DEMOCRACY AND PANDEMICS

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How to Prevent the Next Pandemic

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Australian Government
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THE UNIVERSITY OF
SYDNEY

Australian Government
National Health and
Medical Research Council
NHMRC

Discovery of COVID-19/SARS-CoV-2

- Dec 10/11 2019: First reported cases of COVID-19 symptom onset
- Dec 25: Patient samples sent for sequencing at Vision Medicals
- Dec 26: Fragments of SARS-CoV-2 discovered
- Dec 27: First full virus genome obtained by Vision Medicals
- Dec 27-28: Vision Medicals provide information to China CDC and Wuhan hospitals
- Dec 30: Beijing Genome Institute (BGI) sequence another patient
- Dec 31: BGI report ('SARS-like' virus) leaked on social media

National Health Commission "Gag Order" - Jan 3rd 2020


国家卫生健康委办公厅关于重大突发传染病防控工作中加强生物样本资源及相关科研活动管理工作的通知

国家卫生健康委办公厅关于重大突发传染病防控工作中加强生物样本资源及相关科研活动管理工作的通知
国卫办科教函〔2020〕3号
2020年1月3日于北京市
发布机关：国家卫生健康委员会办公厅

新新闻》惹出全球疫情灾难的"三号文"长这个样子！ 纸质文件翻拍图片@matters.news

国 家 卫 生 健 康 委 员 会 办 公 厅

国卫办科教函〔2020〕3号

Genome sequence data not made public


上 海 市
复旦大学附属 公共卫生临床中心

关于湖北省武汉市华南海鲜市场不明原因发热肺炎疫情的病原学调查报告

国家卫生健康委员会：

我单位（上海市公共卫生临床中心）张永振教授团队与武汉市中心医院、武汉市CDC合作，于2020年1月5日从湖北省武汉市华南海鲜市场一名不明原因发热肺炎病人呼吸道灌洗液中检测出类SARS冠状病毒，经过高通量测序获得了该病毒的全基因组，序列分析发现该病毒与类SARS冠状病毒同源性高达89.11%，命名为Wuhan-Hu-1冠状病毒（WHCV）。由于我们仅有1例重症病人的标本，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是由该新型Wuhan-Hu-1冠状病毒引起。鉴于该病毒与造成SARS疫情的冠状病毒同源，应是经呼吸道传播，建议在公共场所采取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

- 7 patient samples from Wuhan Central Hospital (symptom onset - Dec. 20) sent to Shanghai Public Health Clinical Center and arrived on Jan 3rd 2020
- Jan 5th: Virus genome sequenced by the team of Prof. Yong-Zhen Zhang.
- Jan 5th: Chinese Ministry of Health told the virus was likely respiratory and that people should take precautions

UPL[redacted]
文件预览

[redacted]

QR-D.SY003-03-BABJ A/0 超广谱病原微生物mNGS检测报告[MAPMI v1.1]

三、附录-[MAP[illegible]检测详细技术信息]

（一）检出阳性病原技术信息

1. 病毒筛查结果				
名称	Name	检出序列数	基因组覆盖度	估测浓度[copies/mL]
SARS冠状病毒	Severe_acute_respiratory_syndrome-related_coronavirus	59	1077 bp / 3.58%	3.2E+02
2. 细菌筛查结果				
名称	Name	检出序列数	基因组覆盖度	估测浓度[copies/mL]
铜绿假单胞菌	Pseudomonas_aeruginosa	3803	175949 bp / 2.76%	2.4E+02
肺炎克雷伯菌	Klebsiella_pneumoniae	330	9598 bp / 0.17%	2.3E+01
3. 真菌、寄生虫筛查结果				
名称	Name	检出序列数	基因组覆盖度	估测浓度[copies/mL]
-	-	-	-	-

4. 耐药基因筛查结果				
检测到的耐药基因	检出序列数	基因耐药参考	覆盖度	估测浓度[copies/mL]
-	-	-	-	-

（二）测序质量技术信息

测序平台：	BioelectronSeq4000
测得总reads数：	15463399
过滤去重后reads数(百分比)：	12143527 (81.5%)
> 人源reads总数(百分比)：	8347742 (68.7%)
> 非人源reads总数(百分比)：	3795785 (31.3%)
>> 微生物reads数(百分比)：	717600 (5.9%)
>> Unmapped_reads数(百分比)：	3078185 (25.3%)
用于鉴定的reads平均长度：	151
用于鉴定的reads平均质量：	24


