COVID-19 Research in Shenzhen



□ International cooperation for COVID-19 epidemiological study in Shenzhen

Role: data clean and analysis







Role: epidemiological guidance

Role: data acquisition



□ Rapid spread of SARS-CoV-2 in Wuhan prompted heightened surveillance in Shenzhen.



2. In the past 14 days, 100% persons who have traveled to the key epidemic areas must been quarantined at home;

3. 100% persons with close contact with the case shall be put under centralized isolation;

4. Bidirectional temperature detection shall be carried out for 100% residents in and out of the community;

5. 100% contacting registration for the landlord and lessee of the rental house.

COVID-19 Research in Shenzhen





Graph of COVID-19 index cases and close intimates in Shenzhen

Source: Shenzhen municipal health commission

Modelling Research

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Importation model of COVID-19 in Shenzhen

- Transmission modelling (SEIR) in Shenzhen City
- To estimate the proportion of detected cases in Shenzhen imported from other provinces



Cumulative infected cases in Shenzhen





Source provinces of daily index cases in Shenzhen

Epidemiological Research

□ Target population:

Shenzhen CDC identified 391 SARS-CoV-2 cases and 1286 close contacts from Jan 14 to Feb 12.

D Methods:

Estimation of transmission characteristics for contact-based and symptom-based, respectively.

Results:

Cases were isolated on average 4.6 days after developing symptoms; contact tracing reduced this by 1.9 days.

Conclusions:

- We provide a key piece of evidence supporting intensive contact tracing
- These results paint a positive picture of the impact of heightened surveillance and isolation in Shenzhen.

Highlights:

Scientific evidence of how China flattened the curve

Epidemiology and transmission of COVID-19 in 391 cases and 1286 of their close contacts in Shenzhen, China: a retrospective cohort study. The Lancet Infectious Diseases (2020).





Epidemiological Research

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THE LANCET Infectious Diseases

ARTICLES | VOLUME 20, ISSUE 6, P669-677, JUNE 01, 2020

Estimates of the severity of coronavirus disease 2019: a model-based analysis

Our processed data has shared to Dr. Neil M Ferguson and cited by their recent epidemiological modelling work



Epidemiology and transmission of COVID-19 in 391 cases and 1286 of their close contacts in Shenzhen, China: a retrospective cohort study. The Lancet Infectious Diseases (2020).

Genome Research

Article Open Access Published: 03 February 2020

A new coronavirus associated with human respiratory disease in China

Fan Wu, Su Zhao, Bin Yu, Yan-Mei Chen, Wen Wang, Zhi-Gang Song, Yi Hu, Zhao-Wu Tao, Jun-Hua Tian, Yuan-Yuan Pei, Ming-Li Yuan, Yu-Ling Zhang, Fa-Hui Dai, Yi Liu, Qi-Min Wang, Jiao-Jiao Zheng, Lin Xu, Edward C. Holmes & Yong-Zhen Zhang 🖂

Nature 579, 265–269(2020) Cite this article

366k Accesses 334 Citations 1312 Altmetric Metrics



The organization of genes for WHCV, bat SL-CoVZC45 and SARS-CoV Tor2.

81 different coronavirus gene sequences had been **shared openly via GenBank** and 189 via the China National Genomics Data Centre, which allow scientists to decode the mystery of the virus and hopefully find a treatment or vaccine.



nature > technology features > article a natureresearch journal natureresearch journal Subscribe Subscribe

TECHNOLOGY FEATURE + 24 APRIL 2020

Open science takes on the coronavirus pandemic

Data sharing, open-source designs for medical equipment, and hobbyists are all being harnessed to combat COVID-19.

Mark Zastrow

Yet it wasn't a given that researchers would embrace openness early in the outbreak: data that are made public can be difficult to publish through conventional channels later. And multiple news reports have suggested that health workers and researchers in China were initially subjected to government limits on what information they could release. But when Chinese researchers uploaded the first genome sequence of the SARS-CoV-2 virus to the online repositories virological.org and GenBank, they opened the floodgates for more sequences from China and from the rest of the world, Hodcroft says. "I am very grateful for the scientists who took this risk, because I

Antibody drug Research



Highlights:

- □ 8,558 IgG1+ antigen-binding clonotypes were identified by high-throughput scRNA/VDJ-seq
- **14** potent SARS-CoV-2 neutralizing antibodies were found from 60 convalescent patients
- **BD-368-2** showed high therapeutic and prophylactic efficacy in SARS-CoV-2-infected mice

Human antibody sequences are available on the European Genome-Phenome Archive (EGAS00001004412)





Efficient Neutralizing Antibody Identification through Antigen-Enriched High-Throughput Single-Cell RNA Sequencing



SARS-CoV-2-Infected hACE2 Transgenic Mice

Vaccination Research



Highlights:

- □ The Ad5 vectored COVID-19 vaccine is **tolerable** and **immunogenic** at 28 days post-vaccination.
- □ Humoral responses against SARS-CoV-2 peaked at day 28 post-vaccination in healthy adults
- **D** Rapid specific T-cell responses were noted from day 14 post-vaccination.

