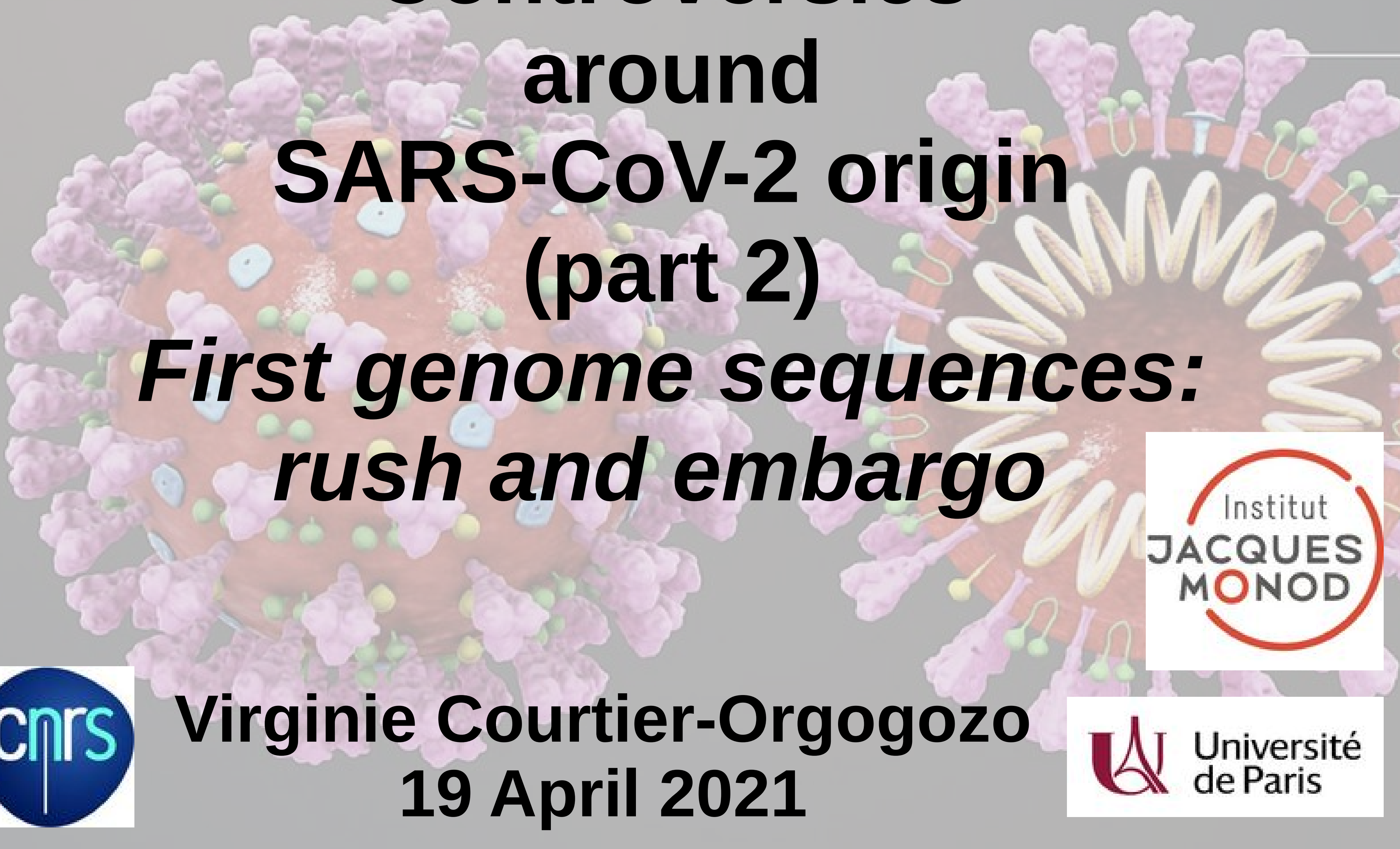
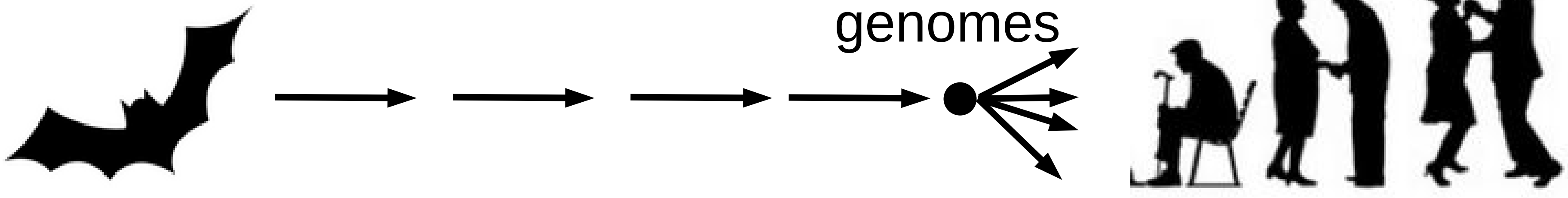


Controversies around SARS-CoV-2 origin (part 2)

First genome sequences: rush and embargo

Virginie Courtier-Orgogozo

19 April 2021



Bats

Mother
of all
genomes

Outbreak in Wuhan

20-30 years
ago

Oct-Nov
2019

December 2019

From Ecology to Genomics
Humans possibly involved
Politics, Fast moving field

Scientific publications, reports

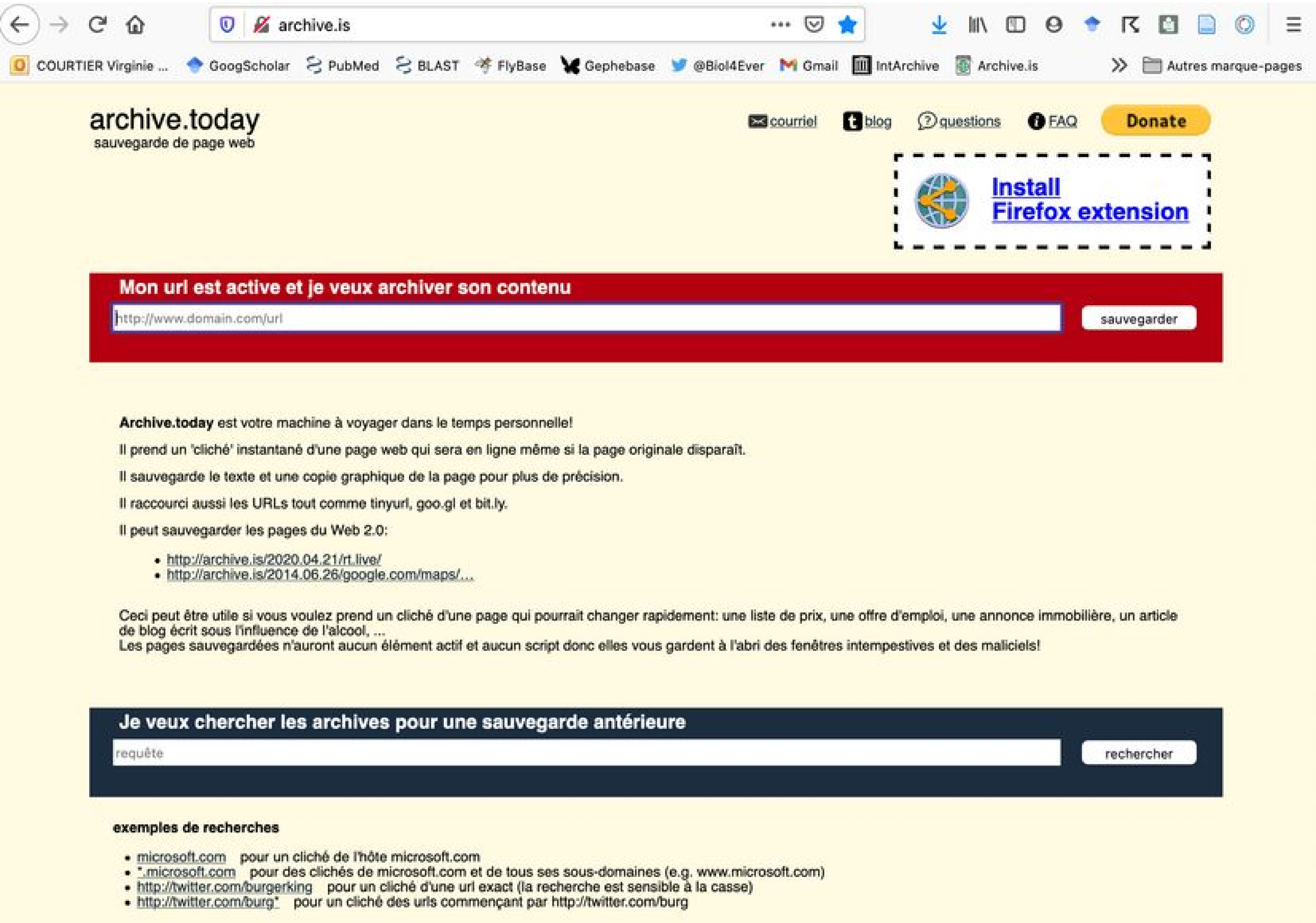
Sequence databases

Press articles, Documentaries

Tweets, Blogs, Conferences

Emails

Sequence analyses



archive.today
sauvegarde de page web

Mon url est active et je veux archiver son contenu

Archive.today est votre machine à voyager dans le temps personnelle!

Il prend un 'cliché' instantané d'une page web qui sera en ligne même si la page originale disparaît.

Il sauvegarde le texte et une copie graphique de la page pour plus de précision.

Il raccourci aussi les URLs tout comme tinyurl, goo.gl et bit.ly.

Il peut sauvegarder les pages du Web 2.0:

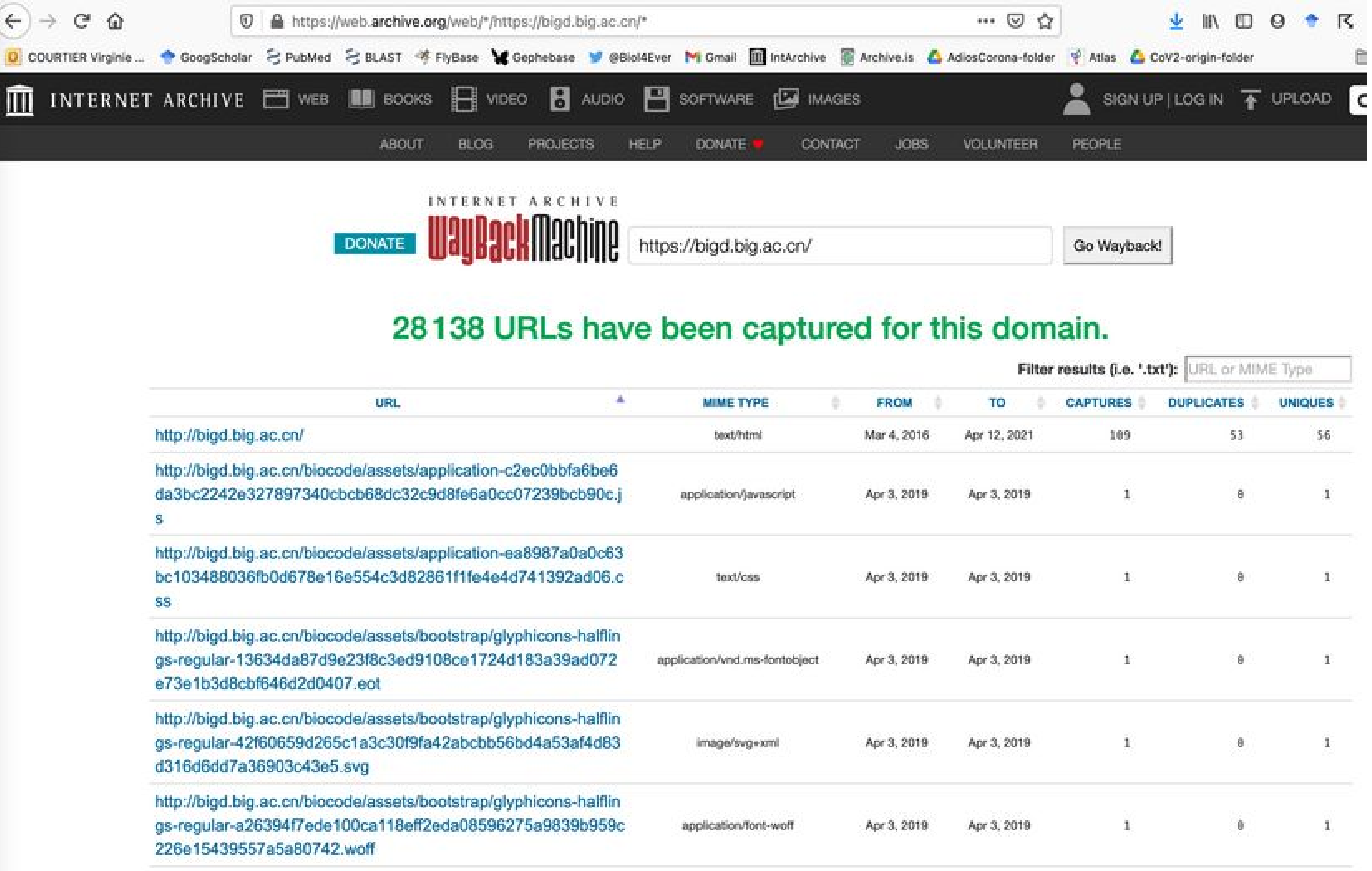
- http://archive.is/2020.04.21/rt.live/
- http://archive.is/2014.06.26/google.com/maps/...

Ceci peut être utile si vous voulez prend un cliché d'une page qui pourrait changer rapidement: une liste de prix, une offre d'emploi, une annonce immobilière, un article de blog écrit sous l'influence de l'alcool, ...
Les pages sauvegardées n'auront aucun élément actif et aucun script donc elles vous gardent à l'abri des fenêtres intempestives et des maliciels!

Je veux chercher les archives pour une sauvegarde antérieure

exemples de recherches

- microsoft.com pour un cliché de l'hôte microsoft.com
- *.microsoft.com pour des clichés de microsoft.com et de tous ses sous-domaines (e.g. www.microsoft.com)
- http://twitter.com/burgerking pour un cliché d'une url exact (la recherche est sensible à la casse)
- http://twitter.com/burg* pour un cliché des urls commençant par http://twitter.com/burg



28138 URLs have been captured for this domain.

Filter results (i.e. '.txt'): URL or MIME Type

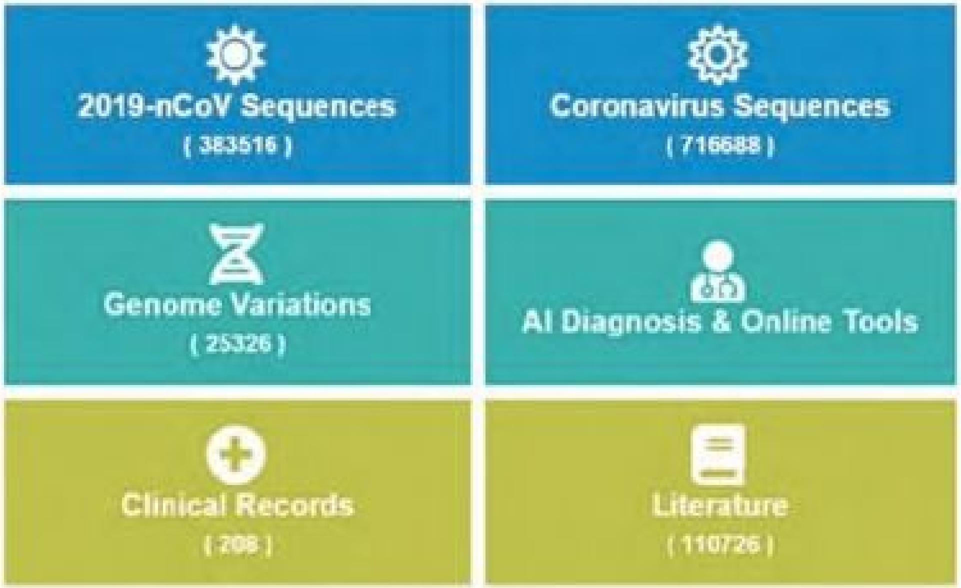
URL	MIME TYPE	FROM	TO	CAPTURES	DUPLICATES	UNIQUES
http://bigd.big.ac.cn/	text/html	Mar 4, 2016	Apr 12, 2021	109	53	56
http://bigd.big.ac.cn/biocode/assets/application-c2ec0bbfa6be6da3bc2242e327897340cbcb68dc32c9d8fe6a0cc07239bcb90c.js	application/javascript	Apr 3, 2019	Apr 3, 2019	1	0	1
http://bigd.big.ac.cn/biocode/assets/application-ea8987a0a0c63bc103488036fb0d678e16e554c3d82861f1fe4e4d741392ad06.css	text/css	Apr 3, 2019	Apr 3, 2019	1	0	1
http://bigd.big.ac.cn/biocode/assets/bootstrap/glyphicons-halflings-regular-13634da87d9e23f8c3ed9108ce1724d183a39ad072e73e1b3d8cbf646d2d0407.eot	application/vnd.ms-fontobject	Apr 3, 2019	Apr 3, 2019	1	0	1
http://bigd.big.ac.cn/biocode/assets/bootstrap/glyphicons-halflings-regular-42f60659d265c1a3c30f9fa42abcbb56bd4a53af4d83d316d6dd7a36903c43e5.svg	image/svg+xml	Apr 3, 2019	Apr 3, 2019	1	0	1
http://bigd.big.ac.cn/biocode/assets/bootstrap/glyphicons-halflings-regular-a26394f7ede100ca118eff2eda08596275a9839b959c226e15439557a5a80742.woff	application/font-woff	Apr 3, 2019	Apr 3, 2019	1	0	1

2019nCoVR

China National Center for Bioinformation

2019 Novel Coronavirus Resource (2019nCoVR)

Six modules



2019-nCoV Sequences
(383516)

Coronavirus Sequences
(716688)

Genome Variations
(25326)

