Covid Origins Debate, Day 1:
where and when Covid-19 started

Is this a good idea?

I asked a few scientists if they wanted to attend this debate. They refused.

Scientists think that science should be settled by peer reviewed papers.

Their critics think that science should be settled in debates, on podcasts, and on Twitter.

Most people don’t read those papers, but they do read the news, listen to podcasts, and scroll Twitter. They hear many lab leak theories, but less about what scientists think.

Many people want to hear better debate and discussion.

I used to think the lab leak theory was possible. I wished I could see a good debate.

So, I’m here to try to have that debate, and I think we’ve come up with a good format.

I’m not a virologist, but I’ll try my best to present the case for a natural origin of Covid.

(Meme stolen from someone on Twitter. Sorry, can’t remember who.)

The lab leak theory makes claims like:

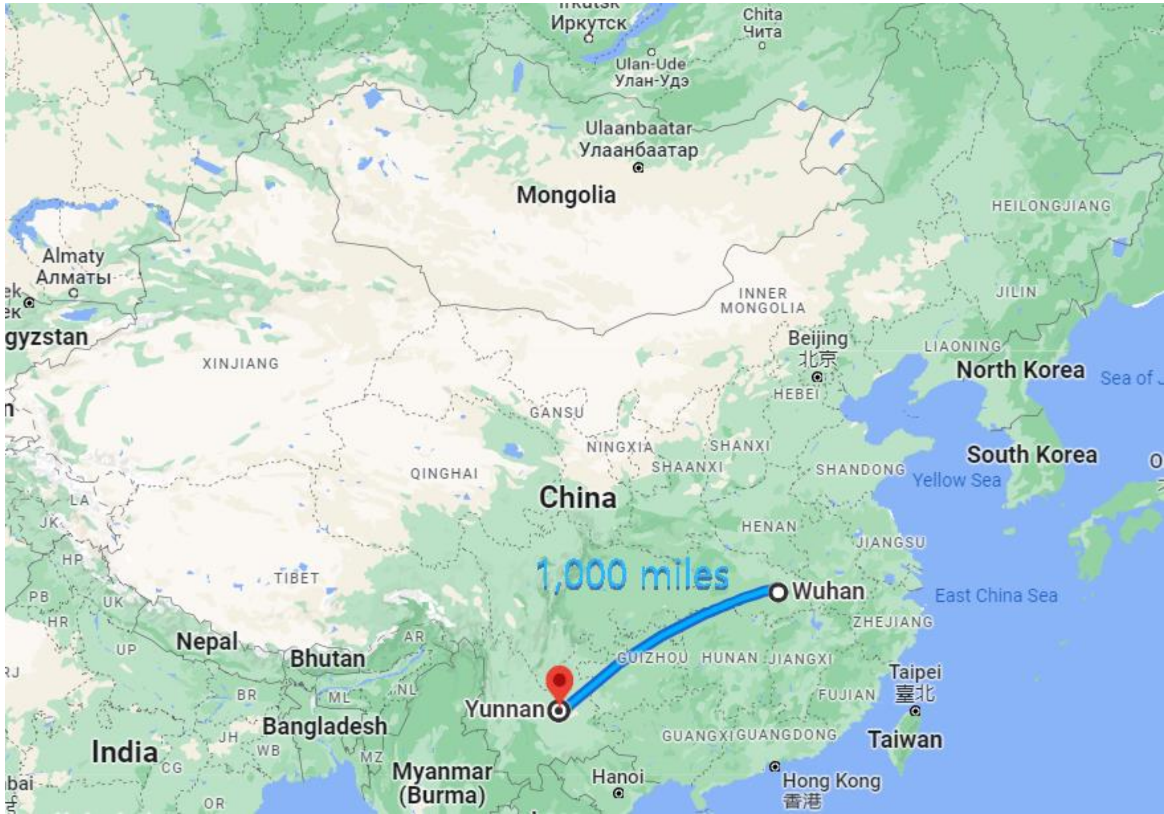
“Wuhan is a very unlikely place for a natural pandemic to start.”

“The closest bats lived 1,000 miles away, there’s no natural way for a virus to get to Wuhan.”

“The pandemic started on the doorstep of China’s best virology lab”.

“The first infected patients were 3 researchers at the Wuhan lab.”

“The virus shows clear signs of genetic engineering.”



I will show that none of that is true:

Wuhan is a fairly likely place for a pandemic to start.

All the evidence points to the pandemic starting at a market in Wuhan that sold wild animals.

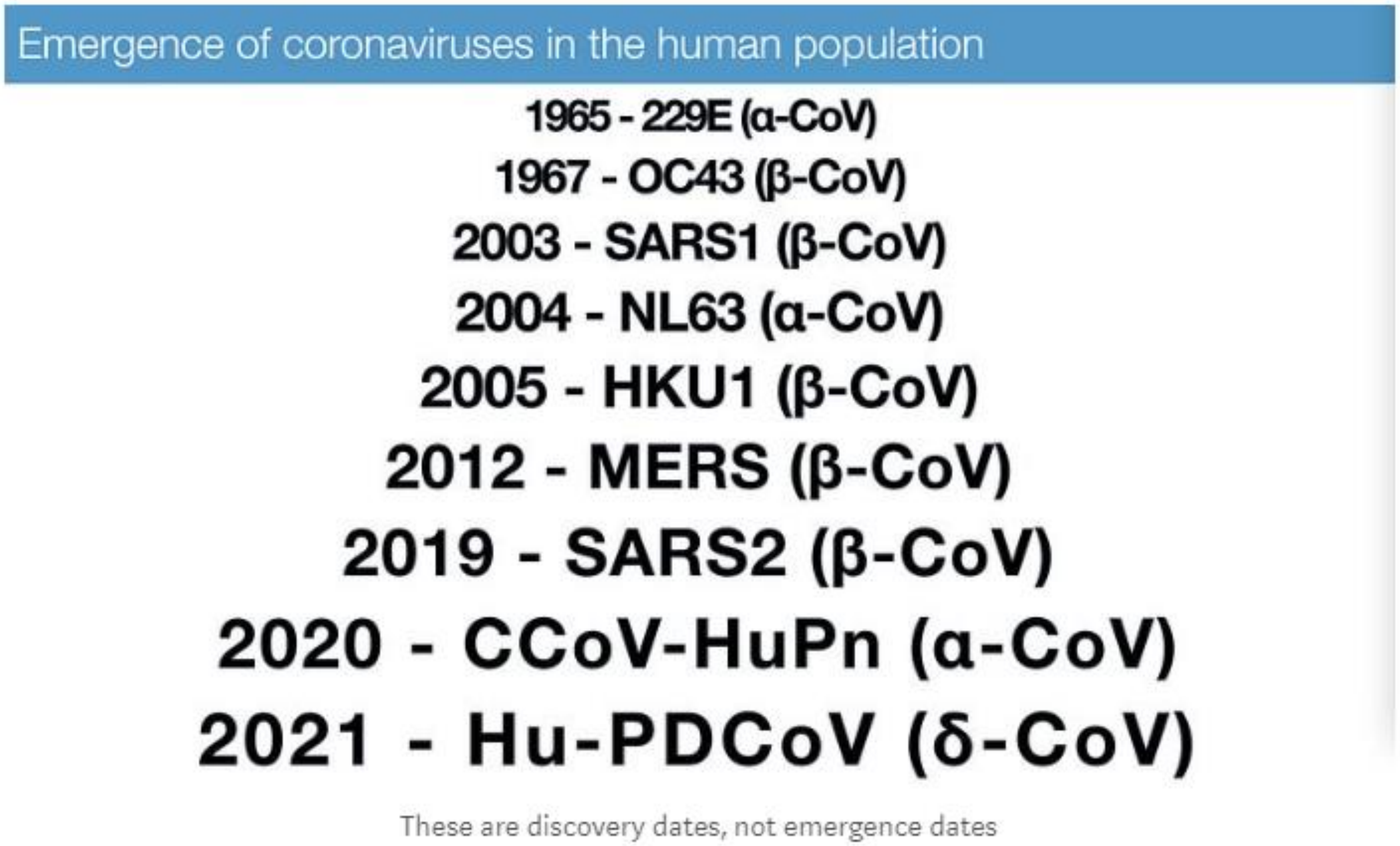
The lab leak theory has a dozen different versions that contradict each other.
It’s sometimes called, “A conspiracy in search of a theory”

The evidence for “3 sick researchers at the lab” appears to be completely made up.