Eddie Holmes @edwardcholmes · Jan 11

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 ...
virological.org

The First Diagnostics & Vaccines

- Jan 23rd 2020: First diagnostic (PCR) test developed by a European group

Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR

Victor M Corman[1], Olfert Landt[2], Marco Kaiser[3], Richard Molenkamp[4], Adam Meijer[5], Daniel KW Chu[6], Tobias Bleicker[1], Sebastian Brünink[1], Julia Schneider[1], Marie Luisa Schmidt[1], Daphne GJC Mulders[4], Bart L Haagmans[4], Bas van der Veer[5], Sharon van den Brink[5], Lisa Wijsman[5], Gabriel Goderski[5], Jean-Louis Romette[7], Joanna Ellis[8], Maria Zambon[8], Malik Peiris[6], Herman Goossens[9], Chantal Reusken[5], Marion PG Koopmans[4], Christian Drosten[1]

Introduction

According to the World Health Organization (WHO), the WHO China Country Office was informed of cases of pneumonia of unknown aetiology in Wuhan City, Hubei Province, on 31 December 2019 [1]. A novel coronavirus currently termed 2019-nCoV was officially announced as the causative agent by Chinese authorities on 7 January. A viral genome sequence was released for immediate public health support via the community online resource virological.org on 10 January (Wuhan-Hu-1, GenBank accession number MN908947 [2]), followed by four other genomes deposited on 12 January in the viral sequence database curated by the Global Initiative on Sharing All Influenza Data (GISAID). The genome sequences suggest presence of a virus closely related to the members of a viral species termed severe acute respiratory syndrome (SARS)-related CoV, a species defined by the agent of the 2002/03 outbreak of SARS in humans [3,4]. The species also comprises a large number of viruses mostly detected in rhinolophid bats in Asia and Europe.

- Jan 13th 2020: NIH/UTexas researchers (Barney Graham, Jason McLellan) and the Moderna designed mRNA vaccine over the same weekend the genome sequence was released
- Pfizer/BioNTech, Oxford/Astra Zeneca quickly followed

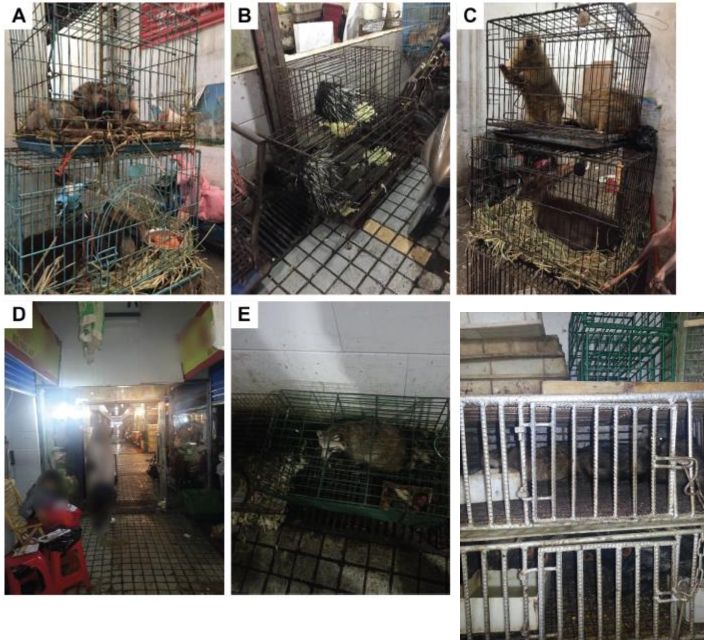
Moderna's groundbreaking coronavirus vaccine was designed in just 2 days