AI Diagnosis & Online Tools

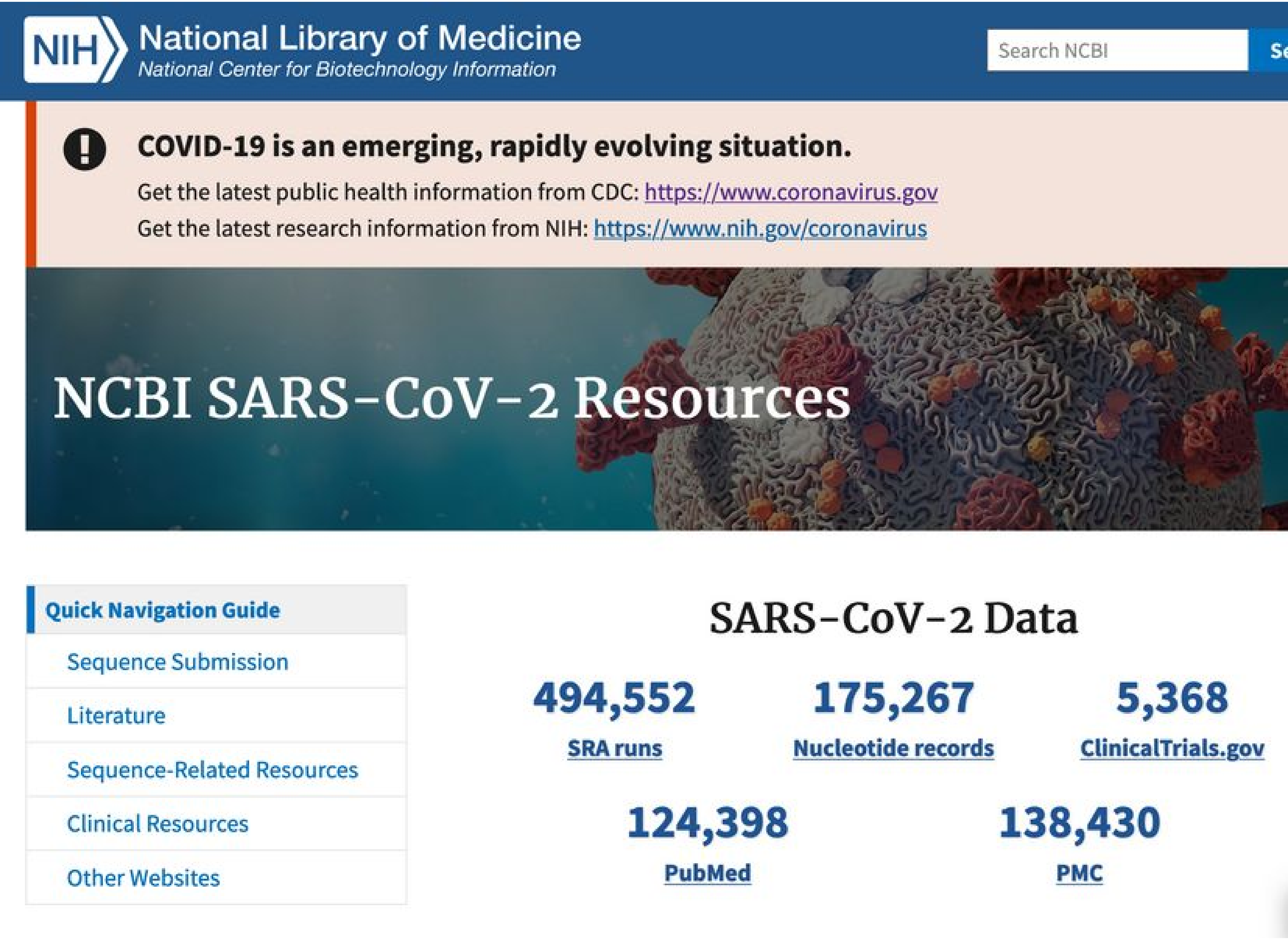
Clinical Records
(208)

Literature
(110726)

https://bigd.big.ac.cn/ncov

Global users

Unique users: >600,000
Countries/regions: 175
Data downloads: >250 million



NIH National Library of Medicine
National Center for Biotechnology Information

Search NCBI

COVID-19 is an emerging, rapidly evolving situation.

Get the latest public health information from CDC: https://www.coronavirus.gov

Get the latest research information from NIH: https://www.nih.gov/coronavirus

NCBI SARS-CoV-2 Resources

Quick Navigation Guide

- Sequence Submission
- Literature
- Sequence-Related Resources
- Clinical Resources
- Other Websites

SARS-CoV-2 Data

494,552
SRA runs

175,267
Nucleotide records

5,368
ClinicalTrials.gov

124,398
PubMed

138,430
PMC

In Focus

Recommended composition of influenza virus vaccines for use in the 2021-2022 Northern Hemisphere Influenza Season announced

(Geneva, Switzerland) An advisory group of experts taking part in a virtual meeting organized by the WHO Global Influenza Programme between 17-25 February 2021 analyzed influenza virus surveillance data generated by the WHO Global Influenza Surveillance and Response System (GISRS), and issued on 26 February 2021, recommendations on the composition of the influenza vaccines for the following influenza season.

These recommendations are used by the national vaccine regulatory agencies and the pharmaceutical companies to develop, produce and license influenza vaccines.

read more:

Genomic epidemiology of hCoV-19

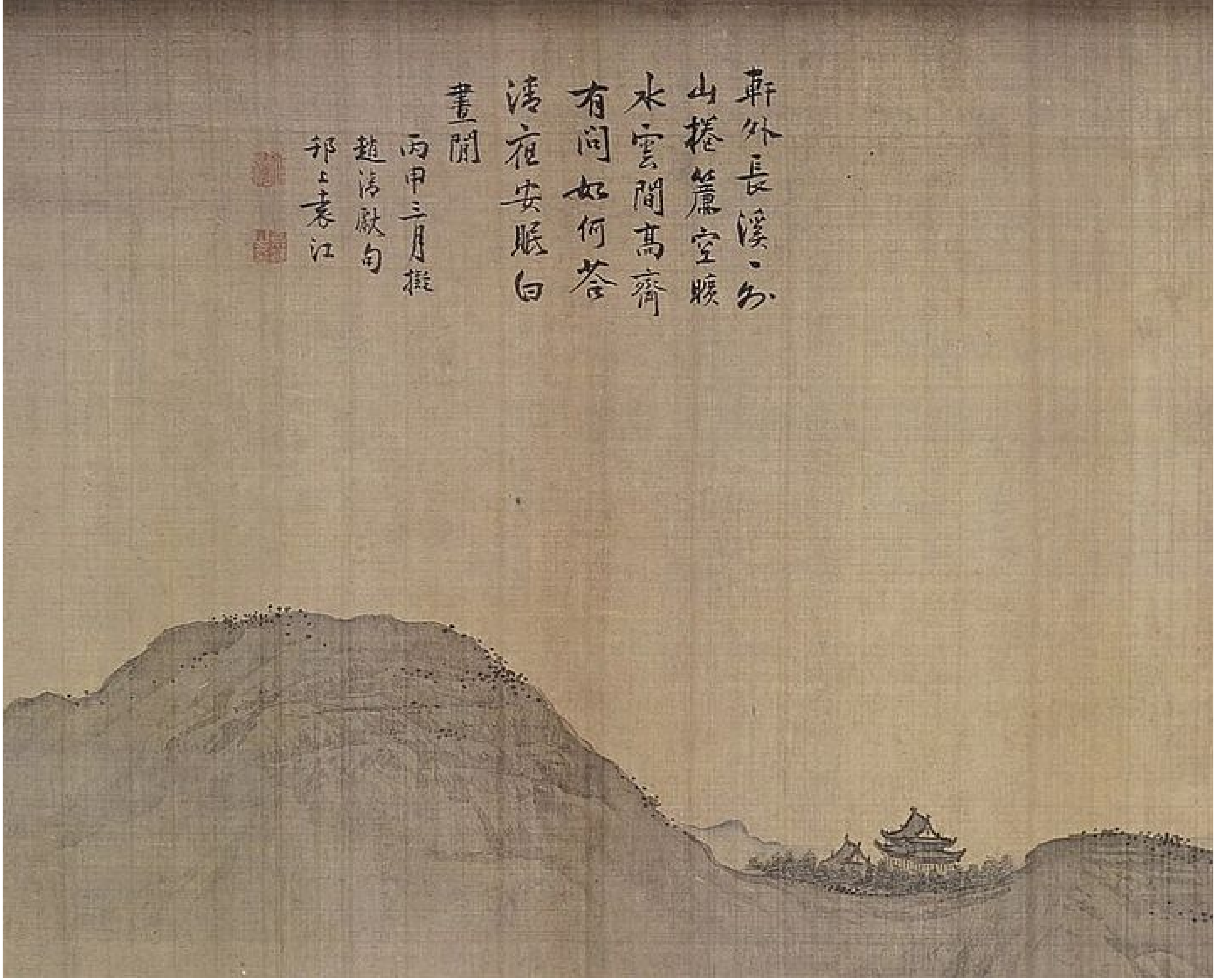
hCoV-19 data sharing via GISAID

1,138,698
submissions

Enabled by data shared via GISAID

CoVizu

Western University (Canada)
Near real-time visualization of hCoV-19 genomic variation



Yuan Jiang, 18th http://www.alaintruong.com/archives/2019/06/07/37411497.html

Charles de la Fosse, 18th

https://www.christies.com/en/lot/lot-6278952

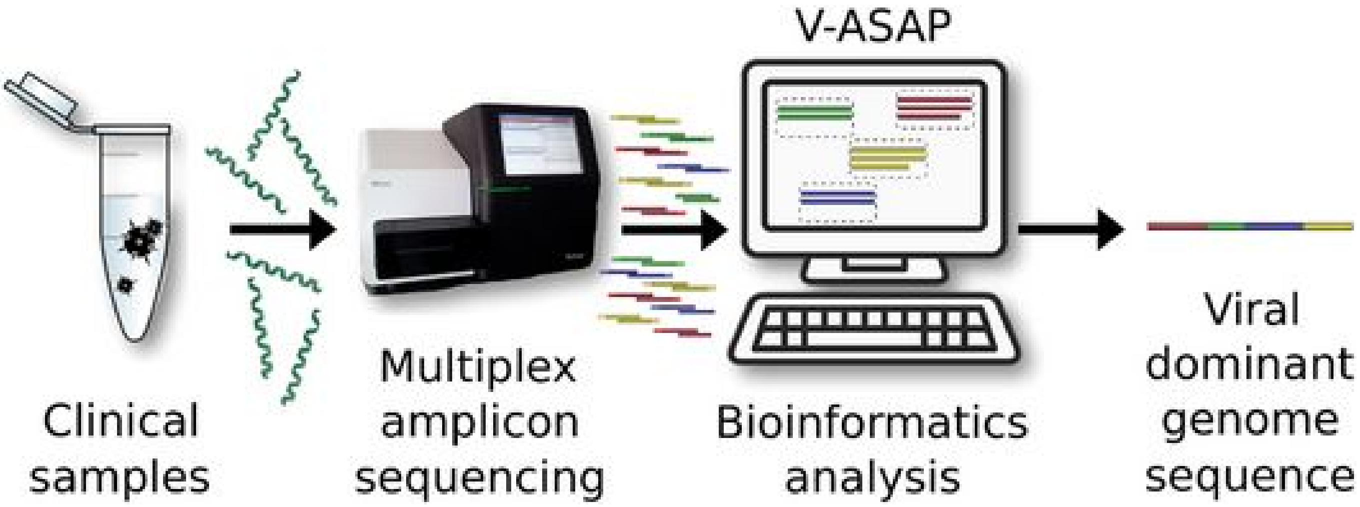
POINTS

FRANÇOIS JULLIEN

La propension des choses

Pour une histoire de l'efficacité en Chine

ESSAIS

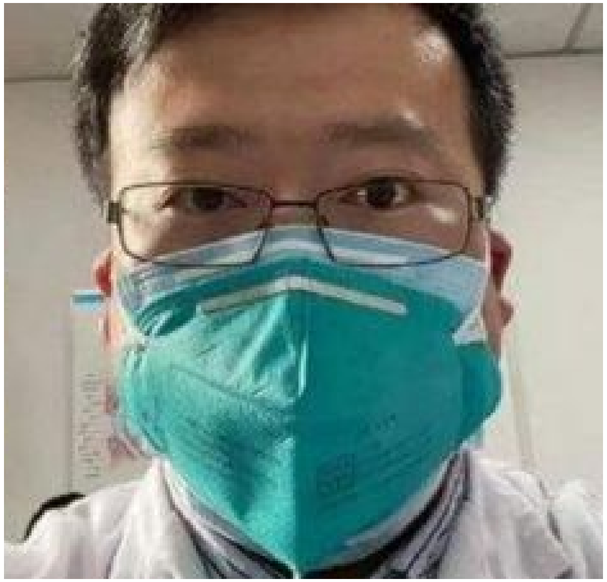


Why is it crucial to sequence the pathogen quickly?

Prevent transmission
Find treatments

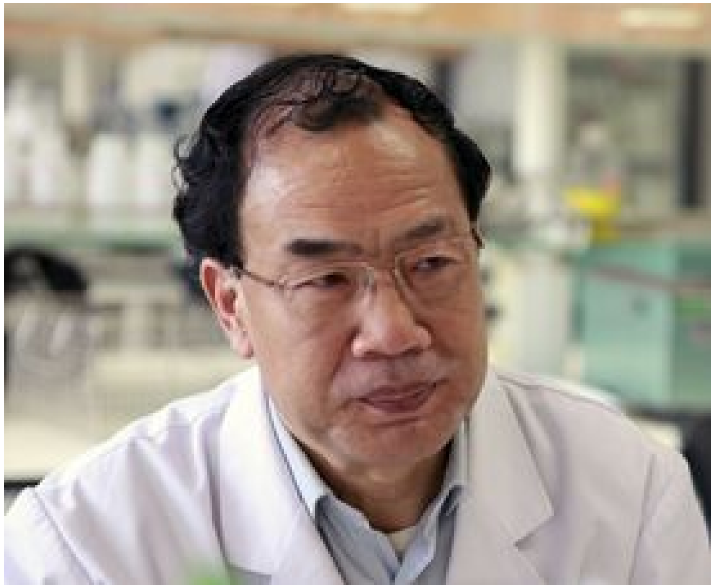
Develop detection tests
Develop vaccines

Genome sequence public on 11 Jan 2020



Li Wenliang

Wuhan Central
Hospital



Yong-Zhen Zhang

Shanghai Public
Health Clinical
Center

Zheng-Li Shi

Wuhan Institute
of Virology

Died
on 6 February 2020
33 years

Li Wenliang

Yong-Zhen Zhang

3rd GigaScience Award for Data Sharing
(Nov 2020)

Nature’s 10 people who helped shape science in 2020

Time’s 100 Most Influential People of 2020
(Sept 2020)

Zheng-Li Shi

"advanced worker of the Chinese Academy of Sciences"

(Jan 2021)

http://gigasciencejournal.com/blog/covid-19-hero-wins-gigascience-prize/
https://www.nature.com/immersive/d41586-020-03435-6/index.html
https://time.com/collection/100-most-influential-people-2020/5888191/zhang-yongzhen/
https://www.globaltimes.cn/page/202101/1212921.shtml

First sample sequenced

15 December 2019: a 65-year-old male deliveryman at the South China Seafood Market began to have fever. On December 18, he came to the emergency department of Wuhan Central Hospital (Nanjing Road District) to see a doctor. The doctor suspected that it might be community-acquired pneumonia and admitted him to the emergency ward of the hospital. Community-acquired pneumonia is a general term for pneumonia caused by bacteria, viruses, chlamydia and mycoplasma. The main clinical symptoms are cough, with or without sputum and chest pain.

On December 22, the patient's condition worsened and entered the ICU. Doctors used various antibiotics to treat it to no avail. Professor Zhao Su, chief physician of the Department of Respiratory Medicine of Wuhan Central Hospital, told Caixin reporters that on **December 24**, a deputy chief physician of the Department of Respiratory Medicine performed a **bronchoscopy sample** on the patient, and then sent the patient’s alveolar lavage fluid sample to the No. The tripartite testing agency **Guangzhou Weiyuan Gene Technology Co., Ltd**. conducts NGS testing (...)

https://web.archive.org/web/20200227094018/http://china.caixin.com/2020-02-26/101520972.html
http://archive.is/yJLzy

EPI_ISL_402123
MT019529
GWHABKF00000000

2019年12月26日 早上09:28

ASRS 都出来了

It found SARS

我天，哪个样本

My goodness, which sample?