There are many reasons why Covid does not look engineered.

This isn’t the first human coronavirus, or the last.

We’ve found 9 human coronaviruses. 5 are endemic.



Emergence of coronaviruses in the human population

1965 - 229E (α-CoV)
1967 - OC43 (β-CoV)
2003 - SARS1 (β-CoV)
2004 - NL63 (α-CoV)
2005 - HKU1 (β-CoV)
2012 - MERS (β-CoV)
2019 - SARS2 (β-CoV)
2020 - CCoV-HuPn (α-CoV)
2021 - Hu-PDCoV (δ-CoV)

These are discovery dates, not emergence dates

Coronaviruses also jump from wild animals into livestock

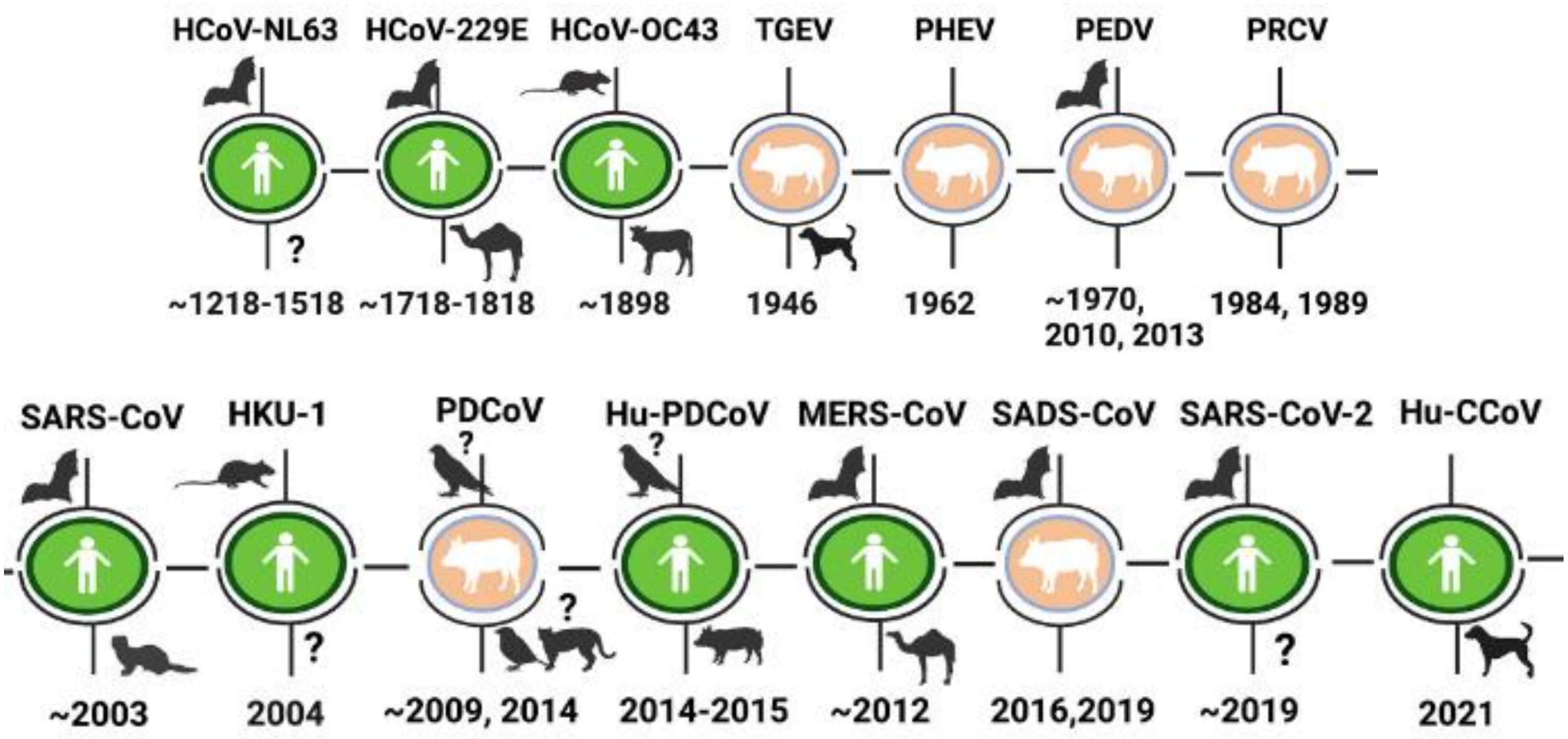


Image from Keusch et al 2022. These are emergence dates.
Top animal is the host species, bottom is the intermediate species.

Sometimes we find the intermediate host, like with SARS in 2003.
Sometimes we can't find it, like with HKU-1 in 2004.

How does Covid-19 compare to the 2003 SARS epidemic?

SARS was found in markets that sold civets and raccoon dogs. Both species carried the virus.

The first known covid cases were at a market that sold civets and raccoon dogs.

First SARS case: November 2002
First covid case: likely November 2019 (first recorded case: early December 2019.

Many human viruses are seasonal in the winter. Bat viruses are seasonal, as well. Infections are higher in September and October because newborn bats have weaker immune systems.

SARS started in Foshan, the 14th largest city in China

Covid started in Wuhan, the 9th largest city in China

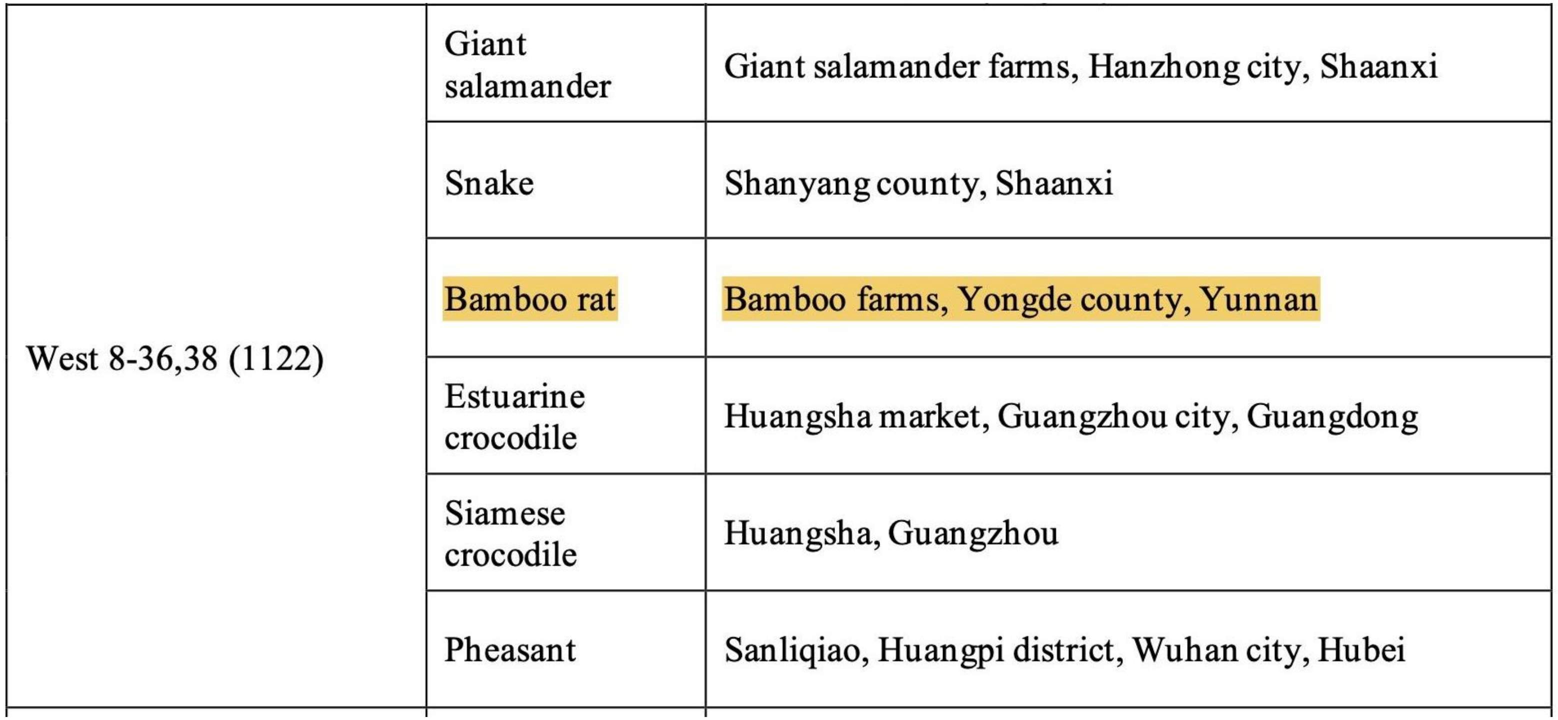
Rank	City	Province	Latest Estimate[5]
1	Shanghai	—	26,875,500
2	Beijing⍟#	—	21,167,303
3	Guangzhou#*	Guangdong	18,810,600
4	Shenzhen#~	Guangdong	17,633,800
5	Chengdu#*	Sichuan	15,025,554
6	Tianjin#†	—	13,929,152
7	Chongqing#*	—	12,313,714
8	Nanjing*	Jiangsu	9,320,689
9	Wuhan#*	Hubei	8,546,775
10	Xi'an#*	Shaanxi	8,438,050
11	Hangzhou*	Zhejiang	7,969,372
13	Dongguan	Guangdong	7,489,198
12	Shenyang*	Liaoning	7,469,474
14	Foshan	Guangdong	7,462,797
15	Harbin*	Heilongjiang	6,612,795