Susie Neilson , Andrew Dunn , and Aria Bendix Dec 20, 2020, 3:51 AM

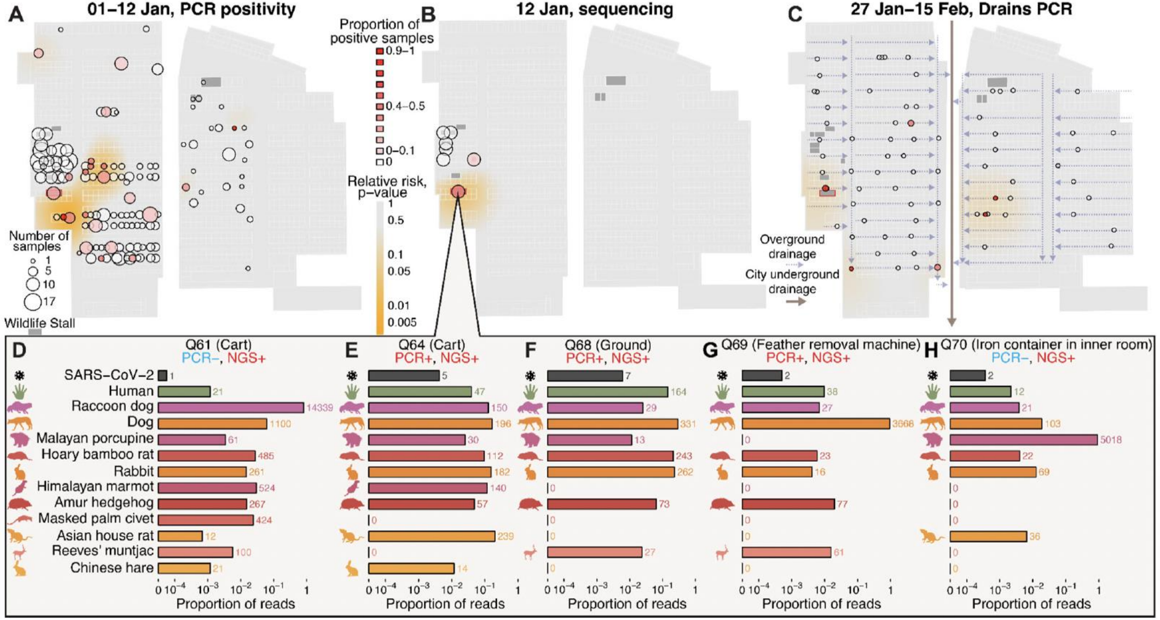
Moderna; Samantha Lee/Business Insider

Wildlife at The Huanan Market, Wuhan

Susceptible wildlife were present in the market in late 2019



Most positive environmental samples (January 2020) fall in locations were wildlife were sold (confirmed by metagenomics)

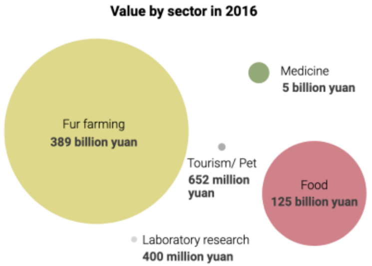


Strong resemblance to the emergence of SARS-CoV-1 in 2002/2003

Crits-Christoph *et al*. *Cell* (2024)

Game Farmed Animals Pose a Risk

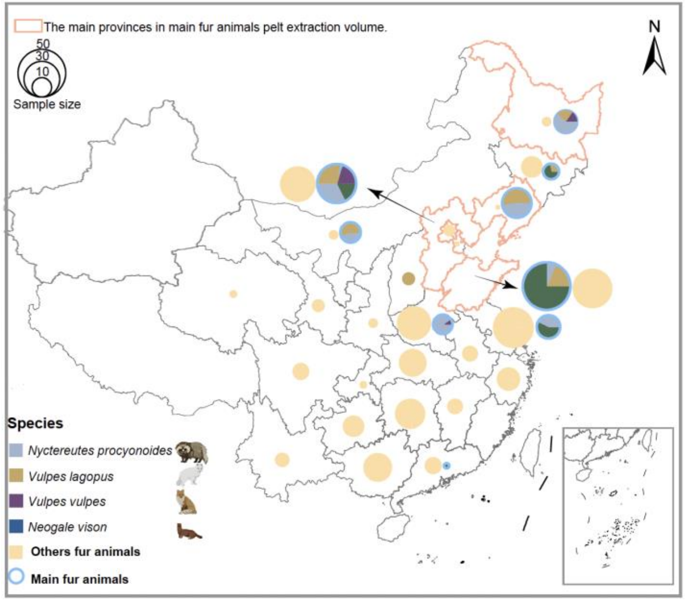
*He et al. Cell **185**, 1-13; 2022.*



- Metagenomic sequencing of 1941 animals from 5 mammalian orders
- 21 viruses at risk of emergence (i.e. jumping species boundaries)
- Examples: Bat alphacoronavirus in a civet; H9N2 avian influenza virus in a civet and Asian badger

Videos courtesy of Drs Mang Shi & Shuo Su

Fur Farmed Animals = Pandemic Incubators?



- Sampled 461 diseased fur farmed animals: 123 viruses, 39 with risk of host jumping
- H1N2, H5N6 and H6N2 influenza A virus in guinea pigs, mink, muskrats with pneumonia
- Raccoon dogs and mink had the highest number of potentially high-risk viruses
- Evidence of human-to-animal transmission

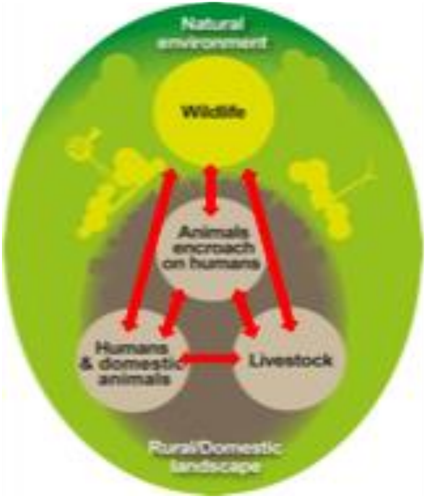
- **7 coronaviruses**: canine *Alphacoronavirus 1* in raccoon dogs and Pipistrellus bat HKU5-like virus in mink with pneumonia (betacoronavirus – *Merbecovirus* – uses ACE2)