这不能开玩笑

This better not be a joke

https://chinadigitaltimes.net/chinese/633514.html

https://medium.com/coronavirus19/%E8%AE%B0%E5%BD%95%E4%B8%80%E4%B8%8B%E9%A6%96%E6%AC%A1%E5%8F%91%E7%8E%B0%E6%96%B0%E5%9E%8B%E5%86%A0%E7%8A%B6%E7%97%85%E6%AF%92%E7%9A%84%E7%BB%8F%E5%8E%86ebb4b5522043

[redacted] 这个样本你单独处理哈

嗯，我在分析

SARS本身就是来自于蝙蝠的

还有果子狸

2019年12月26日 早上10:24

Bat_SARS_like_coronavirus

Check back this sample separately

OK, I am analyzing it

https://chinadigitaltimes.net/chinese/633514.html

就跟这两个最像

Bat_SARS-like_coronavirus_isolate_bat-SL-CoVZXC21

Bat_SARS-like_coronavirus_isolate_bat-SL-CoVZC45

2019年12月26日 晚上18:08

进化树.pdf

1.5 MB

https://chinadigitaltimes.net/chinese/633514.html

communicated with hospitals and disease control (departments) by telephone, and even went to Wuhan on the 29th and 30th to report and exchange all analysis results face-to-face with the leaders of hospitals and disease control centers

http://archive.is/yJLzy

Second sample sequenced

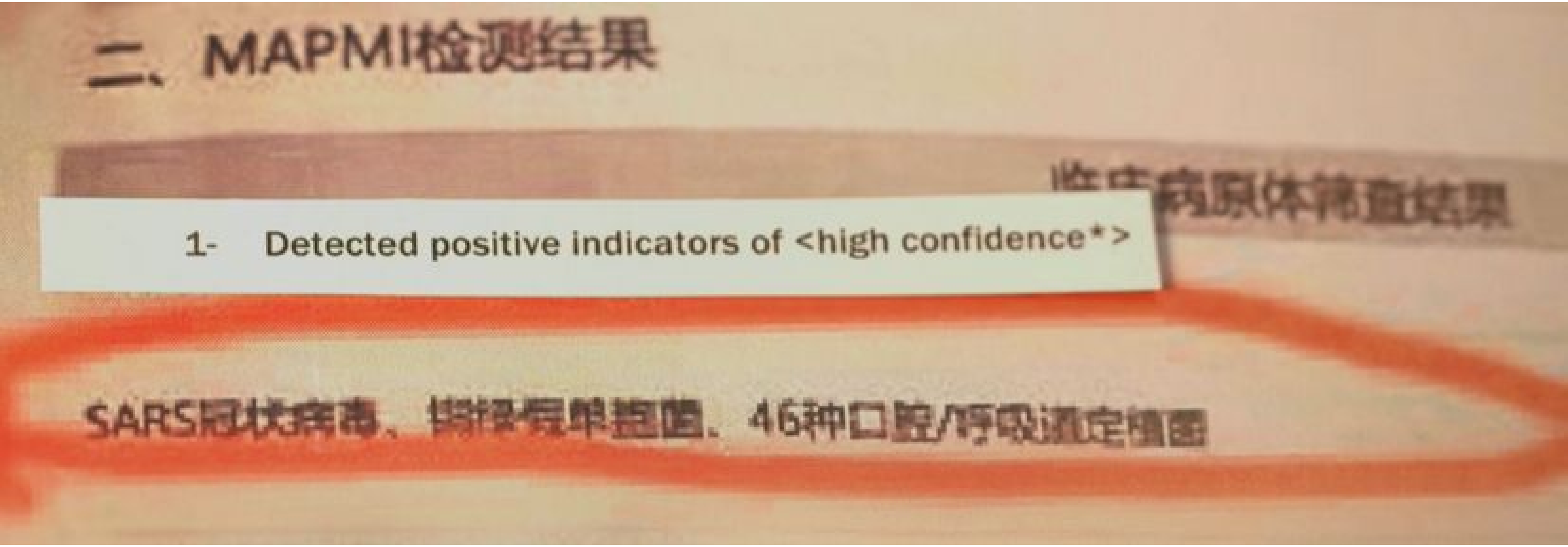
Sampled 26 December 2019
provided by General Hospital of Central Theater Command of People's Liberation Army of China
44M
Patient S03 in WHO-China joint report

EPI_ISL_406798
NMDC60013002-01
LR757998
CNA0007332

Other patients in several hospitals

Mistake in a test result

30 December 2019



二、MAPMI检测结果

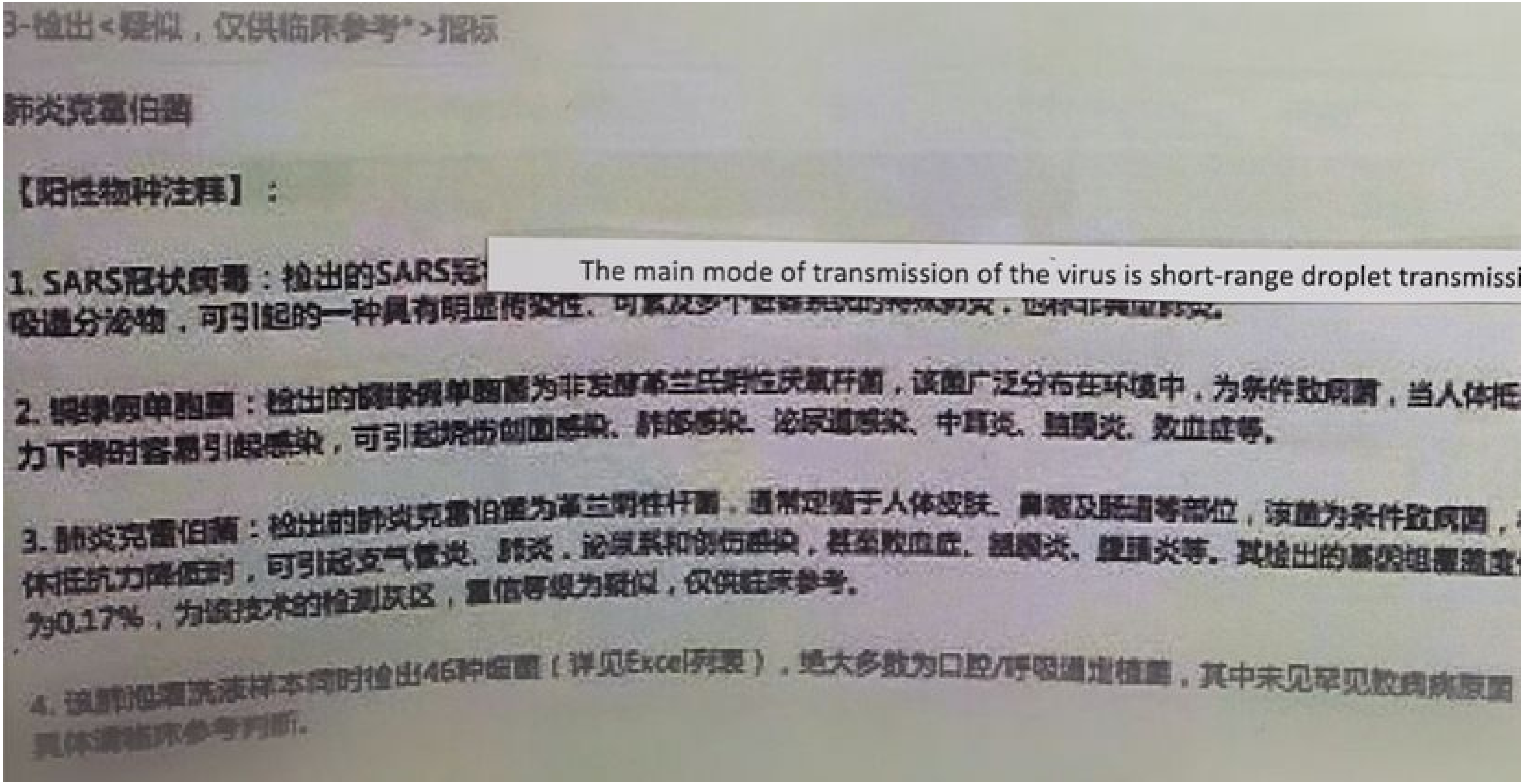
临床病原体筛查结果

1- Detected positive indicators of <high confidence*>

SARS冠状病毒、铜绿假单胞菌、46种口腔/呼吸道定植菌

PBS documentary

Mistake in test result



3-检出<疑似，仅供临床参考*>指标

肺炎克雷伯菌

【阳性物种注释】：

1. SARS冠状病毒：检出的SARS冠

The main mode of transmission of the virus is short-range droplet transmissi

吸道分泌物，可引起的一种具有明显传染性、可累及多个脏器系统的特殊肺炎，也称非典型肺炎。

2. 铜绿假单胞菌：检出的铜绿假单胞菌为非发酵革兰氏阴性需氧杆菌，该菌广泛分布在环境中，为条件致病菌，当人体抵
力下降时容易引起感染，可引起烧伤创面感染、肺部感染、泌尿道感染、中耳炎、角膜炎、败血症等。

3. 肺炎克雷伯菌：检出的肺炎克雷伯菌为革兰阴性杆菌，通常定植于人体皮肤、鼻咽及肠道等部位，该菌为条件致病菌，
体抵抗力降低时，可引起支气管炎、肺炎，泌尿系和创伤感染，甚至败血症、脑膜炎、腹膜炎等。其检出的序列相对丰度
为0.17%，为该技术的检测灰区，置信等级为疑似，仅供临床参考。

4. 该肺泡灌洗液样本同时检出46种细菌（详见Excel列表），绝大多数为口腔/呼吸道定植菌，其中未见罕见致病病原菌
具体请临床参考判断。

PBS documentary

04级 CLASS OF '04

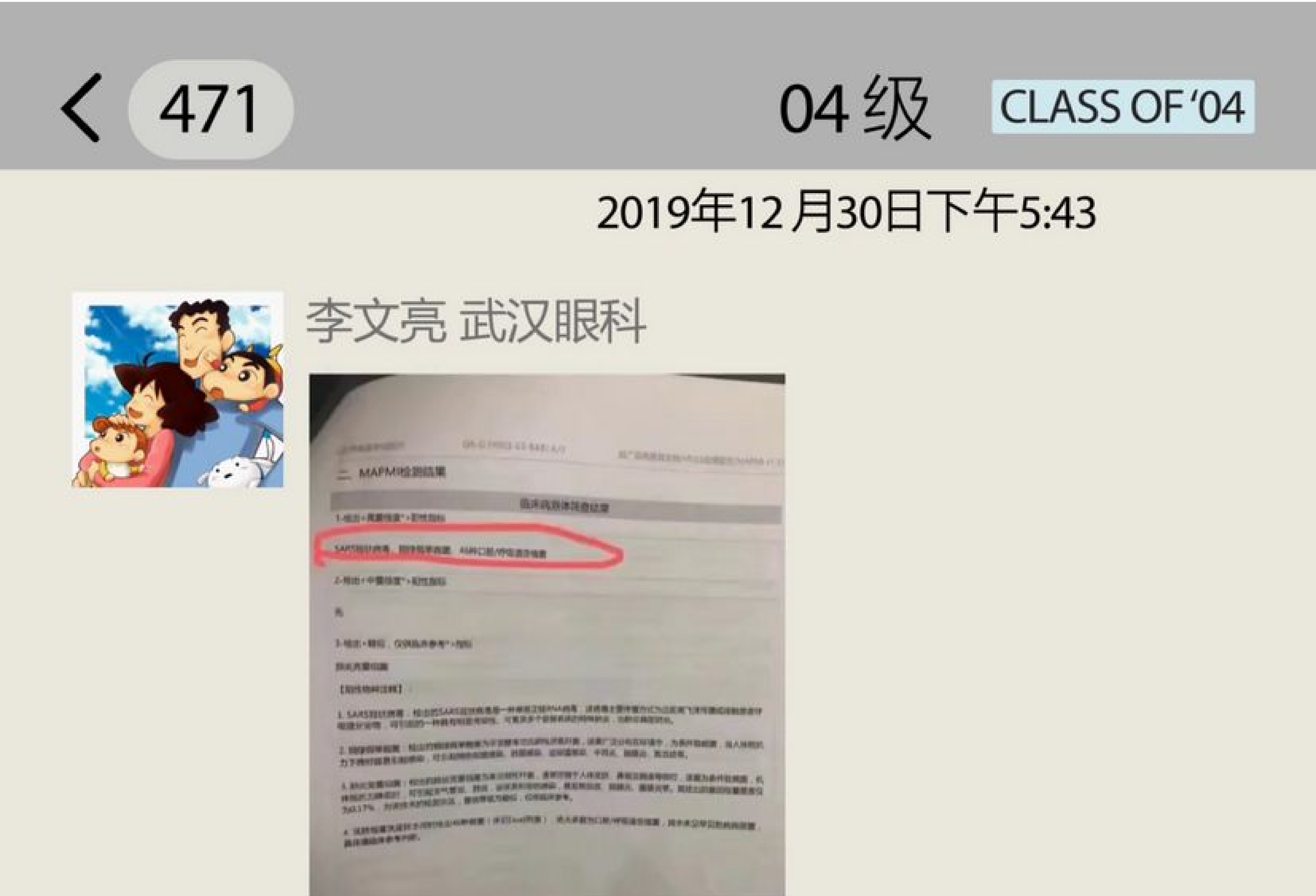
2019年12月30日下午5:43

李文亮 武汉眼科 Li Wenliang Wuhan Opthalmology

华南水果海鲜市场确诊了7例SARS

7 case of SARS have been confirmed at Huanan Seafood Market

PBS documentary



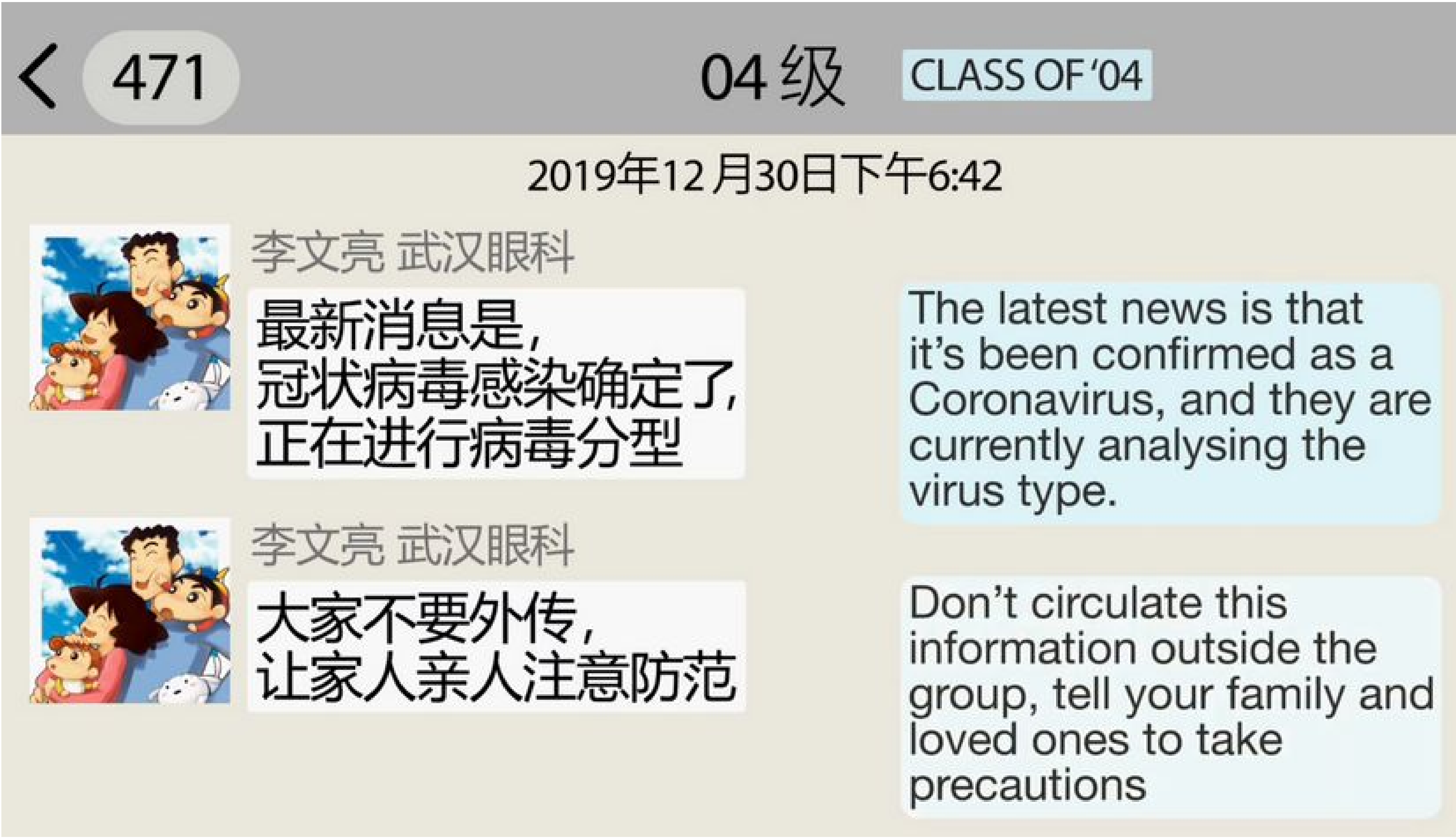
04级

CLASS OF '04

2019年12月30日下午5:43

李文亮 武汉眼科

PBS documentary



2019年12月30日下午6:42

李文亮 武汉眼科

最新消息是，
冠状病毒感染确定了，
正在进行病毒分型

The latest news is that it's been confirmed as a Coronavirus, and they are currently analysing the virus type.

李文亮 武汉眼科

大家不要外传，
让家人亲人注意防范

Don't circulate this information outside the group, tell your family and loved ones to take precautions

PBS documentary

30 December 2019

ProMED
INTERNATIONAL SOCIETY
FOR INFECTIOUS DISEASES

Published Date: 2019-12-30 23:59:00
Subject: PRO/AH/EDR> Undiagnosed pneumonia - China (HU): RFI
Archive Number: 20191230.6864153

UNDIAGNOSED PNEUMONIA - CHINA (HUBEI): REQUEST FOR INFORMATION
****
A ProMED-mail post
http://www.promedmail.org
ProMED-mail is a program of the
International Society for Infectious Diseases
http://www.isid.org

[1]
Date: 30 Dec 2019
Source: Finance Sina [machine translation]
https://finance.sina.cn/2019-12-31/detail-iihnzahk1074832.d.html?from=wap

Wuhan unexplained pneumonia has been isolated test results will be announced [as soon as available]

31 December 2019
Ian Lipkin got a call from Georges Gao on WeChat.

“He had identified the virus, it was a new coronavirus, and it was not highly transmissible”

PBS documentary

31 Dec 2019: WHO picked up on reports of pneumonia cases in Wuhan and asked the Chinese government for more information.

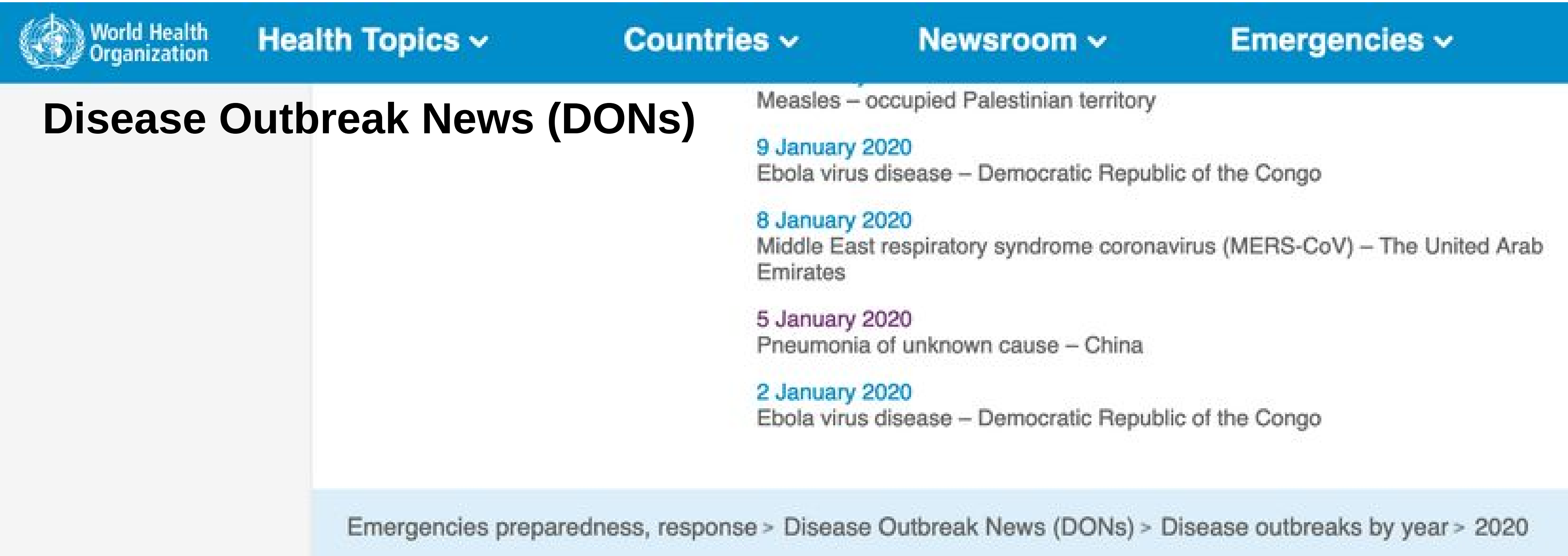
https://www.rte.ie/news/primetime/2021/0318/1204794-covid-19-origins-china-wuhan-bats-lab-leak-frozen-food/

The WHO heard back 2 days later: “there are 44 cases of pneumonia of unknown cause”.

https://apnews.com/article/3c061794970661042b18d5aeaaed9fae

International Health Regulations: When case of Public Health Emergency of International Concern (a new coronavirus meets this criteria), the government is obliged by law to report to the WHO within 24 hours.