Some people ask, “why did Covid start 1,000 miles away from Yunnan province, where the bats live?”

That’s misleading. SARS started in Guangdong province, but was traced back to Yunnan bats.
That’s also 1,000 miles away.

SARS was also found on Hubei farms, so we know these viruses can naturally get to Hubei.

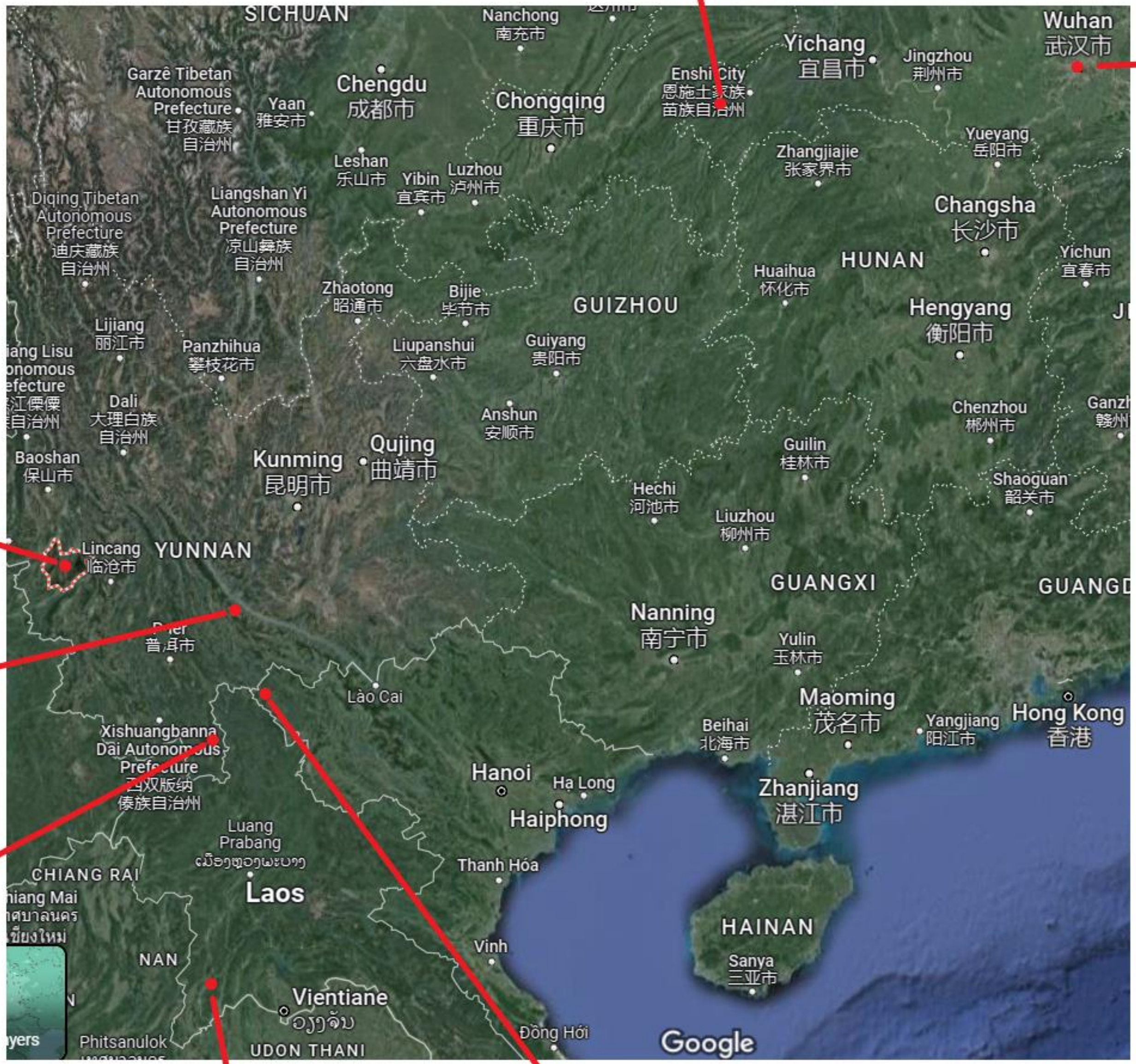
There were some animals from Yunnan sold at the Wuhan market



West 8-36,38 (1122)	Giant salamander	Giant salamander farms, Hanzhong city, Shaanxi
	Snake	Shanyang county, Shaanxi
	Bamboo rat	Bamboo farms, Yongde county, Yunnan
	Estuarine crocodile	Huangsha market, Guangzhou city, Guangdong
	Siamese crocodile	Huangsha, Guangzhou
	Pheasant	Sanliqiao, Huangpi district, Wuhan city, Hubei

Animal sales information, from the WHO report

Those Yunnan farms are near where we found some of the bat viruses closest to Covid



Tenglong cave

Wuhan

Yongde county
bamboo rat farms

Mojiang
(RATG13)