Zhao *et al*. *Nature* (2024)

COVID-19: Lessons Learned

- Porous human-animal interface drives disease emergence events
- Need a global ‘pandemic radar’ to rapidly identify emerging diseases
- Continual research into and funding for cross-protective vaccines and antivirals (coronaviruses, influenza viruses and paramyxoviruses)
- Need a broader set of pandemic plans, not just those based on influenza
- Scientists and public health officials need to share their data as openly and rapidly as possible
- Open global collaboration between scientists
- Governments need to listen to and trust in scientists
- Science must be depoliticised

‘Fault lines’ in Emergence



United States House Select Subcommittee
on the Coronavirus Pandemic, July 11th 2023

A Global Pandemic Radar

- Surveillance at the human-animal interface:
  - wildlife trade, fur farming, animal production and slaughter, live animal markets, animal hunting/bushmeat, living around bat roosts, animal carers etc.
- Surveillance of animal mortality events
- Immunological (e.g. VirScan/GIO) and metagenomic surveillance

GOV.UK

Home > Health and social care > COVID-19

Press release

PM announces plan for 'Global Pandemic Radar'

Prime Minister Boris Johnson announces plan for a new 'Global Pandemic Radar' to identify and track new COVID variants and emerging diseases.

From: Prime Minister's Office, 10 Downing Street and The Rt Hon Boris Johnson
Published 21 May 2021

G7
Cornwall
UK 2021

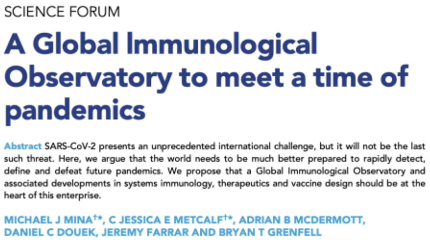
G7 CARBIS BAY HEALTH DECLARATION

v. **We will harness the power and potential of data, digital technologies, science and research to improve prevention, detection and response to future pandemic threats.** We support the establishment of a stronger international pathogen surveillance network, and welcome the WHO's commitment to work with expert partners and countries to help achieve this.

The WHO Hub for Pandemic and Epidemic Intelligence

Better data. Better analytics. Better decisions.

World Health Organization | HUB
Pandemic and Epidemic Intelligence

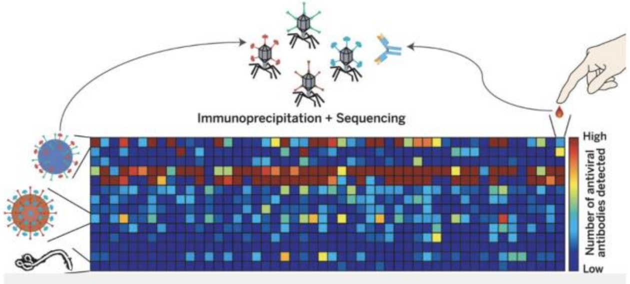


SCIENCE FORUM

A Global Immunological Observatory to meet a time of pandemics

Abstract SARS-CoV-2 presents an unprecedented international challenge, but it will not be the last such threat. Here, we argue that the world needs to be much better prepared to rapidly detect, define and defeat future pandemics. We propose that a Global Immunological Observatory and associated developments in systems immunology, therapeutics and vaccine design should be at the heart of this enterprise.

MICHAEL J MINA†*, C JESSICA E METCALF†*, ADRIAN B MCDERMOTT, DANIEL C DOUEK, JEREMY FARRAR AND BRYAN T GRENFELL



VirScan, or systematic viral epitope scanning, works by displaying bits of protein from more than 1,000 strains of virus. Antibodies in a blood sample latch onto the bits they recognize. Now, scientists have updated VirScan to include the novel coronavirus. Credit: G. Xu et al./*Science* 2015

Steps Toward Pandemic Prevention

- Reduce interactions between humans with wildlife
  - game/fur farms/live animal markets
  - counter deforestation

- Capacity building in low/middle income countries

- Continual global surveillance at the human-animal interface (pandemic radar)

- Zoonotic risk assessment of viruses identified
  - Animal viruses closely related to known human viruses
  - Animal viruses that use human-like cell receptors
  - Animal viruses that are jumping to new hosts

- Immediate and open access data sharing
  - Genome sequences
  - Epidemiological data

- Pre-emptive vaccine design/limitation of risk behaviour

Time following sampling:

- Identification of pathogen
  - 24 hours
- Design of mRNA vaccine
  - 48 hours

Illumina MiSeq 100
~100 million
reads/8 hours