Disease Outbreak News (DONs)



Measles – occupied Palestinian territory

9 January 2020
Ebola virus disease – Democratic Republic of the Congo

8 January 2020
Middle East respiratory syndrome coronavirus (MERS-CoV) – The United Arab Emirates

5 January 2020
Pneumonia of unknown cause – China

2 January 2020
Ebola virus disease – Democratic Republic of the Congo

Emergencies preparedness, response > Disease Outbreak News (DONs) > Disease outbreaks by year > 2020

https://www.who.int/csr/don/archive/year/2020/en/

5 January

Disease Outbreak News (DONs)

World Health Organization

Pneumonia of unknown cause – China

Disease outbreak news
5 January 2020

On 31 December 2019, the WHO China Country Office was informed of cases of pneumonia of unknown etiology (unknown cause) detected in Wuhan City, Hubei Province of China. As of 3 January 2020, a total of 44 patients with pneumonia of unknown etiology have been reported to WHO by the national authorities in China. Of the 44 cases reported, 11 are severely ill, while the remaining 33 patients are in stable condition. According to media reports, the concerned market in Wuhan was closed on 1 January 2020 for environmental sanitation and disinfection.

The causal agent has not yet been identified or confirmed. On 1 January 2020, WHO requested further information from national authorities to assess the risk.

National authorities report that all patients are isolated and receiving treatment in Wuhan medical institutions. The clinical signs and symptoms are mainly fever, with a few patients having difficulty in breathing, and chest radiographs showing invasive lesions of both lungs.

According to the authorities, some patients were operating dealers or vendors in the Huanan Seafood market. Based on the preliminary information from the Chinese investigation team, no evidence of significant human-to-human transmission and no health care worker infections have been reported.

https://www.who.int/csr/don/05-january-2020-pneumonia-of-unkown-cause-china/en/

30 December 2019

武汉市卫生健康委员会

关于做好不明原因肺炎救治工作的紧急通知

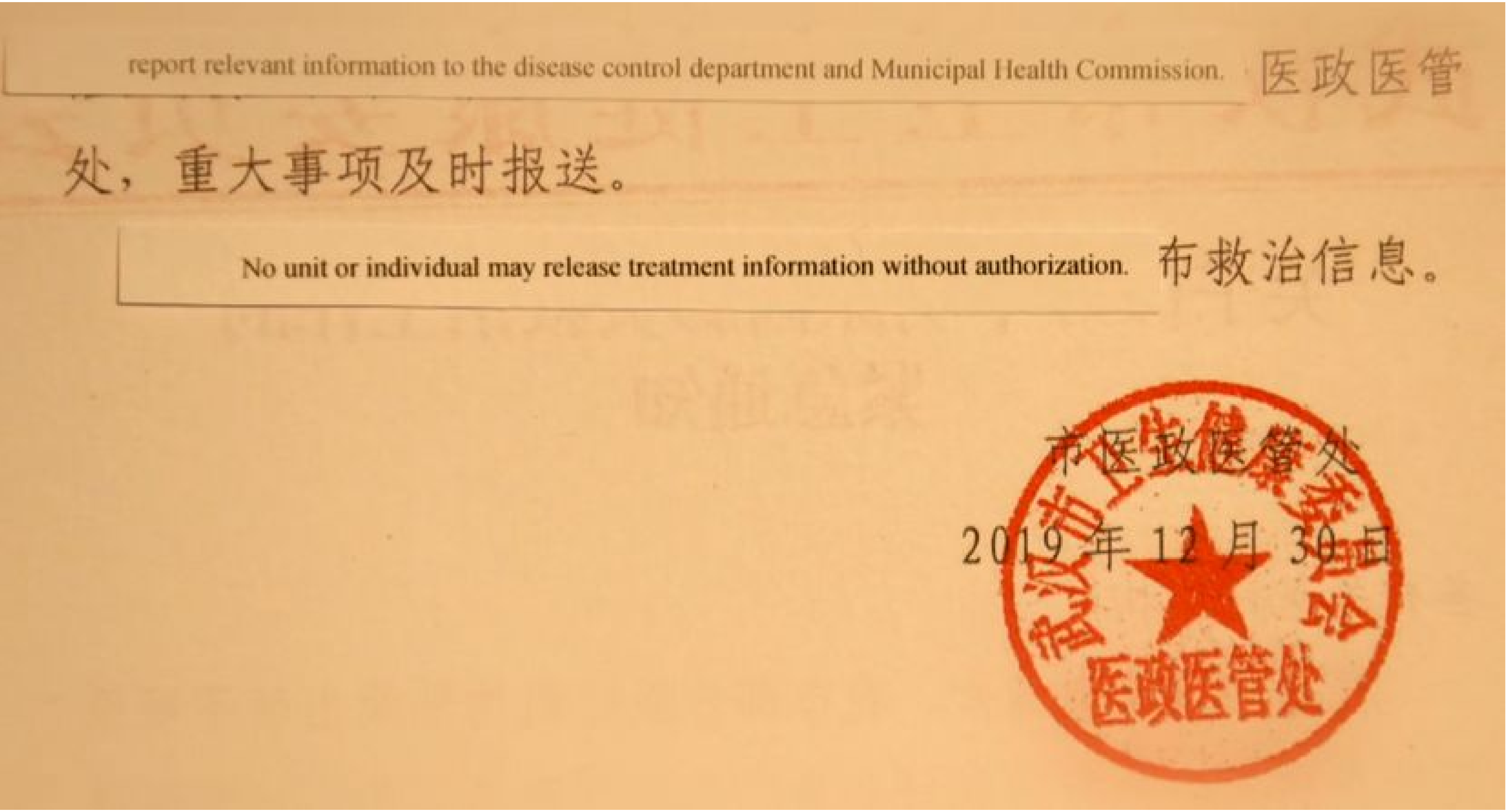
各有关医疗机构：

根据上级紧急通知，我市部分医疗机构陆续出现不明原因肺炎病人，为有效做好此类病人医疗救治工作，切实保障

Urgent Notice on the Treatment
of Pneumonia of Unknown Case
by the Wuhan Municipal Health Commission

http://archive.is/yJLzy

PBS documentary



report relevant information to the disease control department and Municipal Health Commission. 医政医管

处，重大事项及时报送。

No unit or individual may release treatment information without authorization. 布救治信息。

市医政医管处

2019年12月30日

PBS documentary

31 December 2019

2019年12月31日 星期二

First Public Notice
by the Wuhan Municipal Health Commission

武汉市卫健委关于当前我市肺炎疫情的情况通报

发布机构：武汉市卫生健康委员会 | 发布时间：2019-12-31 13:38:05 | 点击数：45101 | 字号：大 中 小

近期部分医疗机构发现接诊的多例肺炎病例与华南海鲜城有关联，市卫健委接到报告后，立即在全市
构开展与华南海鲜城有关联的病例搜索和回顾性调查，目前已发现27例病例，其中7例病情严重，其余病例
控，有2例病情好转拟于近期出院。病例临床表现主要为发热，少数病人呼吸困难，胸片呈双肺浸润性病灶
有病例均已隔离治疗，密切接触者的追踪调查和医学观察正在进行中，对华南海鲜城的卫生学调查和环境
在进行中。

武汉市组织同济医院、省疾控中心、中科院武汉病毒所、武汉市传染病医院及武汉市疾控中心等单位
学、流行病学、病毒学专家进行会诊，专家从病情、治疗转归、流行病学调查、实验室初步检测等方面情
上述病例系病毒性肺炎。到目前为止调查未发现明显人传人现象，未发现医务人员感染。目前对病原的检

http://wjw.wuhan.gov.cn/front/web/showDetail/2019123108989

31 December 2019: censorship

YY, a live-streaming platform in China, added 45 keywords to its blacklist, to censor keywords related to the coronavirus outbreak

List of keywords blacklisted:

Unspecified pneumonia in Wuhan
epidemic pneumonia in Wuhan
Wuhan Seafood Market
Pneumonia outbreak in Wuhan
Severe Acute Respiratory Syndrome (SARS) in Wuhan
Live Monkey Lab
p4 virus laboratory
viral infection
Isolation around South China
Epidemic in Wuhan
7 cases of infection
etc.

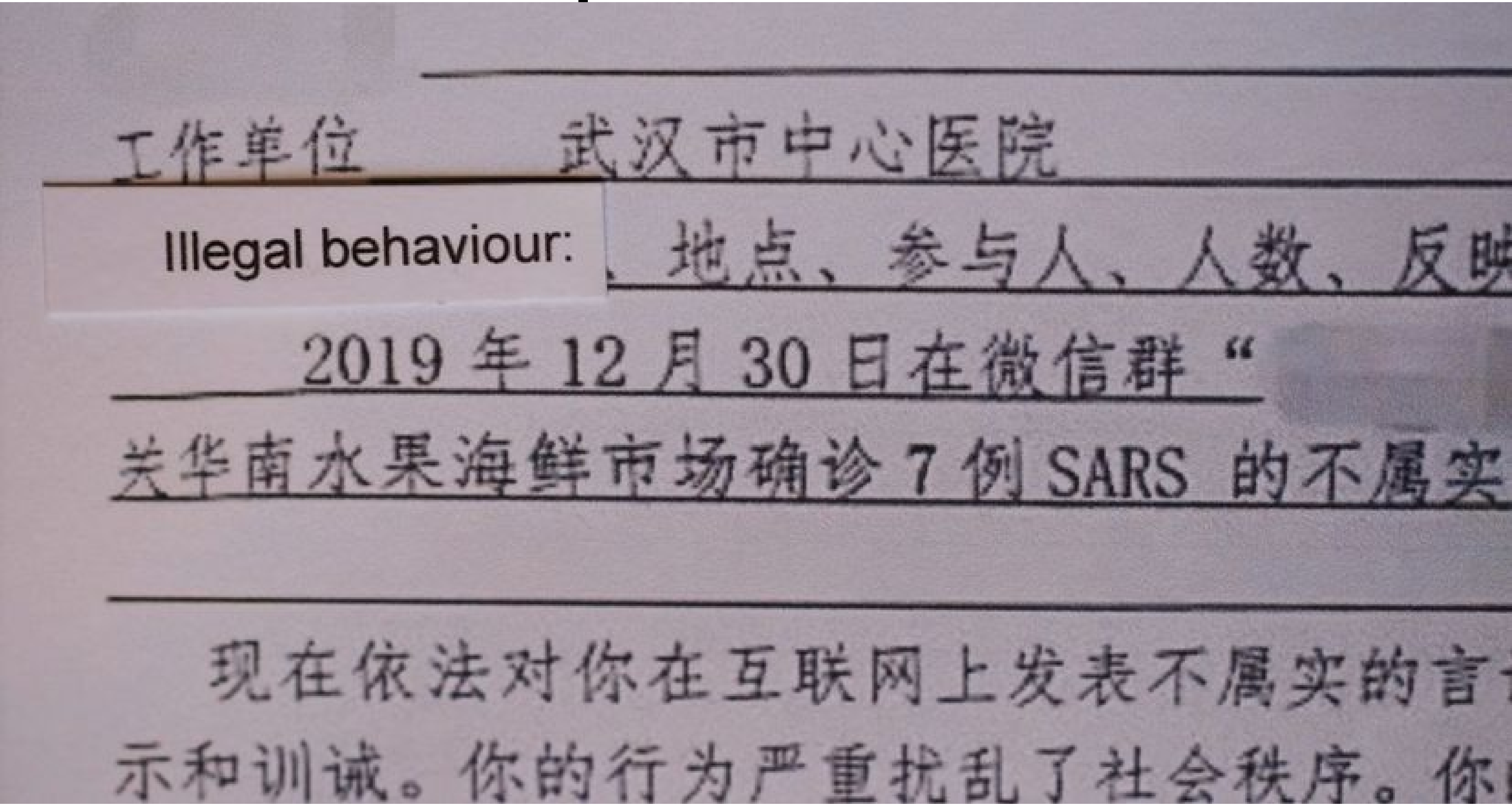
https://citizenlab.ca/2020/03/censored-contagion-how-information-on-the-coronavirus-is-managed-on-chinese-social-media/

1 January 2020

The police will investigate and deal with all illegal acts
that fabricate and spread rumors and disrupt social order.

PBS documentary

3 January: Li Wenliang at the police station



工作单位　武汉市中心医院

Illegal behaviour: 、地点、参与人、人数、反映

2019年12月30日在微信群“[redacted]

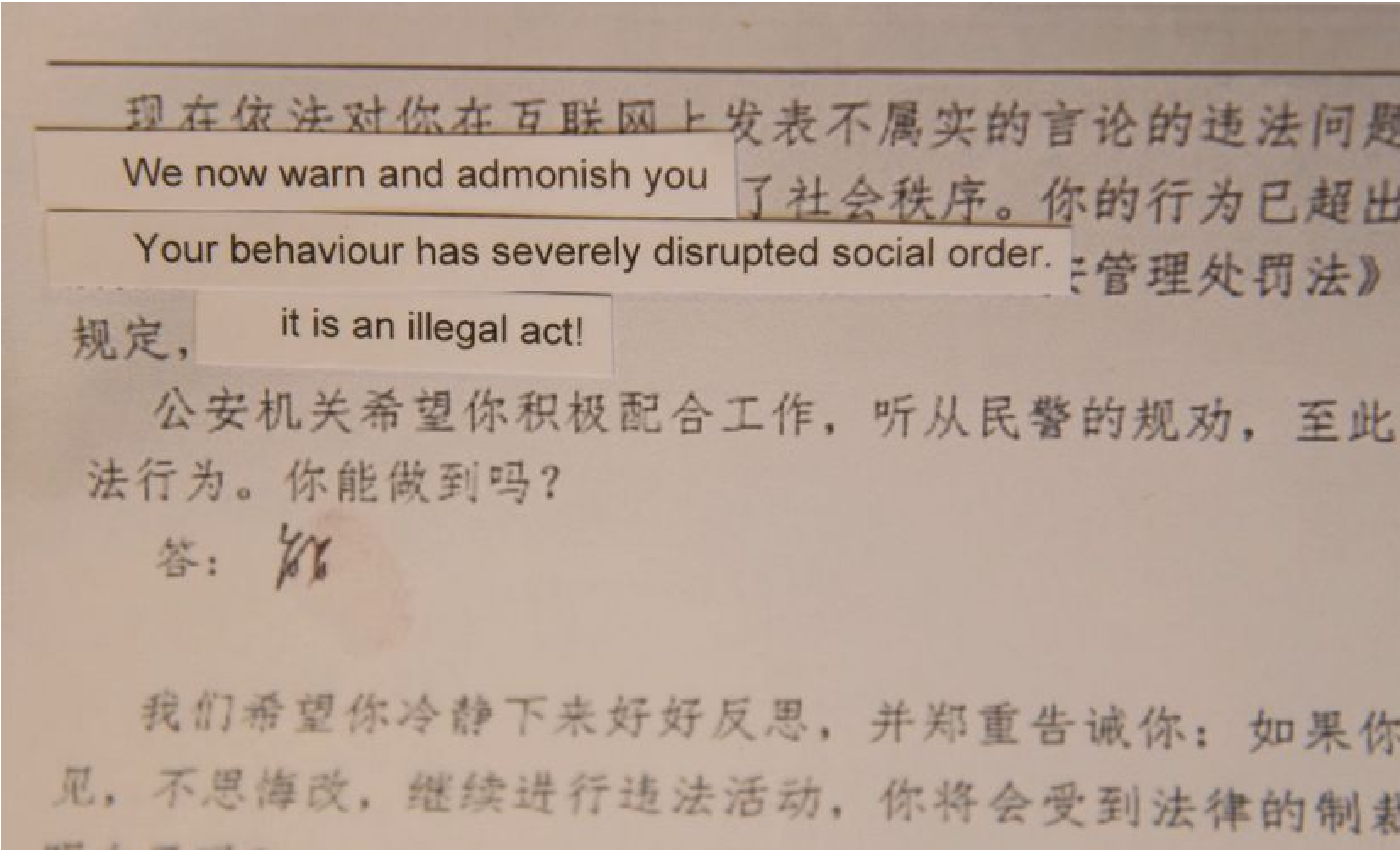
关华南水果海鲜市场确诊7例SARS的不属实

现在依法对你在互联网上发表不属实的言

示和训诫。你的行为严重扰乱了社会秩序。你

https://health.udn.com/health/story/120951/4313771

PBS documentary



现在依法对你在互联网上发表不属实的言论的违法问

We now warn and admonish you 了社会秩序。你的行为已超出

Your behaviour has severely disrupted social order. 管理处罚法》

规定， it is an illegal act!