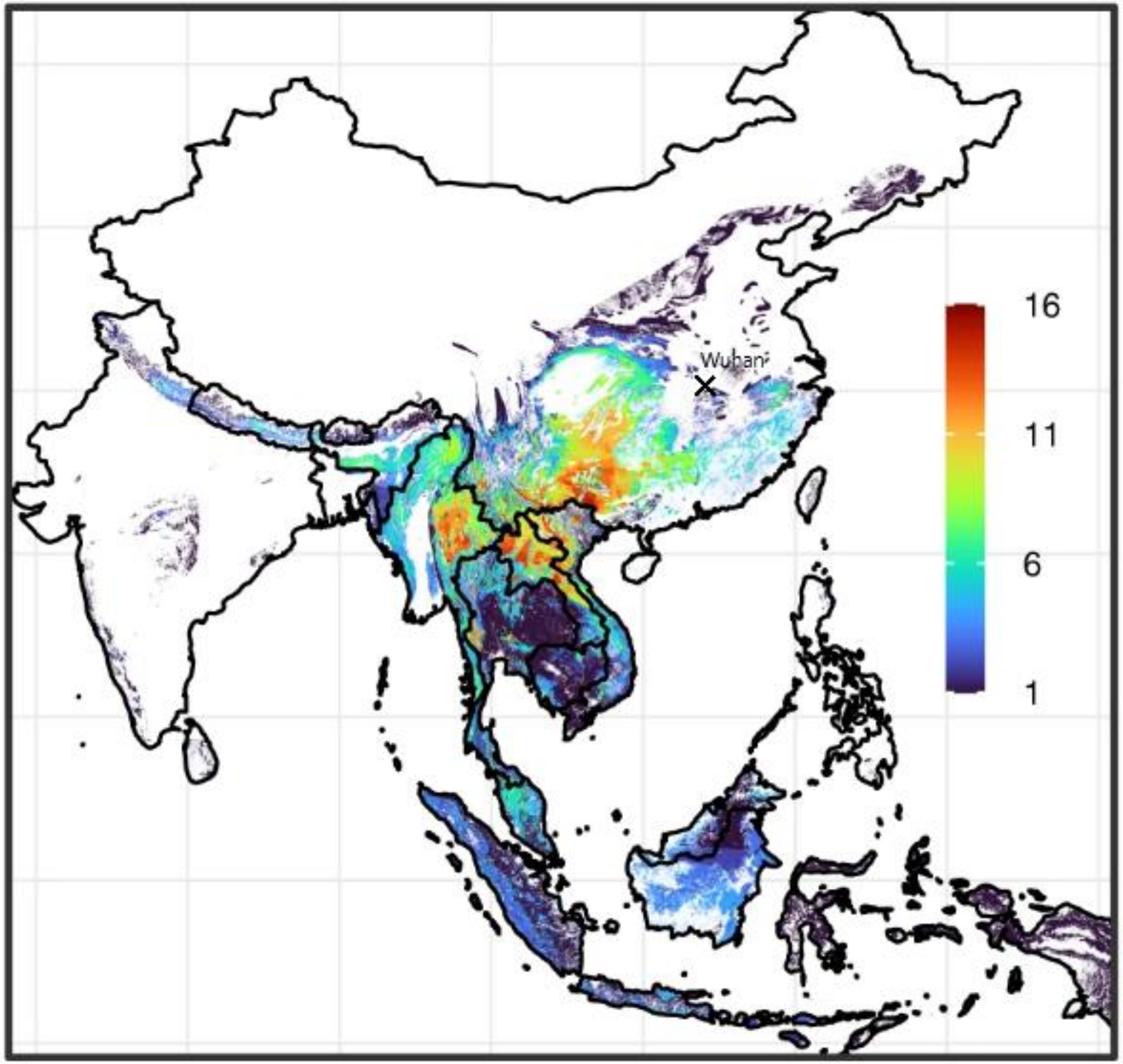
RmYN02

RmBANAL52

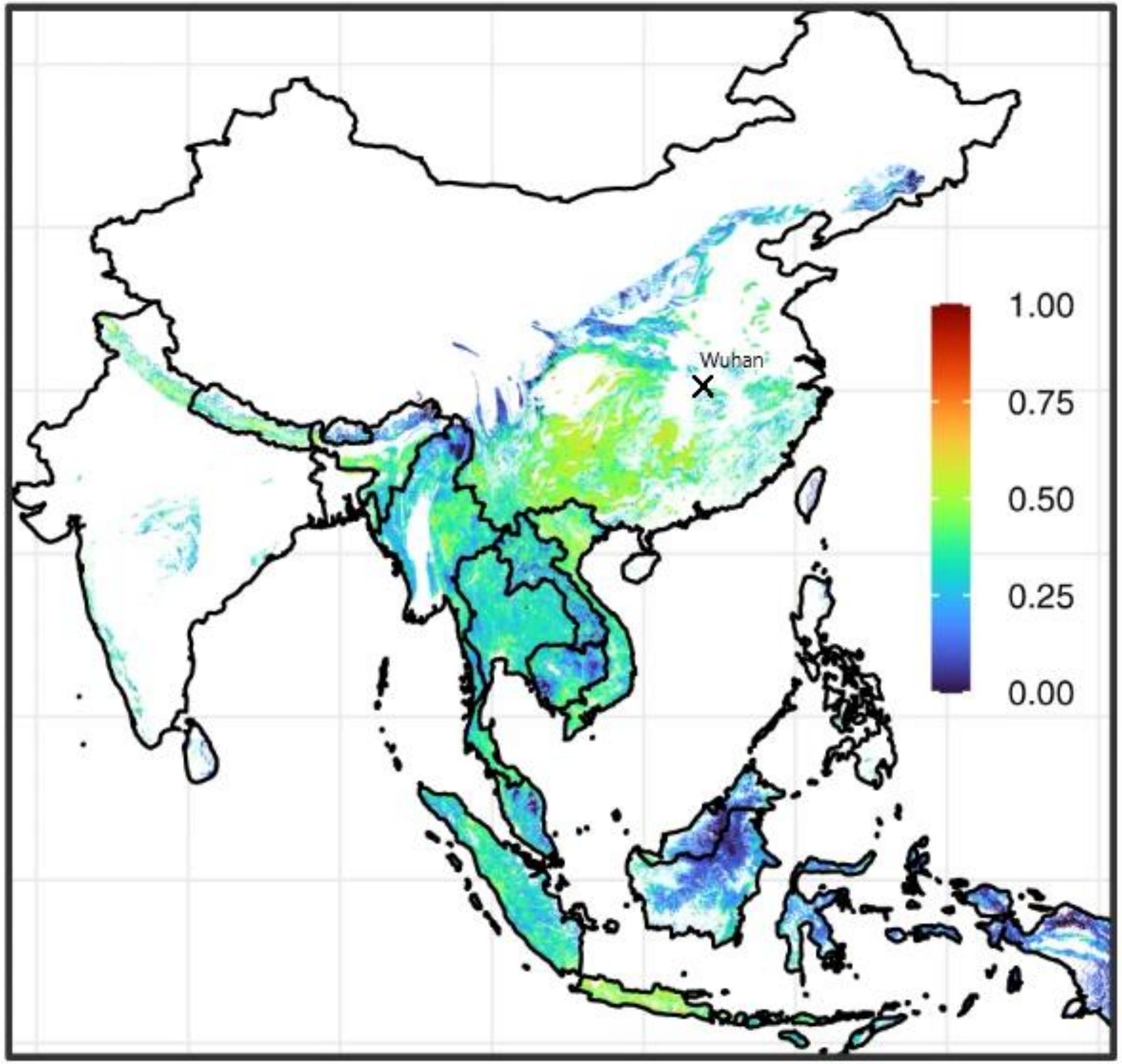
Rp22DB159

There are also caves in Hubei province, with bats in them.
There are civet farms near some of those caves.
Hubei had 631 wildlife farms with 1.1 million animals at the time of the 2019 outbreak.

Bats that can carry SARS viruses are found in many parts of China and Southeast Asia. It's only the density that's highest in Yunnan and Laos:



Yunnan’s human population is also low. The overlap between bats and humans doesn’t stand out as much.



SARS has been found near Wuhan.

A 2005 study found Hubei bats had antibodies against SARS family viruses.

Civets were farmed and sold in Hubei, before the SARS pandemic and after.

Those civets tested positive on multiple occasions:

May 2003 (Hubei, probably Enshi)
April 2004 (Enshi, Hubei)
September 2004 (Wufeng, Hubei)
2005 (SARS related virus, Hubei farms)

Photos: Civet cats released to forests in Wuhan, Hubei

NEWS.SOHU.COM 17:10, May 27, 2003 Xinhuanet

The civet cat was put in a cage and kept circling back and forth, trying to get out

The released civet cat walked to the grass on the side of the road, looking back from time to time

Hubei exported 8,000 civets to Guangdong every year.

SARS infected civets in Hubei had a virus genetically closer to the Guangdong human cases than the Guangdong market civets.

So it's possible that SARS started on Hubei farms.

