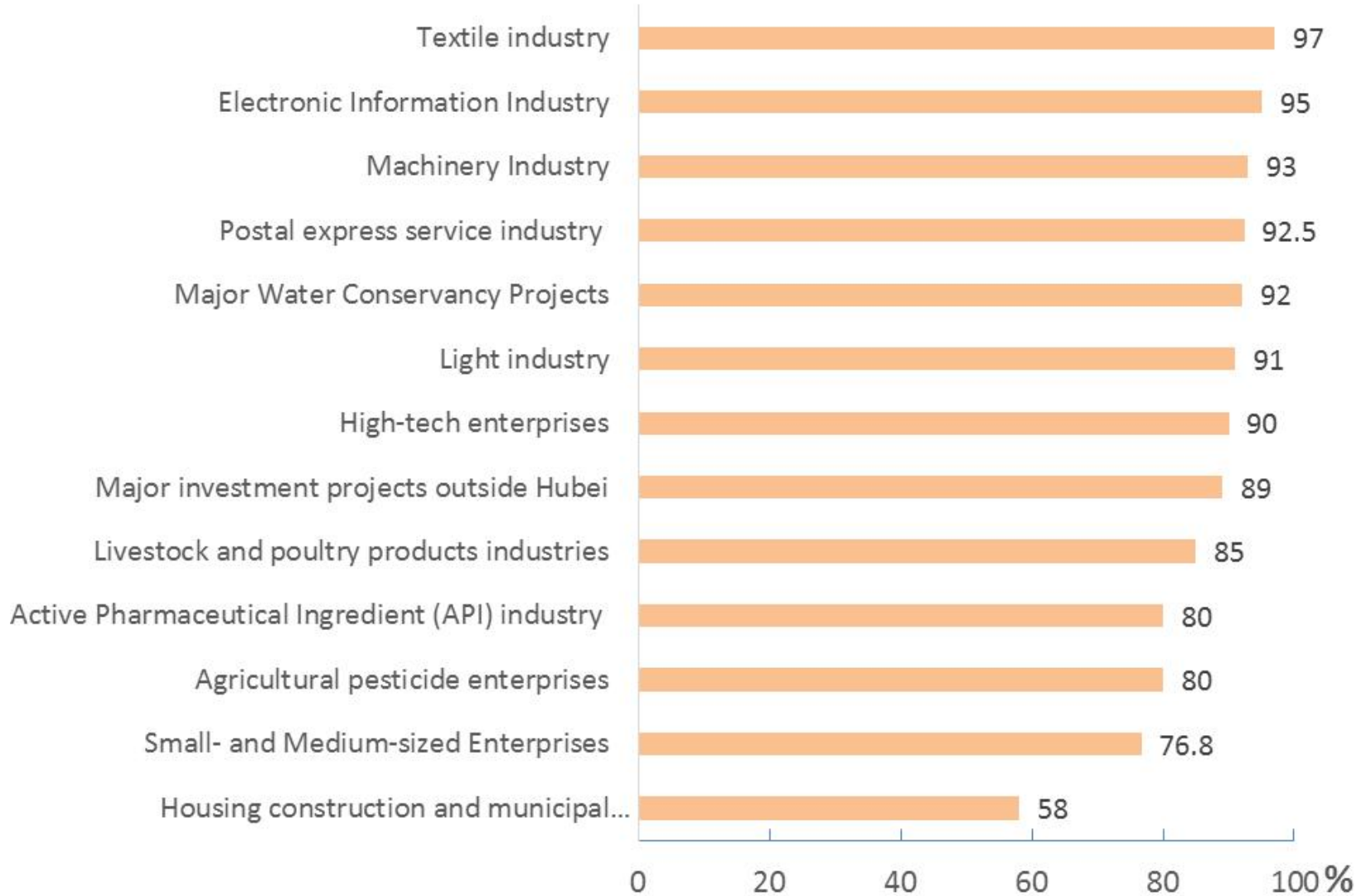
Province	Resuming work %	Province	Resuming work %
Shandong	79.4%	Fujian	75.8%
Jiangsu	75%	Zhejiang	72.2%
Liaoning	71.3%	Shanxi	61.4%
Beijing	61.2%	Guizhou	≥ 60%
Inner Mongolia	56.2%	Sichuan	55.7%
Anhui	51.5%	Shanghai	≥ 50%
Guangdong	≥ 50%	Jiangxi	49.5%
Hunan	46%	Guangxi	41.6%

The same percentage: increased to **>95% outside Hubei** As of Mar 13,
to **>98% nationwide** as of Mar 28, 2020.

* By February 19, Designated Size: annual revenue >20 million CNY



Effectiveness of Resuming by Category





Learned from Transition Stage

- **Risk-based adjustment of strategies and measures adapted to local context by local government**
- **Adhere to Four Early Measures:**
 - Control importation (cross boarder and province), esp. in key and big cities
 - Prevent local spread (epidemiological investigation, close contact tracking and management)
- **Fine-tune approaches to balance the reponses and economic development**
 - strengthen the surveillane to and response measures by employers/workplaces while resuming work
- **Utilize hi-tech such as big data and AI technologies to carry out targeted measures (e.g. contact tracing)**



中国疾病预防控制中心
CHINESE CENTER FOR DISEASE CONTROL AND PREVENTION

Thank You