公安机关希望你积极配合工作，听从民警的规劝，至此

法行为。你能做到吗？

答：能

我们希望你冷静下来好好反思，并郑重告诫你：如果你

见，不思悔改，继续进行违法活动，你将会受到法律的制

PBS documentary

Article

A new coronavirus associated with human respiratory disease in China

https://doi.org/10.1038/s41586-020-2008-3

Received: 7 January 2020

Accepted: 28 January 2020

Fan Wu[1,7], Su Zhao[2,7], Bin Yu[3,7], Yan-Mei Chen[1,7], Wen Wang[4,7], Zhi-Gang S
Zhao-Wu Tao[2], Jun-Hua Tian[3], Yuan-Yuan Pei[1], Ming-Li Yuan[2], Yu-Ling Zh
Yi Liu[1], Qi-Min Wang[1], Jiao-Jiao Zheng[1], Lin Xu[1], Edward C. Holmes[1,5] & Yo

Emerging infectious diseases, such as severe acute respiratory syr

Article

A pneumonia outbreak associated with a new coronavirus of probable bat origin

https://doi.org/10.1038/s41586-020-2012-7

Received: 20 January 2020

Accepted: 29 January 2020

Peng Zhou[1,5], Xing-Lou Yang[1,5], Xian-Guang Wang[2,5], Ben Hu[1], Lei Zhang
Hao-Rui Si[1,3], Yan Zhu[1], Bei Li[1], Chao-Lin Huang[2], Hui-Dong Chen[2], Jing C
Hua Guo[1,3], Ren-Di Jiang[1,3], Mei-Qin Liu[1,3], Ying Chen[1,3], Xu-Rui Shen[1,3], Xi
Xiao-Shuang Zheng[1,3], Kai Zhao[1,3], Quan-Jiao Chen[1], Fei Deng[1], Lin-Lin Li
Fa-Xian Zhan[4], Yan-Yi Wang[1], Geng-Fu Xiao[1] & Zheng-Li Shi[1]✉

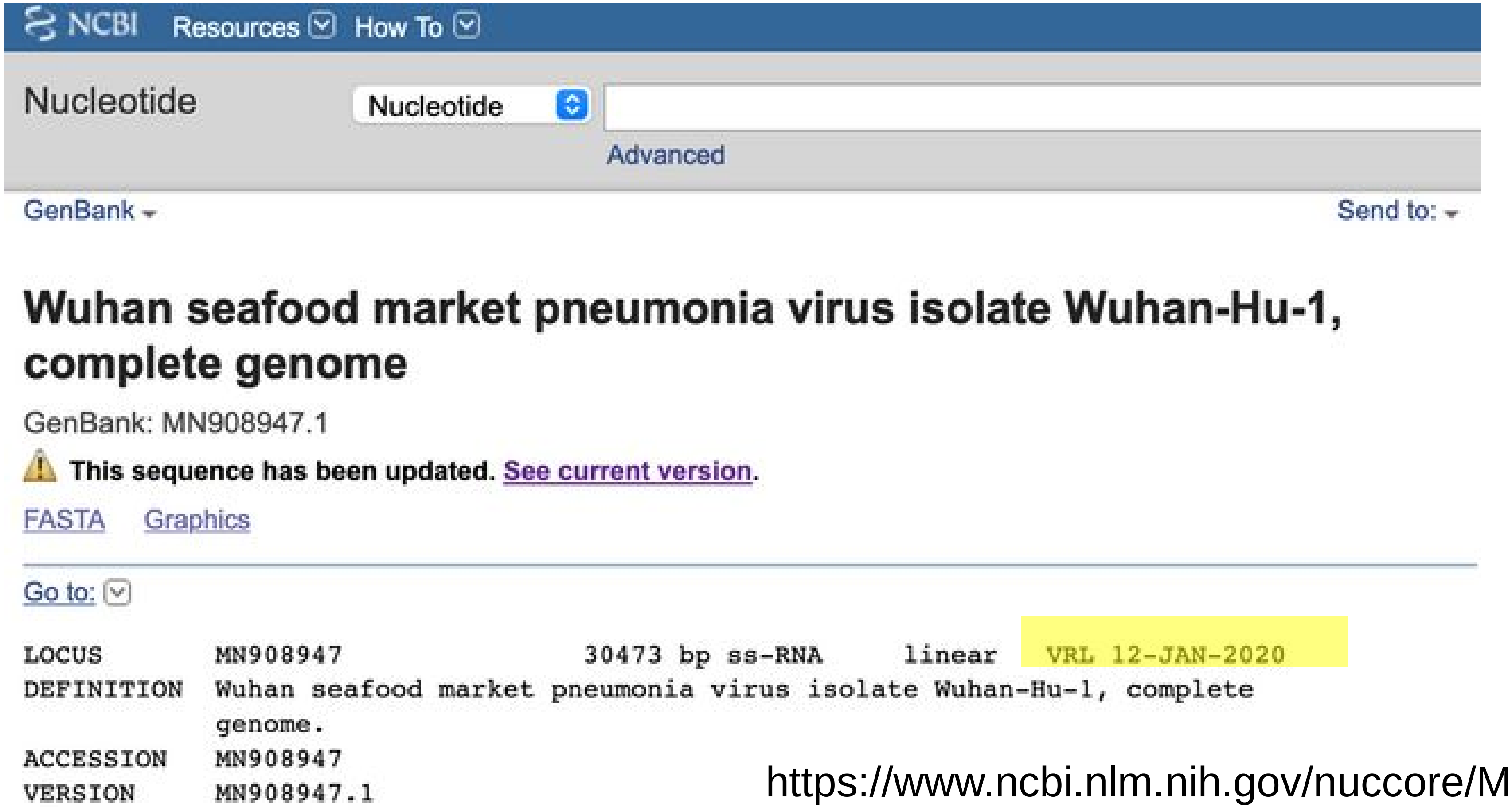
11 January: First sequence made public

Novel 2019 coronavirus genome

10th January 2020 This posting is communicated by Edward C. Holmes, University of Sydney on behalf of the ...

virological.org

https://virological.org/t/novel-2019-coronavirus-genome/319



Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome

GenBank: MN908947.1

⚠ **This sequence has been updated. See current version.**

FASTA Graphics

Go to:

```
LOCUS       MN908947                30473 bp ss-RNA     linear   VRL 12-JAN-2020
DEFINITION  Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete
            genome.
ACCESSION   MN908947
VERSION     MN908947.1
```

https://www.ncbi.nlm.nih.gov/nuccore/MN908947.1

30 Dec 2019
Wuhan Jinyintan Hospital
bronchoalveolar lavage (+oral swab, blood) from at least 7 patients

30/Dec/19	32	M	32M	S04		VIW02	
30/Dec/19	40	M	40M	S12		VIW06	
30/Dec/19	41	M	41M1		S06	(admitted 26 Nov)	Zhang
30/Dec/19	41	M	41M2		?	(admitted 22 Dec)	
30/Dec/19	49	F	49F	S10		VIW04	
30/Dec/19	52	F	52F	S11		VIW05	
30/Dec/19	56	M	56M	S08		VIW07	
30/Dec/19	62	M	62M	-			

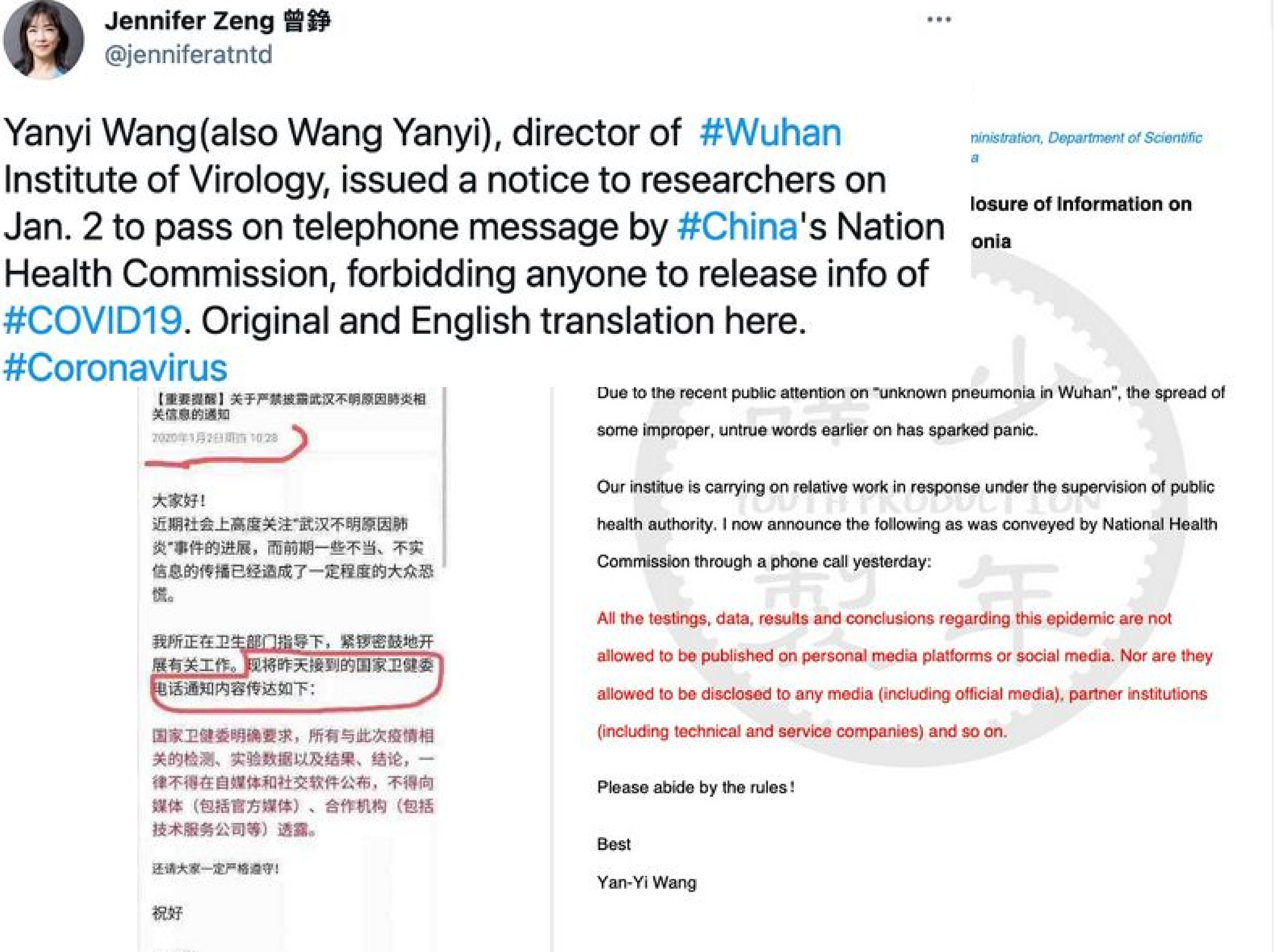
@franciscodeasis

At WIV

- samples arrived in Wuhan Institute of Virology (WIV) at 7PM
- the institute’s director called Zeng-Li Shi after 7PM and asked her to come back immediately from Shanghai

2 January: full genome
5 January: viral strain isolated
11 January: virus sequence submitted to the WHO

http://www.whiov.ac.cn/tzgg_105342/202002/t20200219_5502325.html



Jennifer Zeng 曾錚
@jenniferatntd

Yanyi Wang(also Wang Yanyi), director of #Wuhan Institute of Virology, issued a notice to researchers on Jan. 2 to pass on telephone message by #China's Nation Health Commission, forbidding anyone to release info of #COVID19. Original and English translation here. #Coronavirus

【重要提醒】关于严禁披露武汉不明原因肺炎相关信息的通知

2020年1月2日周四 10:28

大家好！
近期社会上高度关注"武汉不明原因肺炎"事件的进展，而前期一些不当、不实信息的传播已经造成了一定程度的大众恐慌。

我所正在卫生部门指导下，紧锣密鼓地开展有关工作。现将昨天接到的国家卫健委电话通知内容传达如下：

国家卫健委明确要求，所有与此次疫情相关的检测、实验数据以及结果、结论，一律不得在自媒体和社交软件公布，不得向媒体（包括官方媒体）、合作机构（包括技术服务公司等）透露。

还请大家一定严格遵守！

祝好

王延轶

ninistration, Department of Scientific
a

losure of Information on

onia

Due to the recent public attention on "unknown pneumonia in Wuhan", the spread of some improper, untrue words earlier on has sparked panic.

Our institue is carrying on relative work in response under the supervision of public health authority. I now announce the following as was conveyed by National Health Commission through a phone call yesterday:

All the testings, data, results and conclusions regarding this epidemic are not allowed to be published on personal media platforms or social media. Nor are they allowed to be disclosed to any media (including official media), partner institutions (including technical and service companies) and so on.

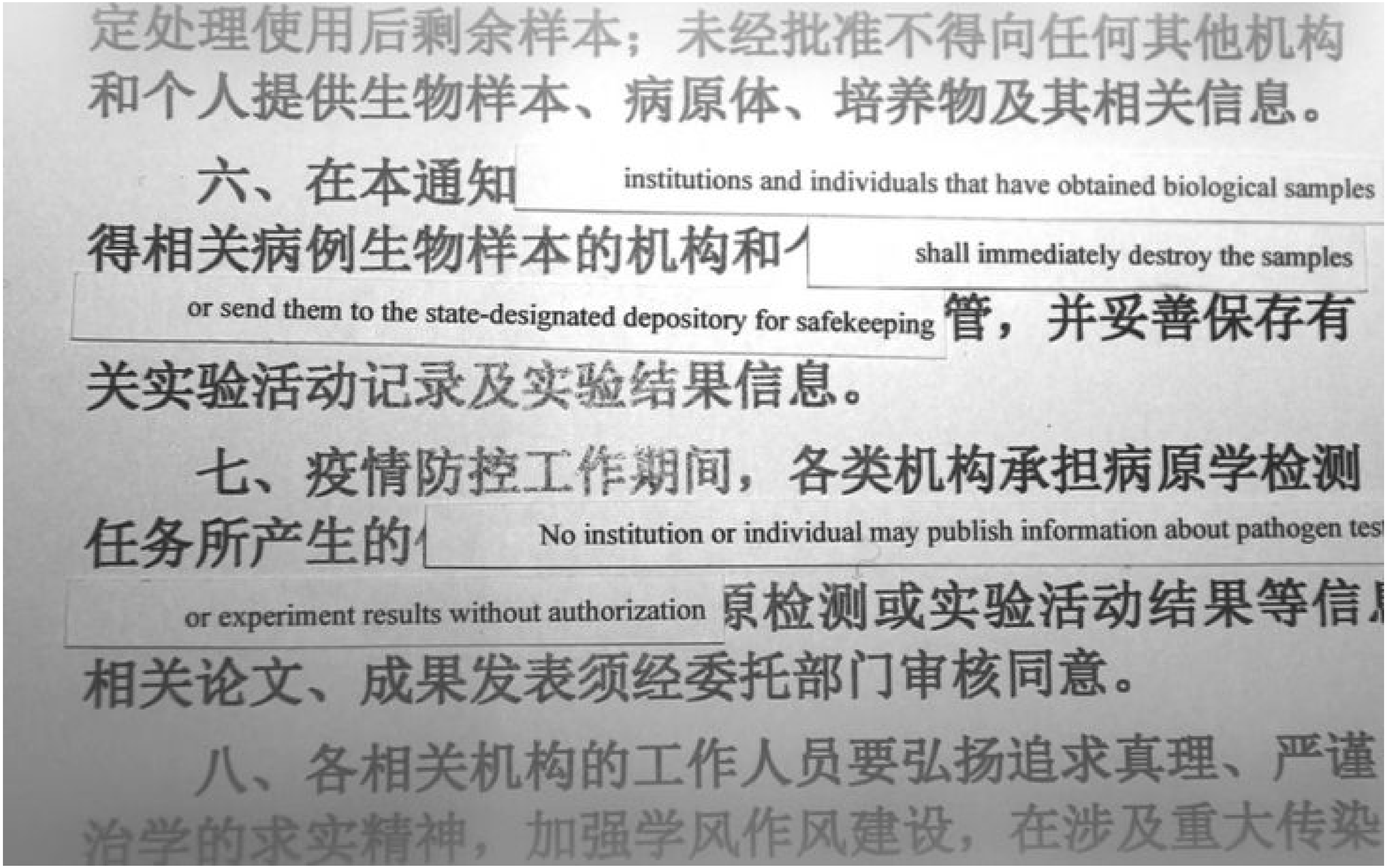
Please abide by the rules！

Best

Yan-Yi Wang

https://twitter.com/jenniferatntd/status/1229421174142140416?s=20

3 January: the National Health Commission issued a confidential notice ordering labs with the virus to either destroy their samples or send them to designated institutes for safekeeping; and forbid labs from publishing about the virus without government authorization.