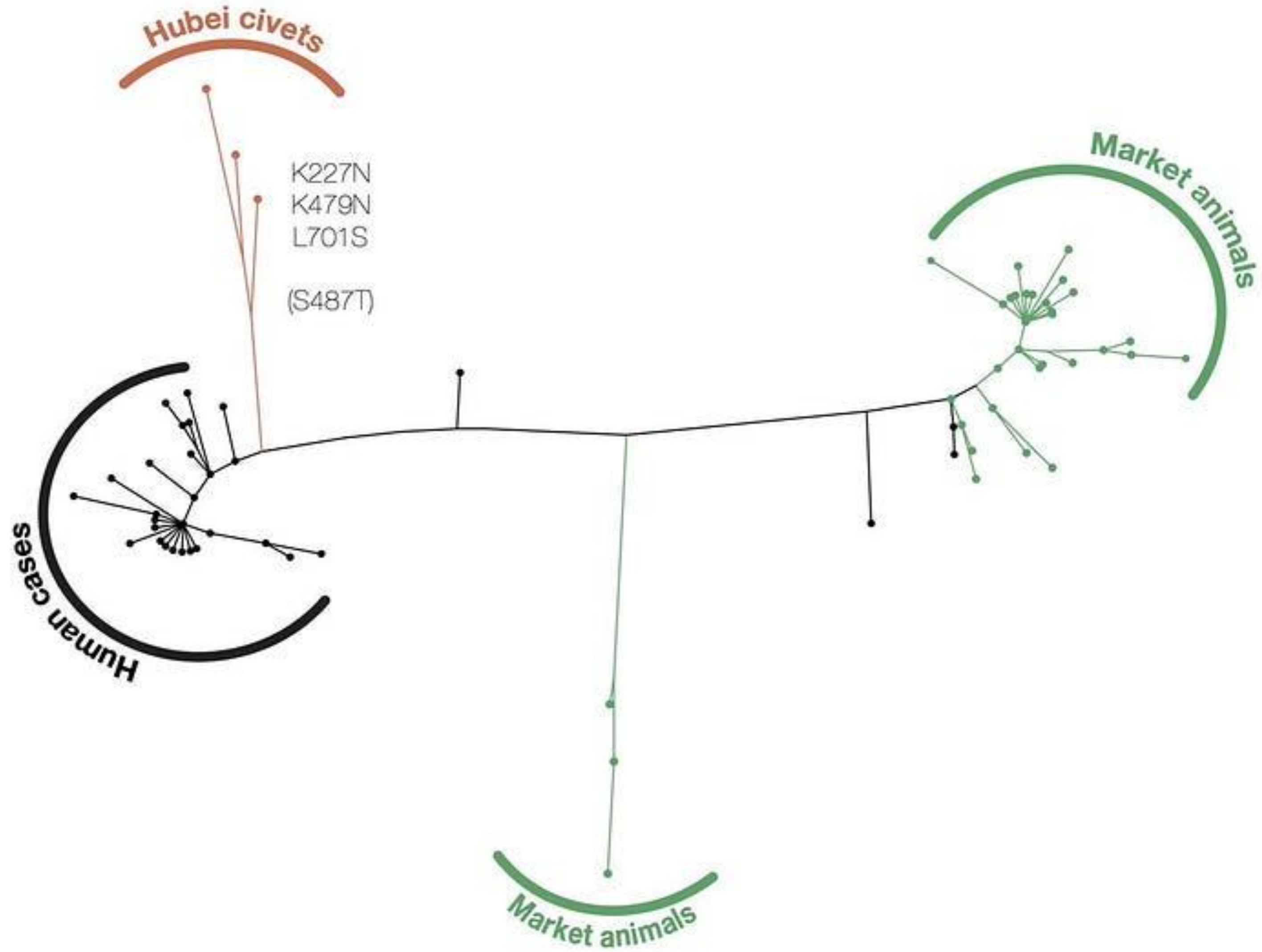


Image source, github link for genetic data

We can track some SARS lineages via deletions in the ORF8 gene

Most of the civet strains have a complete genome here:

```
AY304487|SZ13|Raccoon_Dog|China_Shenzhen_Dongmen-Market|2003/1-8581        TACAGCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTCCTACTGGTTACCAACCTGAATGGAATATAAGGTACAACACTAGGGGTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
AY304488|SZ16|Civet|China_Shenzhen_Dongmen-Market|2003_05_07/1-29731        TACAGCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTCCTACTGGTTACCAACCTGAATGGAATATAAGGTACAACACTAGGGGTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
```

so do some of the earliest Guangzhou cases:

```
AY394985|HSZ-Bb|Human|China_Guangdong_Guangzhou|2003_01/1-29530        TACAGCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTCCTACTGGTTACCAACCTGAATGGAATATAAGGTACAACACTAGGGGTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
AY394994|HSZ-Bc|Human|China_Guangdong_Guangzhou|2003_01/1-29765        TACAGCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTCCTACTGGTTACCAACCTGAATGGAATATAAGGTACAACACTAGGGGTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
```

Later human cases have a 29 nucleotide deletion here, so we can tell those are all related to each other:

```
AY394978|GZ-B|Human|China_Guangdong_Guangzhou|2003_03/1-29640        TACAGCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGT-----------------------------AAGGTACAACACTAGGGGTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
AY461660|SoD|Human|Russia|2003/1-29715                               TACAGCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGT-----------------------------AAGGTACAACACTAGGGGTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
```