Individual participant data will be available beginning 3 months and ending 1 year after publication

	Low dose group (n=36)	Middle dose group (n=36)	High dose group (n=36)	Total (N=108)
All adverse reactions wi	thin 0-7 days			
Any	30 (83%)	30 (83%)	27 (75%)	87 (81%)
Grade 3	2 (6%)	2 (6%)	6 (17%)	10 (9%)
Injection site adverse re	actions within 0-7 day	/s		
Pain	17 (47%)	20 (56%)	21 (58%)	58 (54%)
Induration	2 (6%)	1 (3%)	1 (3%)	4 (4%)
Redness	2 (6%)	1 (3%)	1 (3%)	4 (4%)
Swelling	4 (11%)	4 (11%)	0	8 (7%)
ltch	2 (6%)	3 (8%)	0	5 (5%)
Muscular weakness	0	0	1 (3%)	1 (1%)

Adverse reactions within 7 days and overall adverse events within 28 days after vaccination



Specific T-cell response measured by ELISpot

 <u>FC Zhu, YH Li, XH Guan, et al. Safety,</u> <u>tolerability, and immunogenicity of a</u> <u>recombinant adenovirus type-5 vectored</u> <u>COVID-19 vaccine: a dose-escalation, open-</u> <u>label, non-randomised, first-in-human trial.</u> Lancet, 2020.

COVID-19 in open science



- **Transmission modeling**
- **Epidemiological**
- □ Genome
- □ Antibody drug
- □ Vaccination





COVID-19 Happening in China
 COVID-19 Related Open Science in China
 COVID-19 Related Open Resources from China
 Summary

Public data sets, in Chinese



DXY-COVID-19-Data: COVID-19 Infection Time Series Data Warehouse

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DXY-COVID-19-Crawler: COVID-19 Realtime Infection Crawler and API

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3017052	5982030	260197	7		363001		
Active Cases	Total Cases	Total Recovered			Total Deaths		



Pneumonia-CT-LKM-PP: CT image analysis of pneumonia

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Open source models

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CT Image Analytics for COVID-19: A COVID-19.

- Deep learning model was developed to extract visual features from 3,322 COVID-19 patients (Keya Imaging Ltd)
- CT Image Analytics for COVID-19 suspected cases with 96% accuracy in 20 seconds (Free to apply in AliCloud)
- □ Already deployed in more than 160 hospitals in China and completed 260,000 clinical cases.



Li L, Qin L, Xu Z, et al. Artificial Intelligence Distinguishes COVID-19 from Community Acquired Pneumonia on Chest CT. Radiology. 2020;200905.



Source: AliCloud





- COVID-19 Happening in China
 COVID-19 Related Open Science in China
- COVID-19 Related Open Resources from China
- Summary

Summary



COVID-19 history in China, 4 stages

- Stage I: Early outbreak in Wuhan City, slow, pay for unknown
- Stage II: Central government take action on block COVID-19, very good
- Stage III: Prevention of community spread and importation, very good
- Stage IV: Return to work and production, and school reopening, very good
- □ COVID related open science in China
 - Transmission modeling,
 - Epidemiological
 - Genome
 - Antibody drug
 - Vaccination
- COVID-19 Related Open Resources from China
 - Many related open sourced can be used



Thanks for your attention

"At unprecedented speed, scientists are starting experiments, sharing data and revealing the secrets of the pathogen — a race that is made possible by new scientific tools and cultural norms in the face of a public health emergency."

—Mark Zastrow

Health Encyclopedia Code (HEC)



Application system HEC





Application system HEC





Application scenarios



"One code for one life"

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Emergency patients

Doctor gets the patient's core information instantly

Referral patients

Doctor rely on the patient's HEC for diagnosis, avoiding repeated examination.



Physical examination people

Continuous and comparable tracking of the key indicators for the detection of disease signs. Hospital



One-stop service



深圳CDC应急响应



Motivation



Basic diseases



Three categories :

- □ basic metabolic disorders,
- □ immunodeficiency,
- serious chronic wasting diseases