定处理使用后剩余样本；未经批准不得向任何其他机构
和个人提供生物样本、病原体、培养物及其相关信息。

六、在本通知 institutions and individuals that have obtained biological samples
得相关病例生物样本的机构和个 shall immediately destroy the samples
or send them to the state-designated depository for safekeeping 管，并妥善保存有
关实验活动记录及实验结果信息。

七、疫情防控工作期间，各类机构承担病原学检测
任务所产生的 No institution or individual may publish information about pathogen tes
or experiment results without authorization 原检测或实验活动结果等信
相关论文、成果发表须经委托部门审核同意。

八、各相关机构的工作人员要弘扬追求真理、严谨
治学的求实精神，加强学风作风建设，在涉及重大传染

https://apnews.com/article/3c061794970661042b18d5aeaaed9fae

PBS documentary

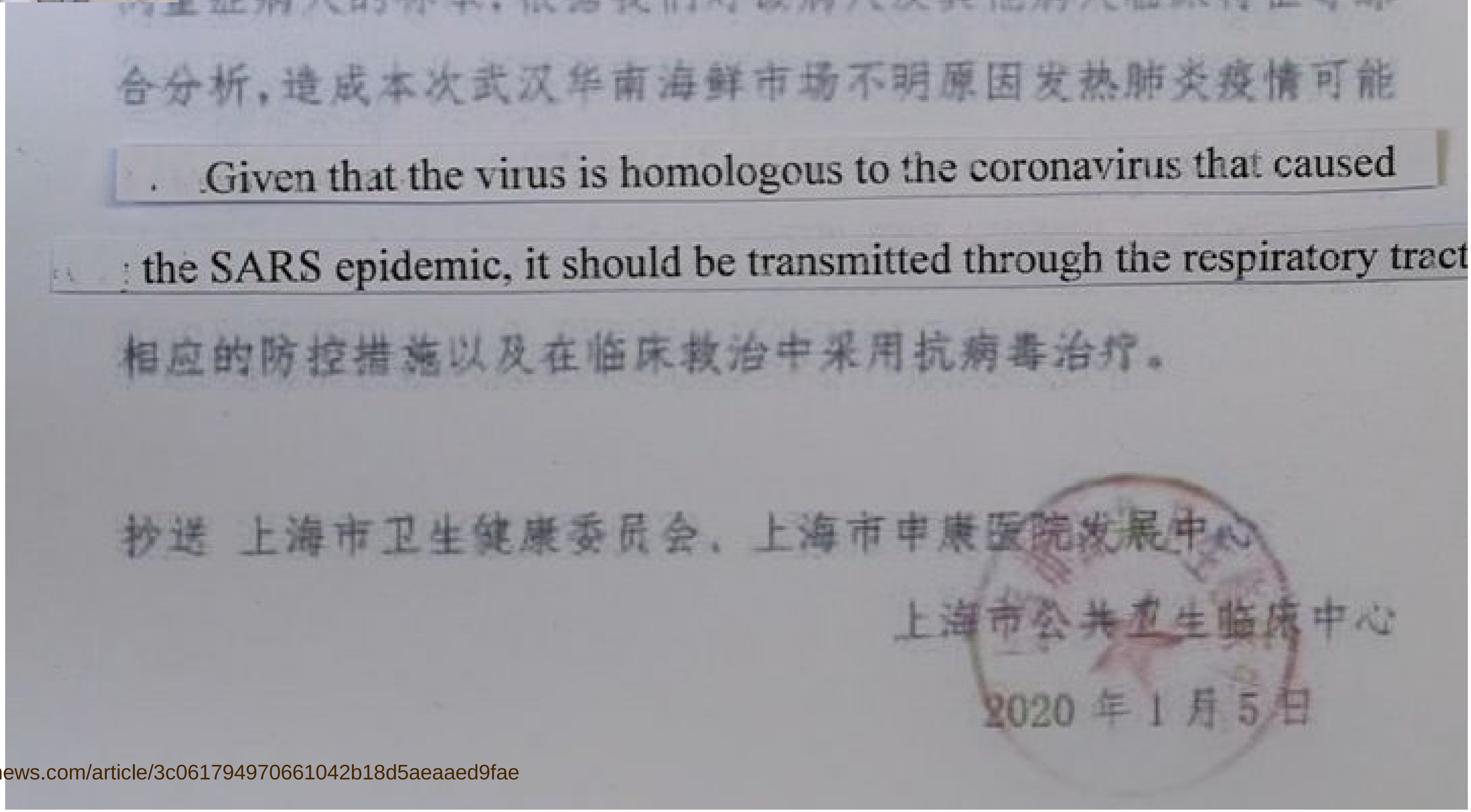
in Shanghai

2 Jan 2020

- samples sent by high-speed train to Shanghai

5 Jan 2020

- full genome obtained, submitted to GenBank (MN908947)
- Pr Zhang’s office wrote to National Health Commission



11%。命名为 Wuhan-Hu-1 冠状病毒（WHCV）。由于我们仅有 1

重症病人的标本，根据我们对该病人及其他病人临床特征等综

合分析，造成本次武汉华南海鲜市场不明原因发热肺炎疫情可能

Given that the virus is homologous to the coronavirus that caused

the SARS epidemic, it should be transmitted through the respiratory tract

相应的防控措施以及在临床救治中采用抗病毒治疗。

抄送 上海市卫生健康委员会、上海市申康医院发展中心

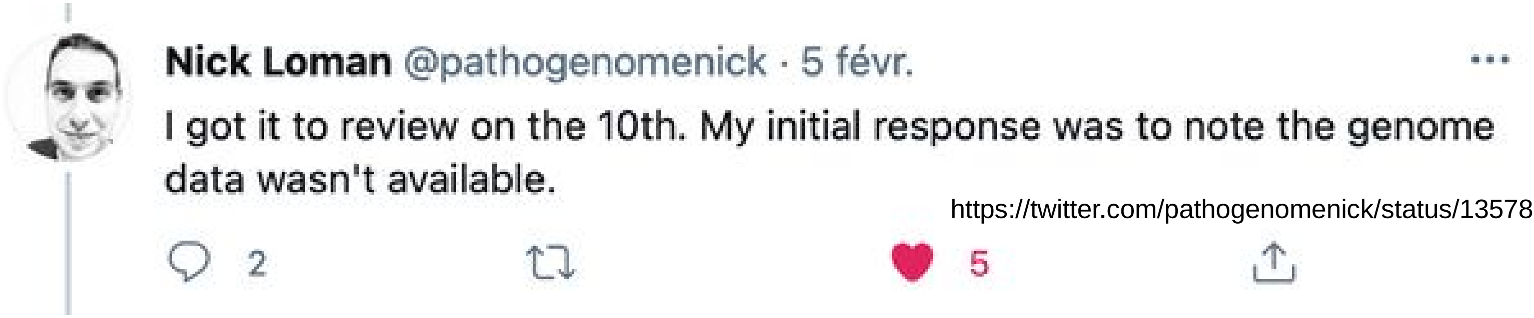
上海市公共卫生临床中心

2020 年 1 月 5 日

https://apnews.com/article/3c061794970661042b18d5aeaaed9fae

7 Jan 2020

Yong-Zhen Zhang submits his paper to Nature



Nick Loman @pathogenomenick · 5 févr.

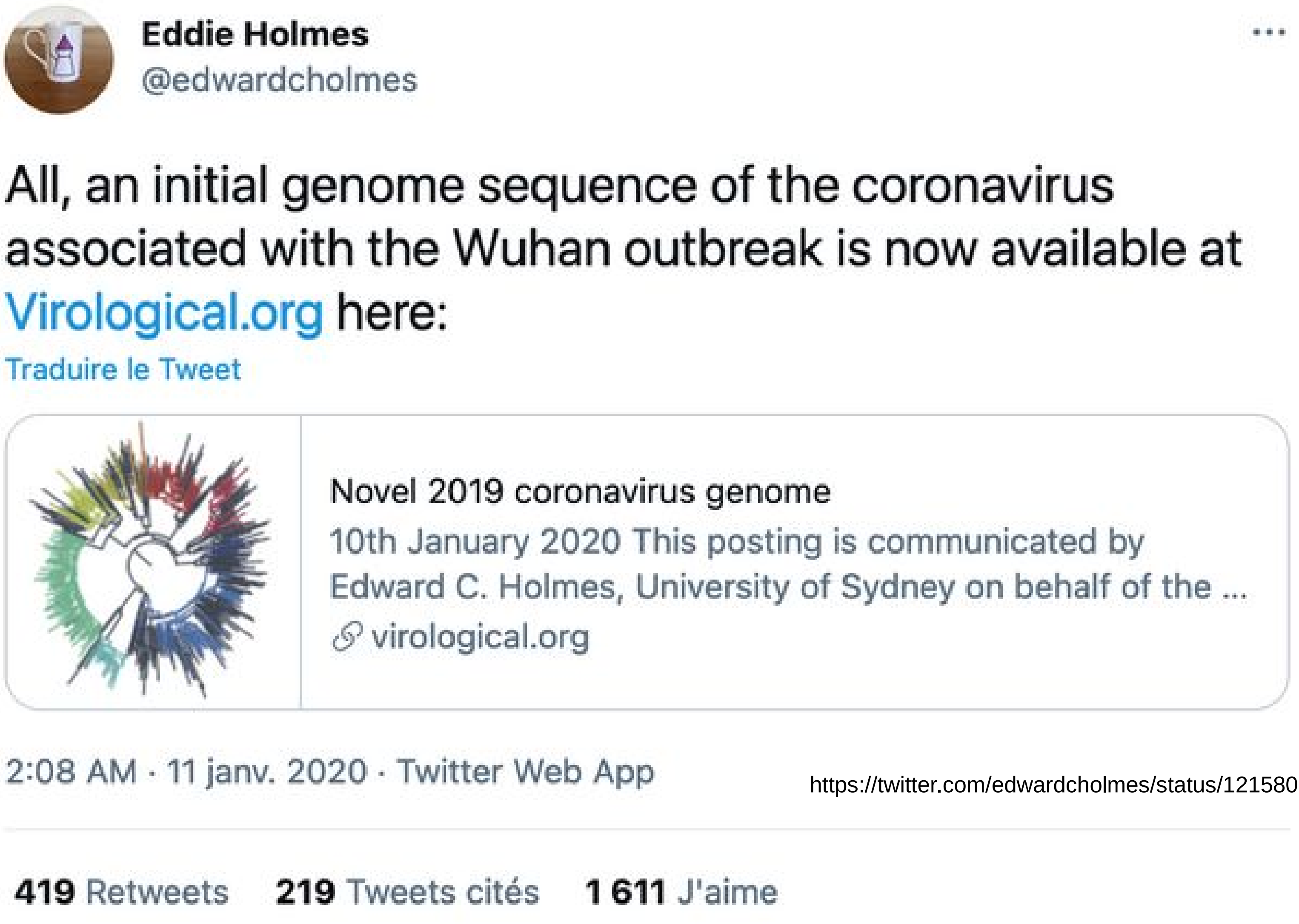
I got it to review on the 10th. My initial response was to note the genome data wasn't available.

https://twitter.com/pathogenomenick/status/1357808339321827337?s=20

Jeremy Farrar @JeremyFarrar · 10 janv. 2020

If rumours of publications on the Wuhan Pneumonia situation are being prepared & submitted to @nature @NEJM are true & that critical public health information is not being shared immediately with @WHO - something is very wrong

https://twitter.com/JeremyFarrar/status/1215647022893670401?s=20



Eddie Holmes
@edwardcholmes

All, an initial genome sequence of the coronavirus associated with the Wuhan outbreak is now available at Virological.org here:

Novel 2019 coronavirus genome
10th January 2020 This posting is communicated by Edward C. Holmes, University of Sydney on behalf of the ...
virological.org

2:08 AM · 11 janv. 2020 · Twitter Web App

419 Retweets **219** Tweets cités **1 611** J'aime

https://twitter.com/edwardcholmes/status/1215802670176276482?s=20

12 Jan 2020
Yong-Zhen Zhang’s lab closed for "rectification" (for a few days)

https://www.scmp.com/news/china/society/article/3052966/chinese-laboratory-first-shared-coronavirus-genome-world-ordered

First SARS-CoV-2 genome from Shanghai team

Show difference between I and II as GenBank/GenPept Diff

Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

29,903 bp linear RNA

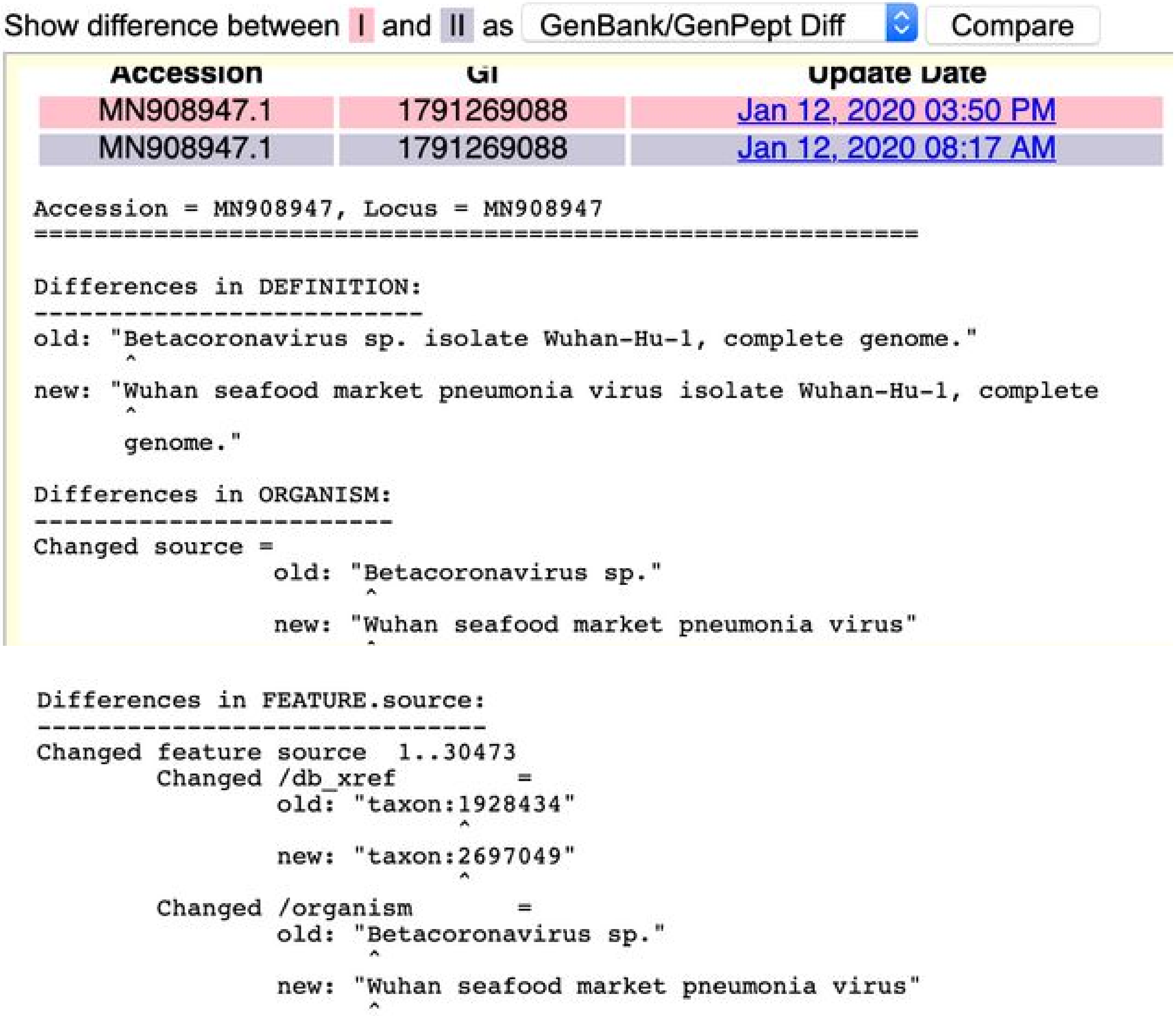
Accession: MN908947.3 GI: 1798172431

Current status: live

I	II	Version	Gi	Accession	Update Date	Action
●	○	3	1798172431	MN908947.3	Mar 18, 2020 09:36 AM	
○	○	3	1798172431	MN908947.3	Feb 11, 2020 04:38 PM	
○	○	3	1798172431	MN908947.3	Feb 11, 2020 02:17 PM	
○	○	3	1798172431	MN908947.3	Feb 11, 2020 01:00 PM	
○	○	3	1798172431	MN908947.3	Jan 23, 2020 08:32 AM	
○	○	3	1798172431	MN908947.3	Jan 17, 2020 12:44 PM	
○	○	3	1798172431	MN908947.3	Jan 17, 2020 12:41 PM	
○	○	2	1796487982	MN908947.2	Jan 14, 2020 08:59 AM	
○	○	1	1791269088	MN908947.1	Jan 12, 2020 03:50 PM	
○	●	1	1791269088	MN908947.1	Jan 12, 2020 08:17 AM	

Accession MN908947 was first seen at NCBI on Jan 12, 2020 08:17 AM

https://www.ncbi.nlm.nih.gov/nuccore/MN908947.3?report=girevhist



Show difference between I and II as GenBank/GenPept Diff Compare

Accession	GI	Update Date
MN908947.1	1791269088	Jan 12, 2020 03:50 PM
MN908947.1	1791269088	Jan 12, 2020 08:17 AM

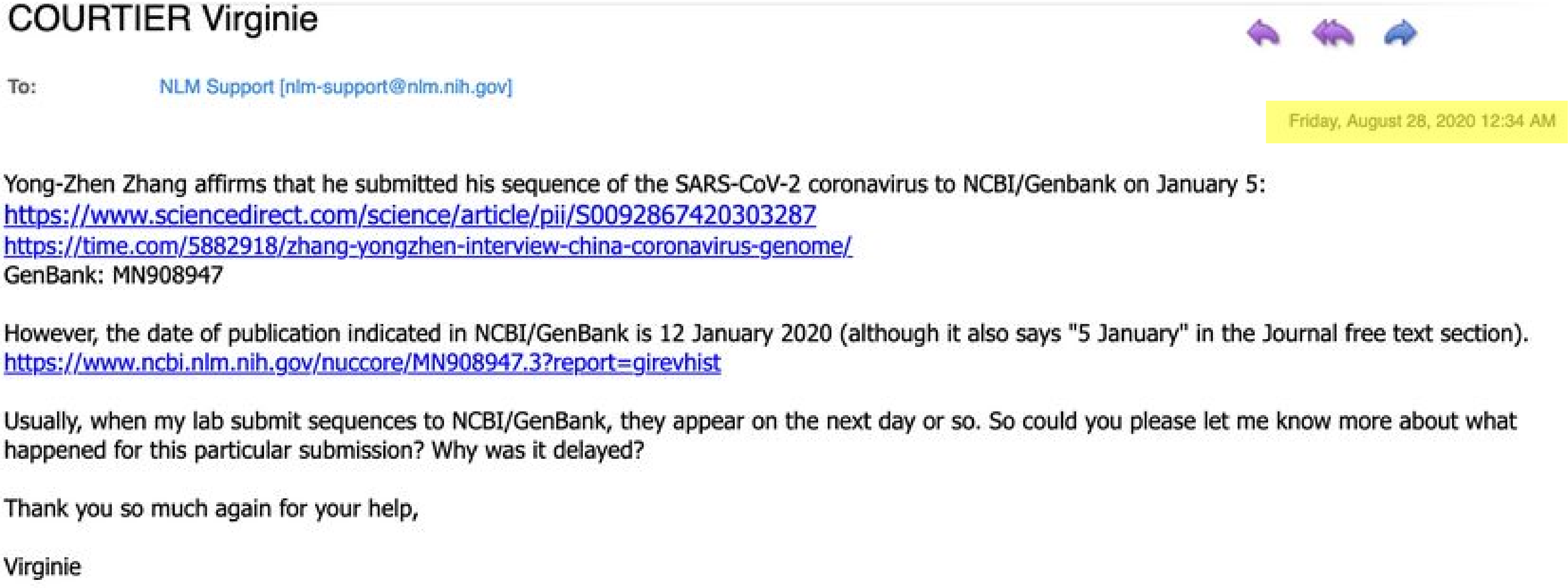
```
Accession = MN908947, Locus = MN908947
===========================================================

Differences in DEFINITION:
--------------------------
old: "Betacoronavirus sp. isolate Wuhan-Hu-1, complete genome."
      ^
new: "Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete
      ^
      genome."

Differences in ORGANISM:
------------------------
Changed source =
                old: "Betacoronavirus sp."
                      ^
                new: "Wuhan seafood market pneumonia virus"
                      ^

Differences in FEATURE.source:
------------------------------
Changed feature source  1..30473
        Changed /db_xref        =
                old: "taxon:1928434"
                            ^
                new: "taxon:2697049"
                            ^
        Changed /organism       =
                old: "Betacoronavirus sp."
                      ^
                new: "Wuhan seafood market pneumonia virus"
                      ^
```

GenBank/NCBI:
What happened from 5 Jan to 12 Jan?