But some early Guangdong human cases have this rare 82 nucleotide deletion instead:

```
AY394996|ZS-B|Human|China_Guangdong_Zhongshan|2003_01/1-29683        TACAGCGCTGTGCATCTAA----------------------------------------------------------------------------------TATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
AY394997|ZS-A|Human|China_Guangdong_Zhongshan|2003_01/1-29683        TACAGCGCTGTGCATCTAA----------------------------------------------------------------------------------TATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
AY395003|ZS_C|Human|China_Guangdong_Zhongshan|2003_01/1-29647        TACAGCGCTGTGCATCTAA----------------------------------------------------------------------------------TATAGCACTGCTTGGCTTTGTGCTCTAGGAAA
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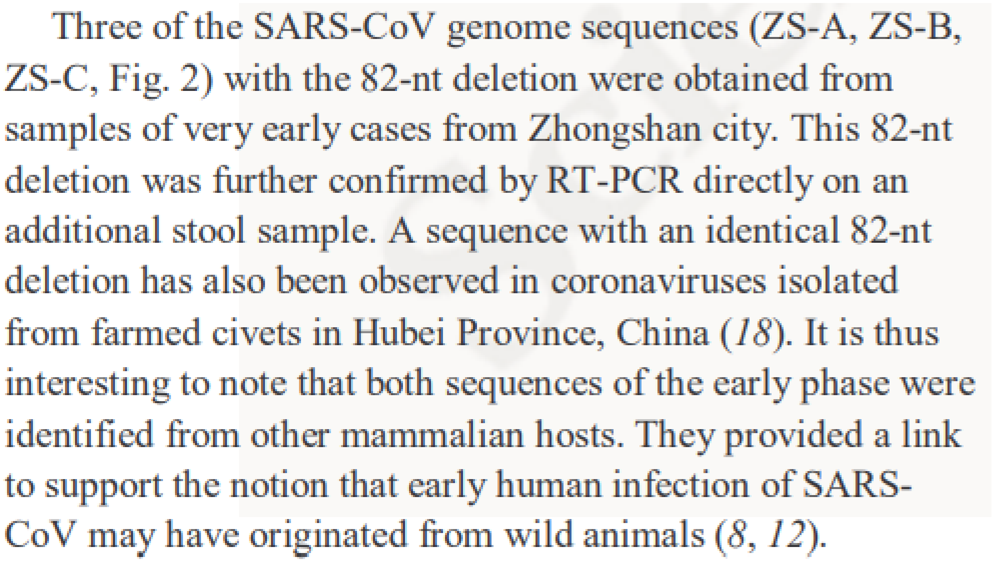
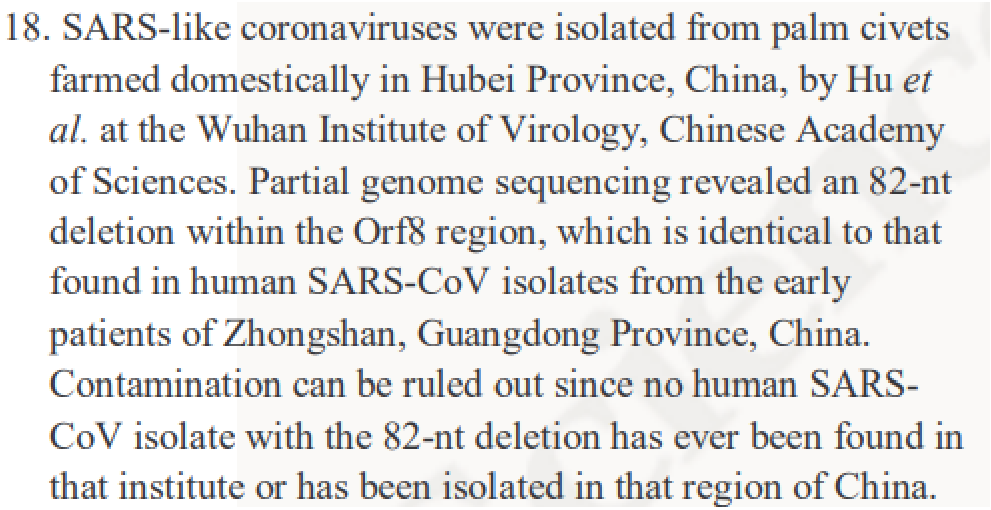
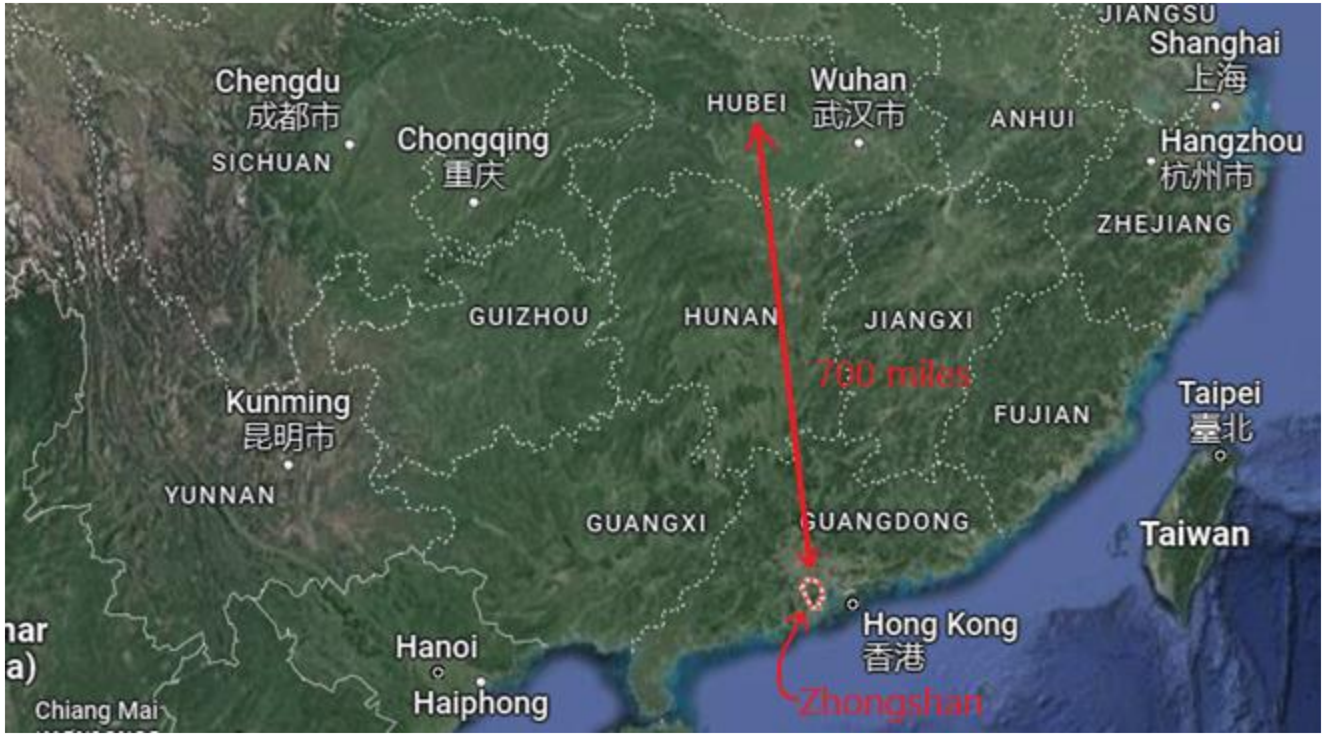
That 82 nucleotide mutation was also found in farmed civets in Hubei, in May 2003.



Three of the SARS-CoV genome sequences (ZS-A, ZS-B, ZS-C, Fig. 2) with the 82-nt deletion were obtained from samples of very early cases from Zhongshan city. This 82-nt deletion was further confirmed by RT-PCR directly on an additional stool sample. A sequence with an identical 82-nt deletion has also been observed in coronaviruses isolated from farmed civets in Hubei Province, China (*18*). It is thus interesting to note that both sequences of the early phase were identified from other mammalian hosts. They provided a link to support the notion that early human infection of SARS-CoV may have originated from wild animals (*8*, *12*).



18. SARS-like coronaviruses were isolated from palm civets farmed domestically in Hubei Province, China, by Hu *et al.* at the Wuhan Institute of Virology, Chinese Academy of Sciences. Partial genome sequencing revealed an 82-nt deletion within the Orf8 region, which is identical to that found in human SARS-CoV isolates from the early patients of Zhongshan, Guangdong Province, China. Contamination can be ruled out since no human SARS-CoV isolate with the 82-nt deletion has ever been found in that institute or has been isolated in that region of China.

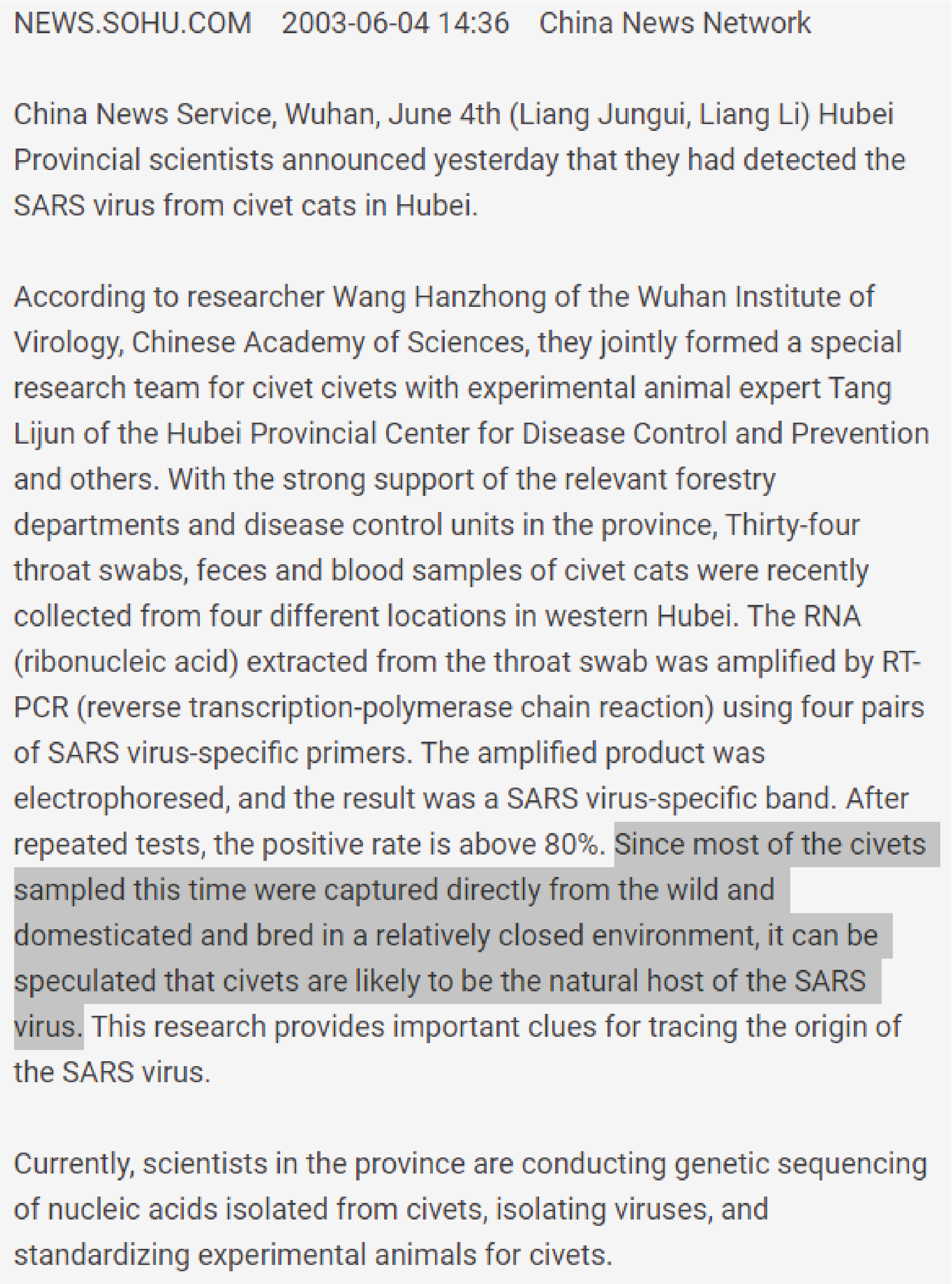


That virus most likely started on Hubei farms and was exported to Zhongshan markets.

Source paper

How did those Hubei civets get sick?

They were captured from the wild and then farmed.



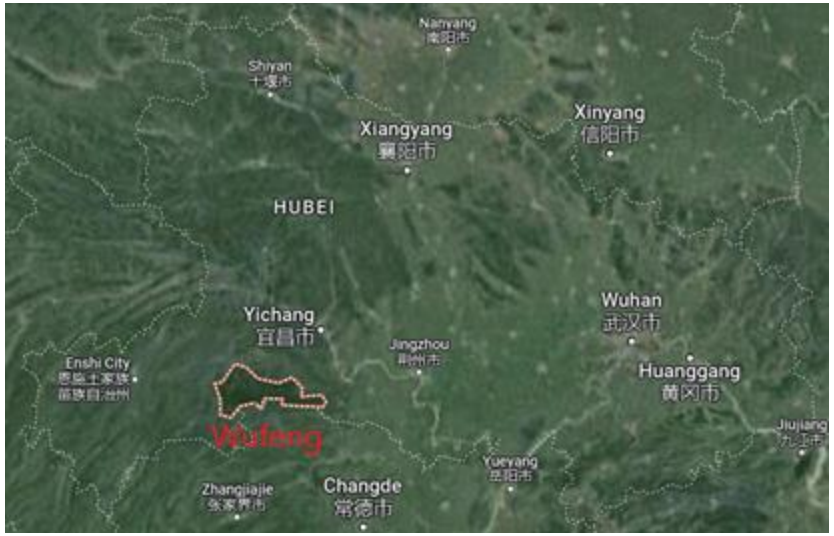
NEWS.SOHU.COM 2003-06-04 14:36 China News Network