COURTIER Virginie

To: NLM Support [nlm-support@nlm.nih.gov]

Friday, August 28, 2020 12:34 AM

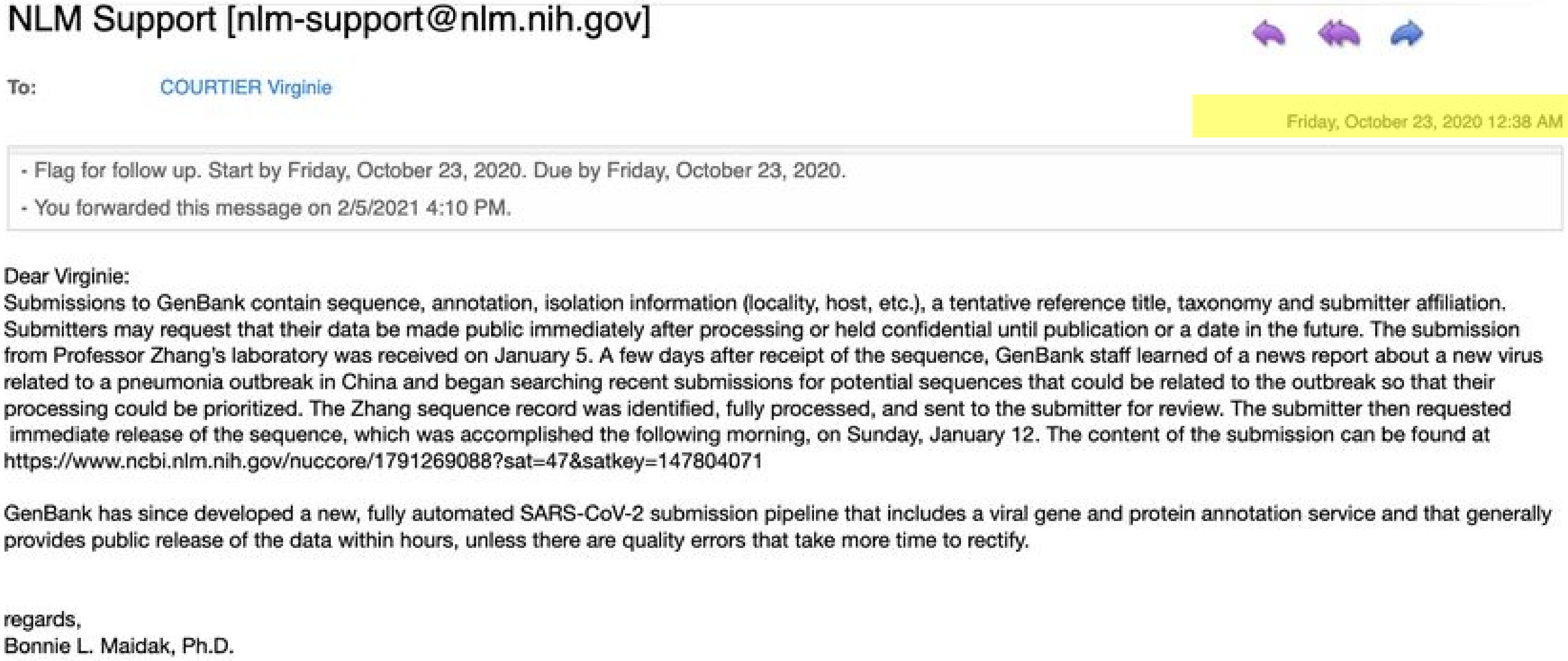
Yong-Zhen Zhang affirms that he submitted his sequence of the SARS-CoV-2 coronavirus to NCBI/Genbank on January 5:
https://www.sciencedirect.com/science/article/pii/S0092867420303287
https://time.com/5882918/zhang-yongzhen-interview-china-coronavirus-genome/
GenBank: MN908947

However, the date of publication indicated in NCBI/GenBank is 12 January 2020 (although it also says "5 January" in the Journal free text section).
https://www.ncbi.nlm.nih.gov/nuccore/MN908947.3?report=girevhist

Usually, when my lab submit sequences to NCBI/GenBank, they appear on the next day or so. So could you please let me know more about what happened for this particular submission? Why was it delayed?

Thank you so much again for your help,

Virginie



NLM Support [nlm-support@nlm.nih.gov]

To: COURTIER Virginie

Friday, October 23, 2020 12:38 AM

- Flag for follow up. Start by Friday, October 23, 2020. Due by Friday, October 23, 2020.
- You forwarded this message on 2/5/2021 4:10 PM.

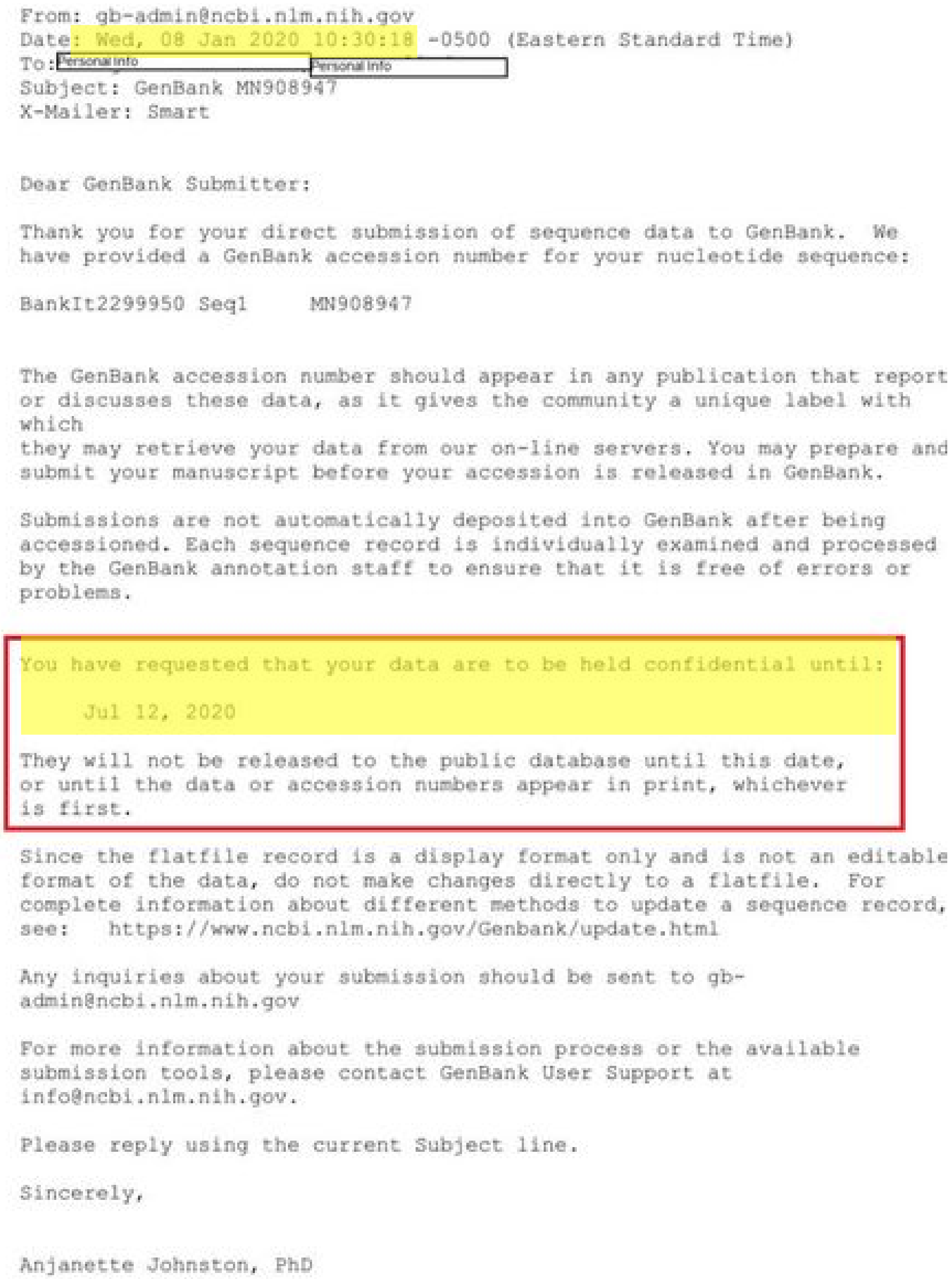
Dear Virginie:
Submissions to GenBank contain sequence, annotation, isolation information (locality, host, etc.), a tentative reference title, taxonomy and submitter affiliation. Submitters may request that their data be made public immediately after processing or held confidential until publication or a date in the future. The submission from Professor Zhang's laboratory was received on January 5. A few days after receipt of the sequence, GenBank staff learned of a news report about a new virus related to a pneumonia outbreak in China and began searching recent submissions for potential sequences that could be related to the outbreak so that their processing could be prioritized. The Zhang sequence record was identified, fully processed, and sent to the submitter for review. The submitter then requested immediate release of the sequence, which was accomplished the following morning, on Sunday, January 12. The content of the submission can be found at https://www.ncbi.nlm.nih.gov/nuccore/1791269088?sat=47&satkey=147804071

GenBank has since developed a new, fully automated SARS-CoV-2 submission pipeline that includes a viral gene and protein annotation service and that generally provides public release of the data within hours, unless there are quality errors that take more time to rectify.

regards,
Bonnie L. Maidak, Ph.D.

The sequence was under embargo at GenBank

Email obtained
via FOAI request



From: gb-admin@ncbi.nlm.nih.gov
Date: Wed, 08 Jan 2020 10:30:18 -0500 (Eastern Standard Time)
To: [redacted] [redacted]
Subject: GenBank MN908947
X-Mailer: Smart

Dear GenBank Submitter:

Thank you for your direct submission of sequence data to GenBank. We have provided a GenBank accession number for your nucleotide sequence:

BankIt2299950 Seq1   MN908947

The GenBank accession number should appear in any publication that report or discusses these data, as it gives the community a unique label with which they may retrieve your data from our on-line servers. You may prepare and submit your manuscript before your accession is released in GenBank.

Submissions are not automatically deposited into GenBank after being accessioned. Each sequence record is individually examined and processed by the GenBank annotation staff to ensure that it is free of errors or problems.

You have requested that your data are to be held confidential until:

Jul 12, 2020

They will not be released to the public database until this date, or until the data or accession numbers appear in print, whichever is first.

Since the flatfile record is a display format only and is not an editable format of the data, do not make changes directly to a flatfile. For complete information about different methods to update a sequence record, see: https://www.ncbi.nlm.nih.gov/Genbank/update.html

Any inquiries about your submission should be sent to gb-admin@ncbi.nlm.nih.gov

For more information about the submission process or the available submission tools, please contact GenBank User Support at info@ncbi.nlm.nih.gov.

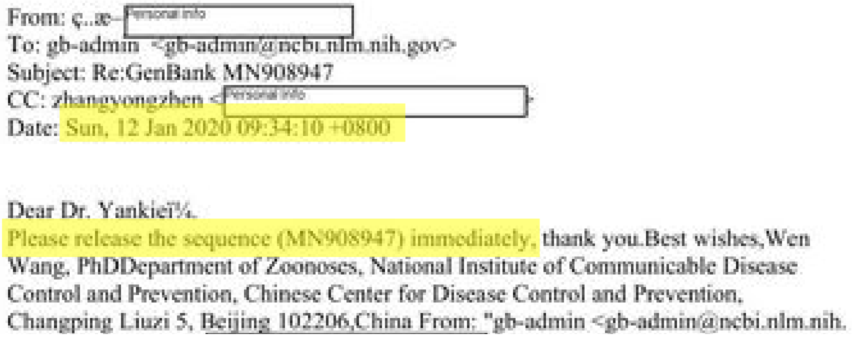
Please reply using the current Subject line.

Sincerely,

Anjanette Johnston, PhD

https://twitter.com/coroldo1/status/1363430389142839306?s=20

12 Jan, 9am GMT+8 (3am Paris): Submitter: “please release immediately”



From: ç..æ– Personal info
To: gb-admin <gb-admin@ncbi.nlm.nih.gov>
Subject: Re:GenBank MN908947
CC: zhangyongzhen <Personal info>
Date: Sun, 12 Jan 2020 09:34:10 +0800

Dear Dr. Yankieï¾,
Please release the sequence (MN908947) immediately, thank you.Best wishes,Wen Wang, PhDDepartment of Zoonoses, National Institute of Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Changping Liuzi 5, Beijing 102206,China From: "gb-admin <gb-admin@ncbi.nlm.nih.

12 Jan, 8am EST: NCBI: “MN908947 is public”

From: gb-admin@ncbi.nlm.nih.gov
Date: Sun, 12 Jan 2020 08:18:56 -0500 (Eastern Standard Time)
To: Personal info
Bcc: yankie@ncbi.nlm.nih.gov
Subject: GenBank MN908947
X-Mailer: Smart

Dear GenBank Submitter:

We have released your GenBank submission MN908947 and it is available at:

https://www.ncbi.nlm.nih.gov/nuccore/MN908947

If you have additional information about your sequence or wish to make further revisions, see: https://www.ncbi.nlm.nih.gov/Genbank/update.html for proper update formats

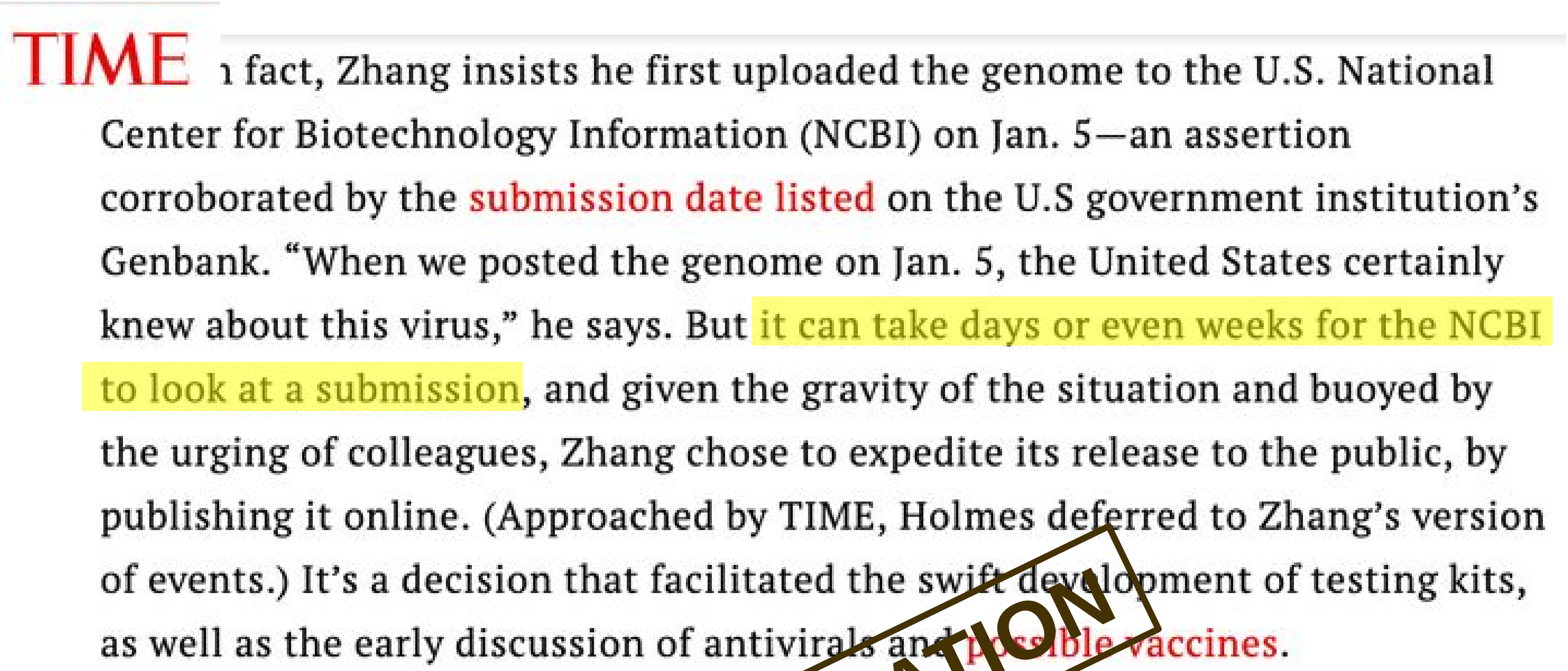
Since the flatfile record is a display format only and is not an editable format of the data, do not make changes directly to a flatfile. Thank you for your update notification.

Please reply using the current Subject line.

Sincerely,

Linda Yankie, PhD
The GenBank Submissions Staff
Bethesda, Maryland USA
****
gb-admin@ncbi.nlm.nih.gov (for replies/updates to records in GenBank)
info@ncbi.nlm.nih.gov (for general questions regarding GenBank)
****

https://twitter.com/coroldo1/status/1363430389142839306?s=20



TIME

n fact, Zhang insists he first uploaded the genome to the U.S. National Center for Biotechnology Information (NCBI) on Jan. 5—an assertion corroborated by the submission date listed on the U.S government institution's Genbank. "When we posted the genome on Jan. 5, the United States certainly knew about this virus," he says. But it can take days or even weeks for the NCBI to look at a submission, and given the gravity of the situation and buoyed by the urging of colleagues, Zhang chose to expedite its release to the public, by publishing it online. (Approached by TIME, Holmes deferred to Zhang's version of events.) It's a decision that facilitated the swift development of testing kits, as well as the early discussion of antivirals and possible vaccines.

https://time.com/5882918/zhang-yongzhen-interview-china-coronavirus-genome/

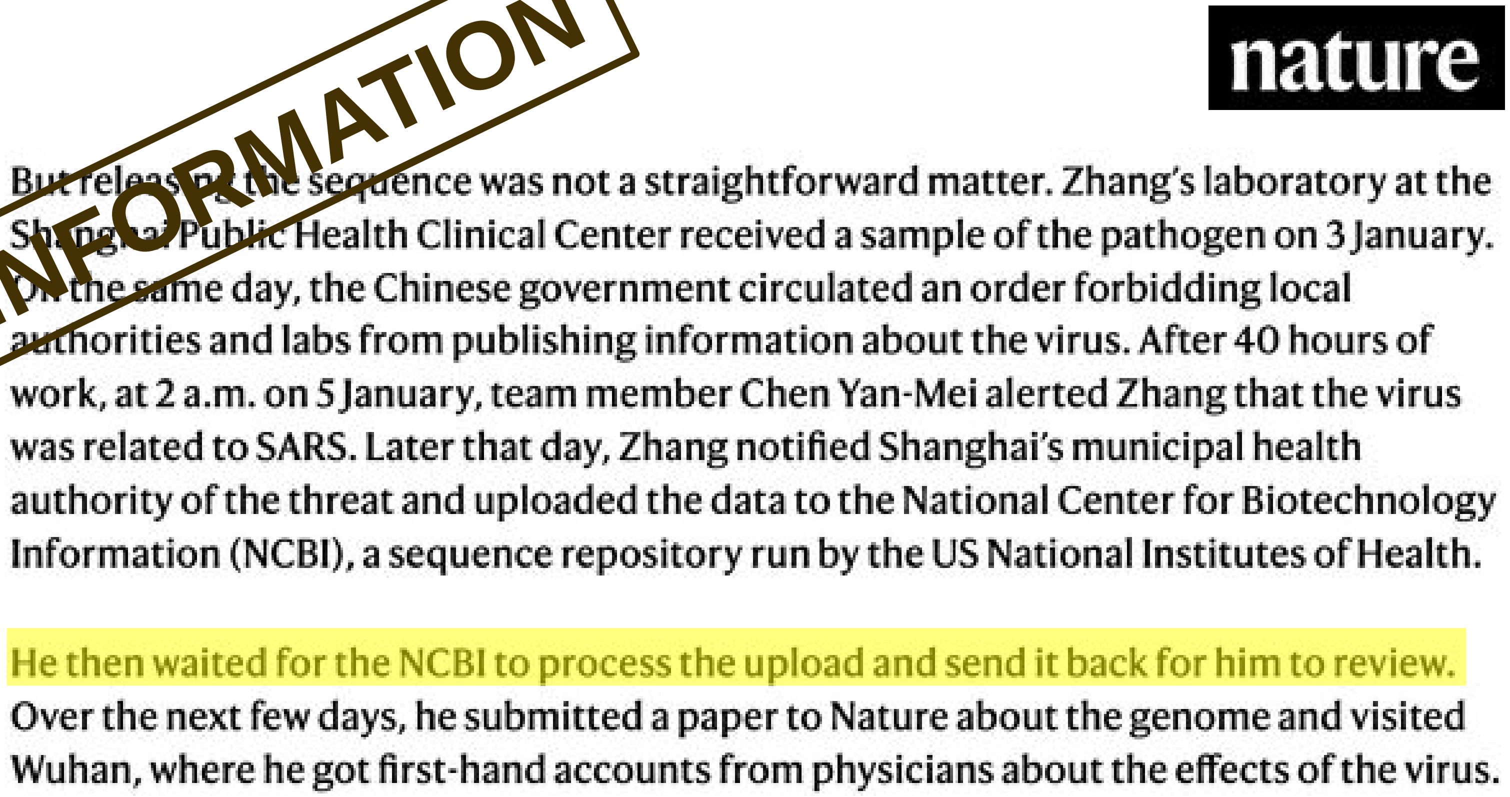
MISINFORMATION

IAN M. MACKAY, PHD @Mac... · 11 janv. 2020 ···

Virological has become the go-to **for** emerging virus sequence. **Genbank is not helpful for rapid response.** Or any timely sequence release in my lengthy experience

https://twitter.com/MackayIM/status/1215841817184198656?s=20

MISINFORMATION



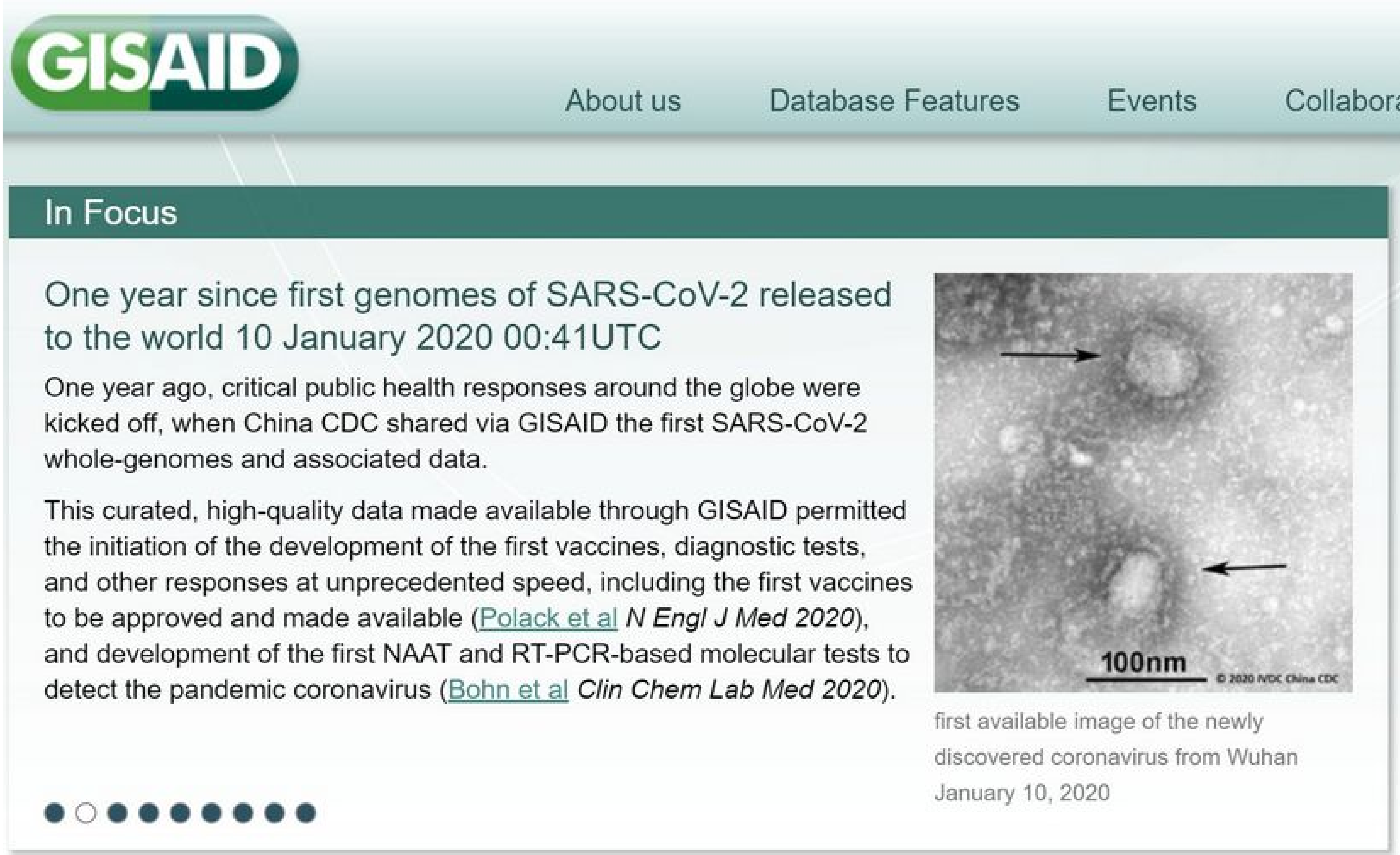
nature

But releasing the sequence was not a straightforward matter. Zhang's laboratory at the Shanghai Public Health Clinical Center received a sample of the pathogen on 3 January. On the same day, the Chinese government circulated an order forbidding local authorities and labs from publishing information about the virus. After 40 hours of work, at 2 a.m. on 5 January, team member Chen Yan-Mei alerted Zhang that the virus was related to SARS. Later that day, Zhang notified Shanghai's municipal health authority of the threat and uploaded the data to the National Center for Biotechnology Information (NCBI), a sequence repository run by the US National Institutes of Health.

He then waited for the NCBI to process the upload and send it back for him to review. Over the next few days, he submitted a paper to Nature about the genome and visited Wuhan, where he got first-hand accounts from physicians about the effects of the virus.

https://www.nature.com/immersive/d41586-020-03435-6/index.html

Controversy still ongoing



In Focus

One year since first genomes of SARS-CoV-2 released to the world 10 January 2020 00:41UTC

One year ago, critical public health responses around the globe were kicked off, when China CDC shared via GISAID the first SARS-CoV-2 whole-genomes and associated data.

This curated, high-quality data made available through GISAID permitted the initiation of the development of the first vaccines, diagnostic tests, and other responses at unprecedented speed, including the first vaccines to be approved and made available (Polack et al *N Engl J Med 2020*), and development of the first NAAT and RT-PCR-based molecular tests to detect the pandemic coronavirus (Bohn et al *Clin Chem Lab Med 2020*).

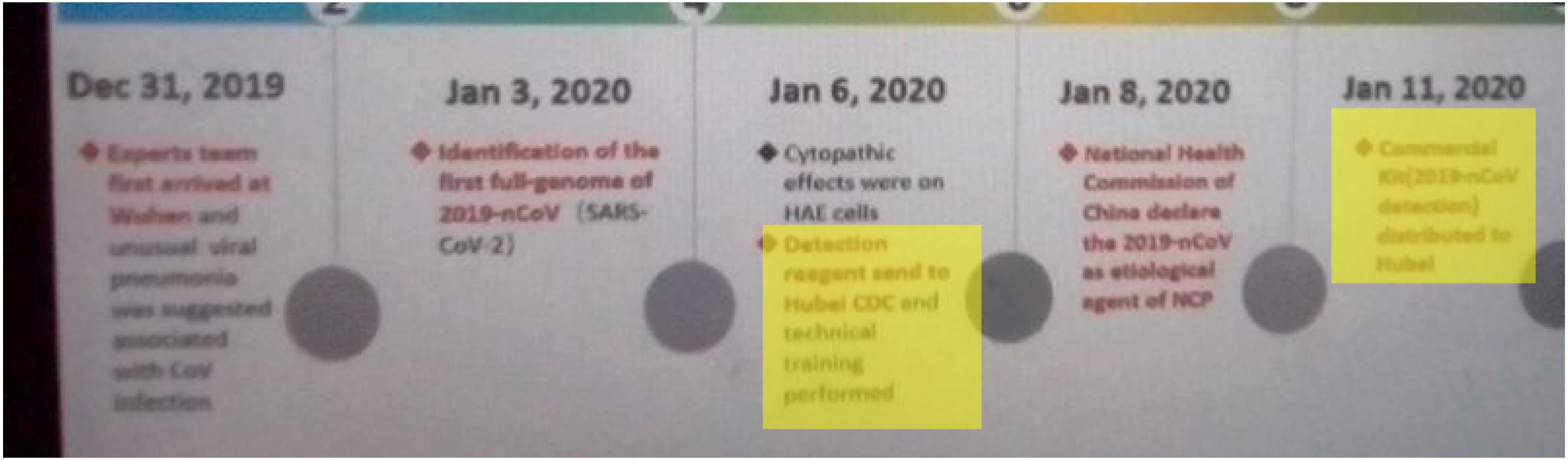
first available image of the newly discovered coronavirus from Wuhan January 10, 2020

IVDC's 'initial' submission of IVDC-01/05 on GISAID on 10th Jan, 2020

https://twitter.com/coroldo1/status/1366643799926087683?s=20

6-11 Jan 2020: China had detection RT-PCR tests

slide by CCDC George Gao Fu at an online conference



Dec 31, 2019

- Experts team first arrived at Wuhan and unusual viral pneumonia was suggested associated with CoV infection

Jan 3, 2020

- Identification of the first full-genome of 2019-nCoV（SARS-CoV-2）

Jan 6, 2020

- Cytopathic effects were on HAE cells
- Detection reagent send to Hubei CDC and technical training performed

Jan 8, 2020

- National Health Commission of China declare the 2019-nCoV as etiological agent of NCP

Jan 11, 2020

- Commercial Kit(2019-nCoV detection) distributed to Hubei

https://twitter.com/BillyBostickson/status/1359004931483598852?s=20

https://twitter.com/amicocolorido/status/1365354159223013376?s=20

13 Jan 2020: Moderna teams finalized the targeted genetic sequence for its vaccine

https://www.sec.gov/Archives/edgar/data/1682852/000119312520074867/d884510dex992.htm

https://archive.is/yfG0B

12 Jan 2020: Thailand sent data to WHO

8 Jan: A sick woman from Wuhan at Thai airport. Chulalongkorn University professor Supaporn Wacharapluesadee’s team found the woman was infected with a new coronavirus, much like what Chinese officials had described, and **reported its partial sequence** to the Thai government.

Thailand informed the WHO, said Tanarak Plipat, deputy director-general of the Department of Disease Control at Thailand’s Ministry of Public Health.

hCoV-19/Thailand/61/2020
EPI_ISL_403962
(submitted 17 Jan to GISAID)

https://apnews.com/article/3c061794970661042b18d5aeaaed9fae

Thanks

Sequencing started 24 Dec 2019
Genome public on 11 Jan 2020
Official notifications

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DRASTIC, others

PBS Documentary

Article

A new coronavirus associated with human respiratory disease in China

5,220 citations

https://doi.org/10.1038/s41586-020-2008-3

Received: 7 January 2020

Accepted: 28 January 2020

Fan Wu[1,7], Su Zhao[2,7], Bin Yu[3,7], Yan-Mei Chen[1,7], Wen Wang[4,7], Zhi-Gang S
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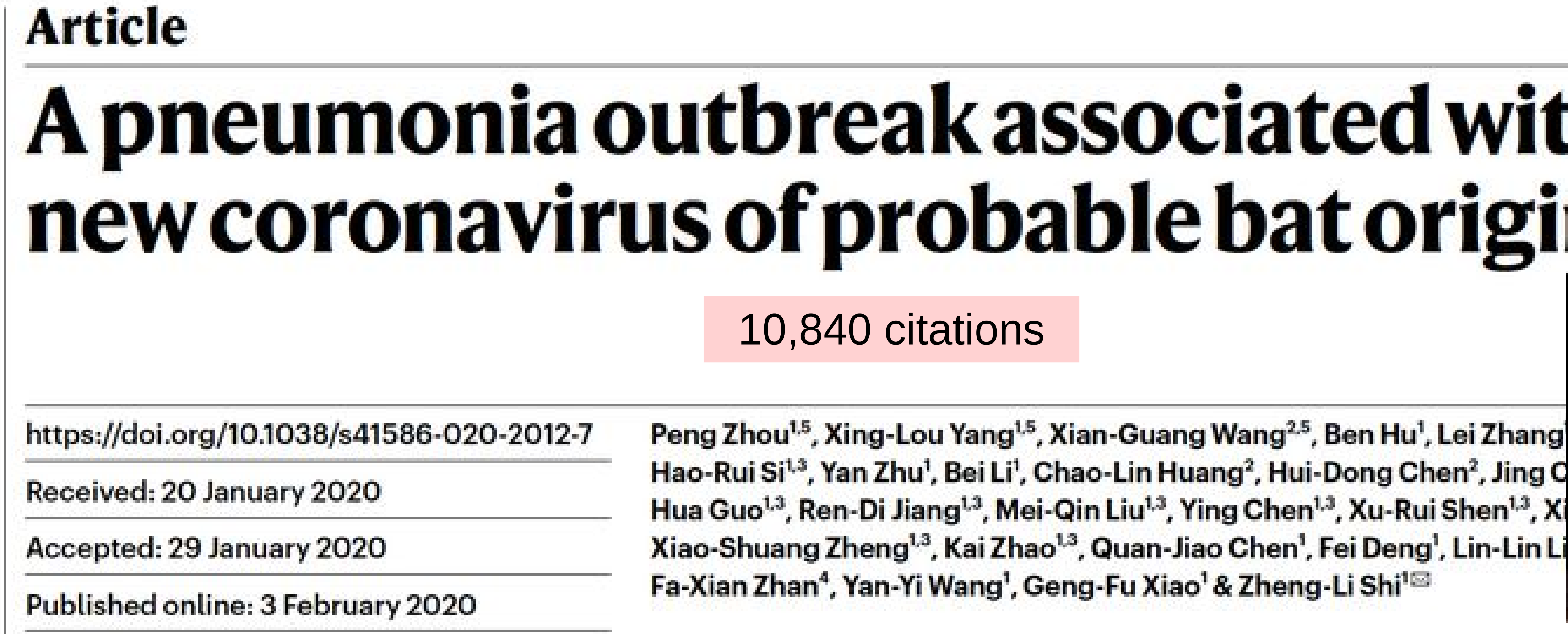
Emerging infectious diseases, such as severe acute respiratory syr



Article

A pneumonia outbreak associated with a new coronavirus of probable bat origin

10,840 citations

https://doi.org/10.1038/s41586-020-2012-7

Received: 20 January 2020

Accepted: 29 January 2020

Peng Zhou[1,5], Xing-Lou Yang[1,5], Xian-Guang Wang[2,5], Ben Hu[1], Lei Zhang
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Hua Guo[1,3], Ren-Di Jiang[1,3], Mei-Qin Liu[1,3], Ying Chen[1,3], Xu-Rui Shen[1,3], Xi
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Fa-Xian Zhan[4], Yan-Yi Wang[1], Geng-Fu Xiao[1] & Zheng-Li Shi[1] ✉