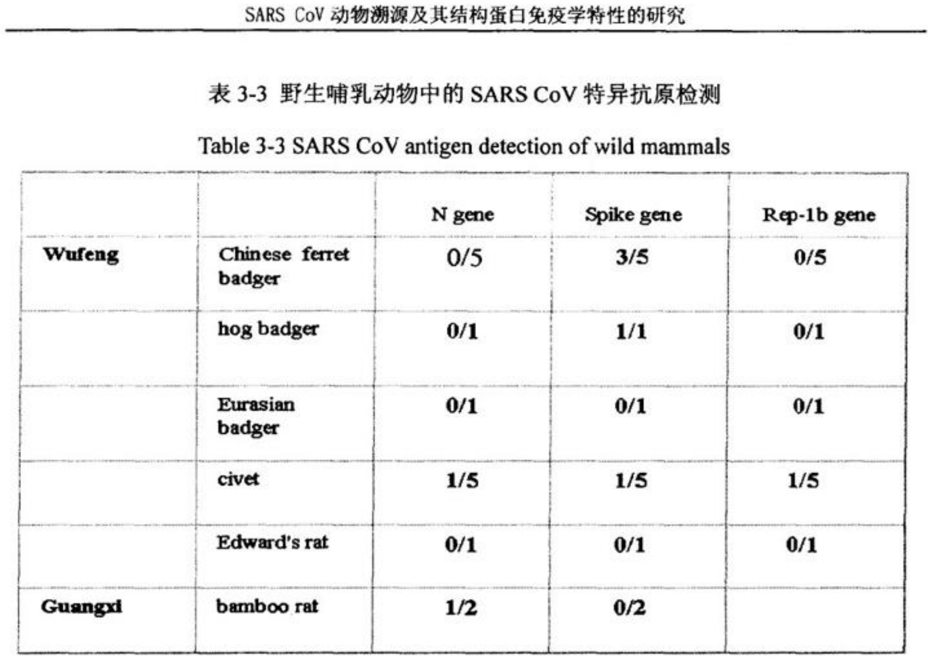
China News Service, Wuhan, June 4th (Liang Jungui, Liang Li) Hubei Provincial scientists announced yesterday that they had detected the SARS virus from civet cats in Hubei.

According to researcher Wang Hanzhong of the Wuhan Institute of Virology, Chinese Academy of Sciences, they jointly formed a special research team for civet civets with experimental animal expert Tang Lijun of the Hubei Provincial Center for Disease Control and Prevention and others. With the strong support of the relevant forestry departments and disease control units in the province, Thirty-four throat swabs, feces and blood samples of civet cats were recently collected from four different locations in western Hubei. The RNA (ribonucleic acid) extracted from the throat swab was amplified by RT-PCR (reverse transcription-polymerase chain reaction) using four pairs of SARS virus-specific primers. The amplified product was electrophoresed, and the result was a SARS virus-specific band. After repeated tests, the positive rate is above 80%. Since most of the civets sampled this time were captured directly from the wild and domesticated and bred in a relatively closed environment, it can be speculated that civets are likely to be the natural host of the SARS virus. This research provides important clues for tracing the origin of the SARS virus.

Currently, scientists in the province are conducting genetic sequencing of nucleic acids isolated from civets, isolating viruses, and standardizing experimental animals for civets.

A 2004 study (translated here) looked at wild animals in Hubei and found several species with SARS antibodies. The same study also found higher infection rates among farmed civets than wild civets.





SARS CoV 动物溯源及其结构蛋白免疫学特性的研究

表 3-3 野生哺乳动物中的 SARS CoV 特异抗原检测

Table 3-3 SARS CoV antigen detection of wild mammals

		N gene	Spike gene	Rep-1b gene
Wufeng	Chinese ferret badger	0/5	3/5	0/5
	hog badger	0/1	1/1	0/1
	Eurasian badger	0/1	0/1	0/1
	civet	1/5	1/5	1/5
	Edward's rat	0/1	0/1	0/1
Guangxi	bamboo rat	1/2	0/2	

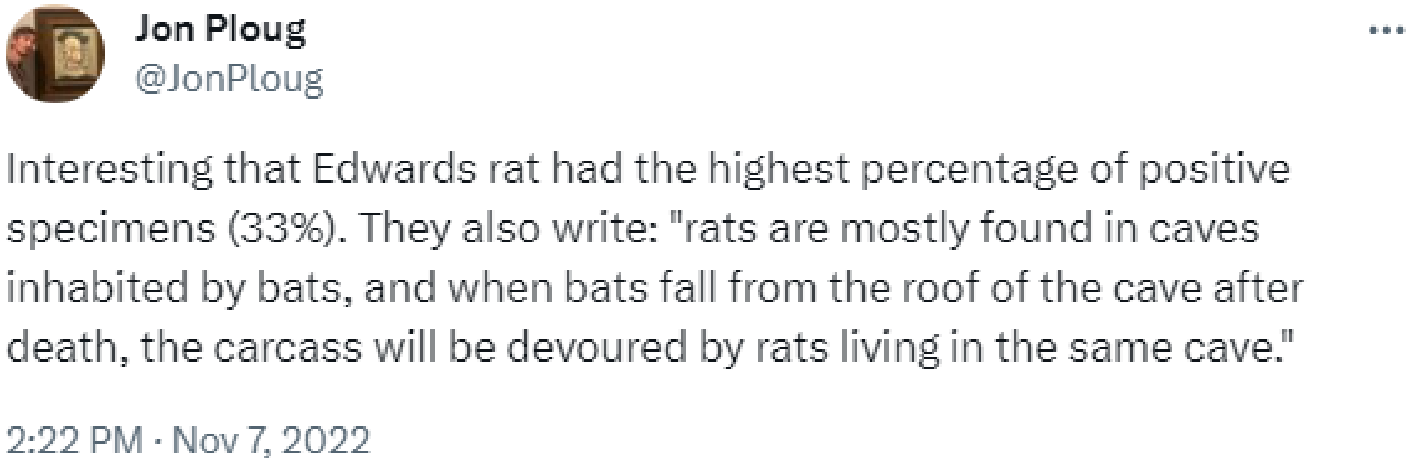
表 3-4 野生哺乳动物中的 SARS CoV 特异抗体检测

Table 3-4 SARS CoV specific antibody detection of wild mammals

Samples	Number of specimens	Number of positive specimens (%)
Chinese ferret badger (*Melogale moschata*)	24	4 (16.67)
Hog badger (*Arctonyx collaris*)	7	1 (14.29)
Eurasian badger (*Meles meles*)	3	0 (0.00)
Edward's rat (*Leopoldamys edwardsi*)	18	6 (33.33)
Wild civet (*Paguma larvata*)	37	2 (5.41)
Domestic dog (*Canis lupus familiaris*)	5	0 (0.00)
Domestic cat (*Felis silvestris catus*)	3	0 (0.00)
Domestic pig (*Sus scrofa domesticus*)	7	0 (0.00)

How did these wild animals get sick?

The paper gives one possible explanation:



Jon Ploug
@JonPloug

Interesting that Edwards rat had the highest percentage of positive specimens (33%). They also write: "rats are mostly found in caves inhabited by bats, and when bats fall from the roof of the cave after death, the carcass will be devoured by rats living in the same cave."

2:22 PM · Nov 7, 2022

The full SARS spillover scenario might be something like this:

Hubei rat eats dead bat in a cave -> wild civet eats infected rat -> trapped wild civets are put on a farm -> Hubei farmed civets are shipped to Guangdong -> people in Guangdong get sick.

The spillover for Covid might be something similar.

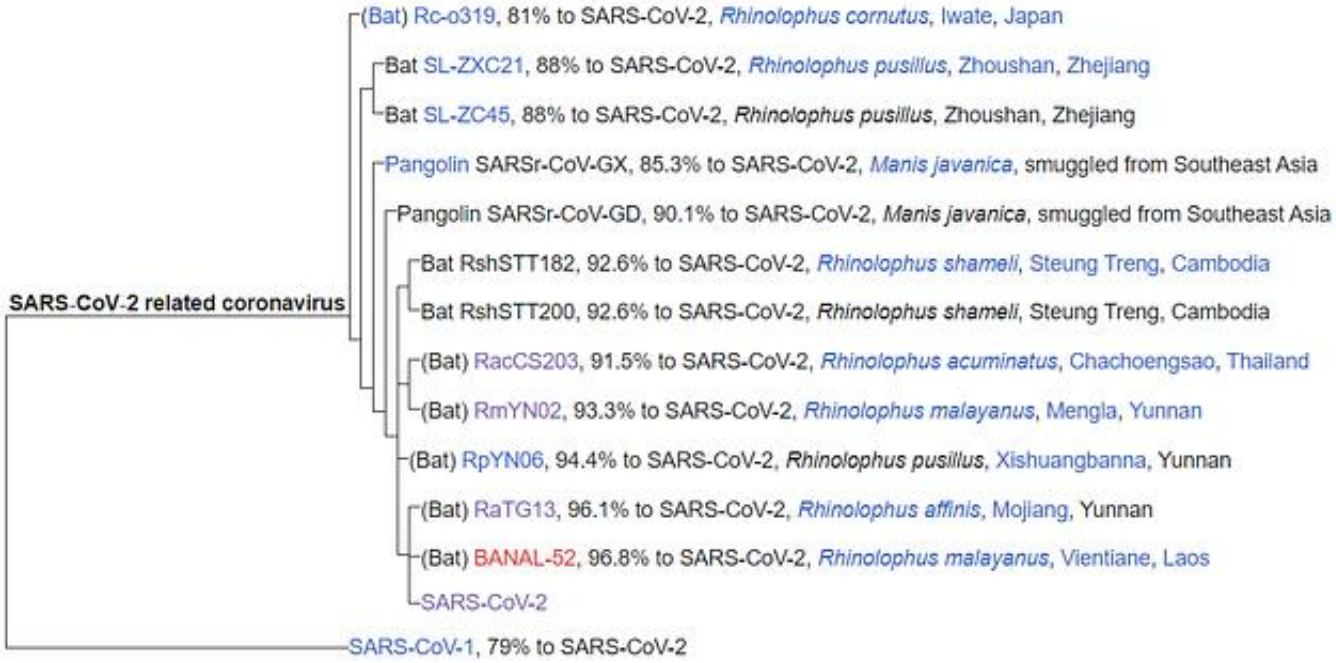
There are multiple pathways for a virus to get to the market:

Hubei bats -> Hubei farms -> Wuhan market
Yunnan bats -> Yunnan farms -> Wuhan market
Yunnan bats -> Yunnan animals -> Hubei farms -> Wuhan market
Yunnan bats -> Yunnan animals -> Yunnan person -> Wuhan market

For both SARS and Covid, we've found 3 bat viruses 94-97% similar.

The closest bat virus is closer to Covid than the closest one is to SARS.

SARS virus family tree, from Wikipedia



Covid virus family tree from Wikipedia

We can also look for "recombinant ancestors"

These viruses frequently recombine with each other, so it's not a simple family tree.
We can look at SARS or Covid as the combination of various bat viruses we've found.
The closest recombinant ancestor is 98.6% for SARS and 98.8% for Covid.

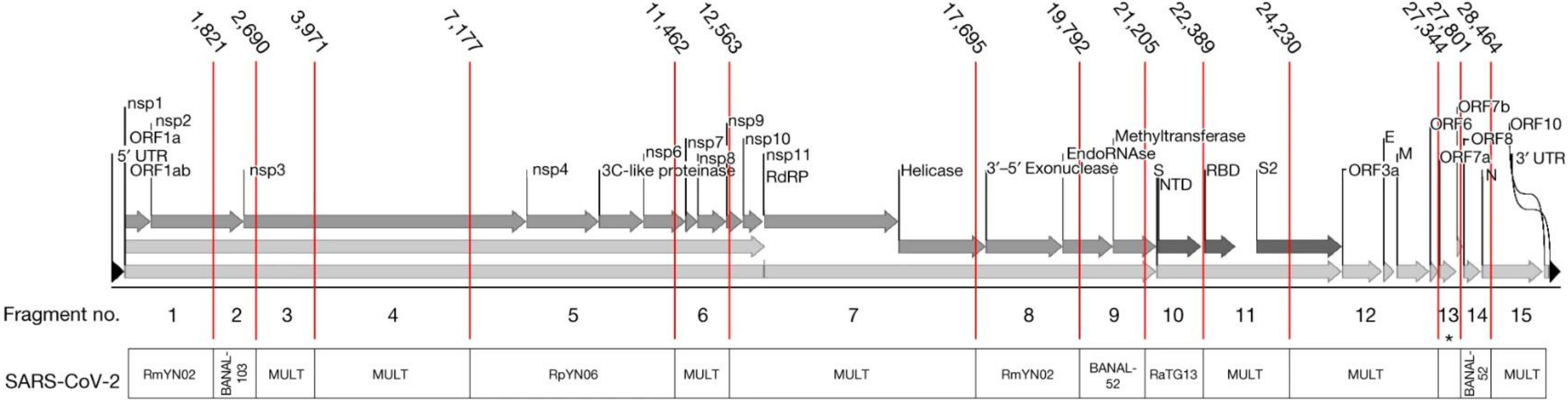


Figure from Temmam et al 2021, showing the segments of Covid. We'll get more into genetics like this in the next debate.

Is it unlikely for a pandemic to start in Wuhan?

Some people ask, “what are the odds Covid would start on the doorstep of China’s best virology lab?”

That’s not literally true. The first known cases were at a market in Wuhan. It’s a 30 minute drive from the lab.

What are the odds a pandemic would start in Wuhan?

The Wuhan lab did coronavirus research, so this could be more than a coincidence.

Let’s try to calculate the odds.

There are 8.6 million people in Wuhan and 1.4 billion in China.

If patient zero is one randomly chosen person, the odds are 1 in 170 they live in Wuhan.

Outbreaks happen in cities

Jonathan Pekar did outbreak simulations: the virus would go extinct if it started in a rural area (95-99% of the time)

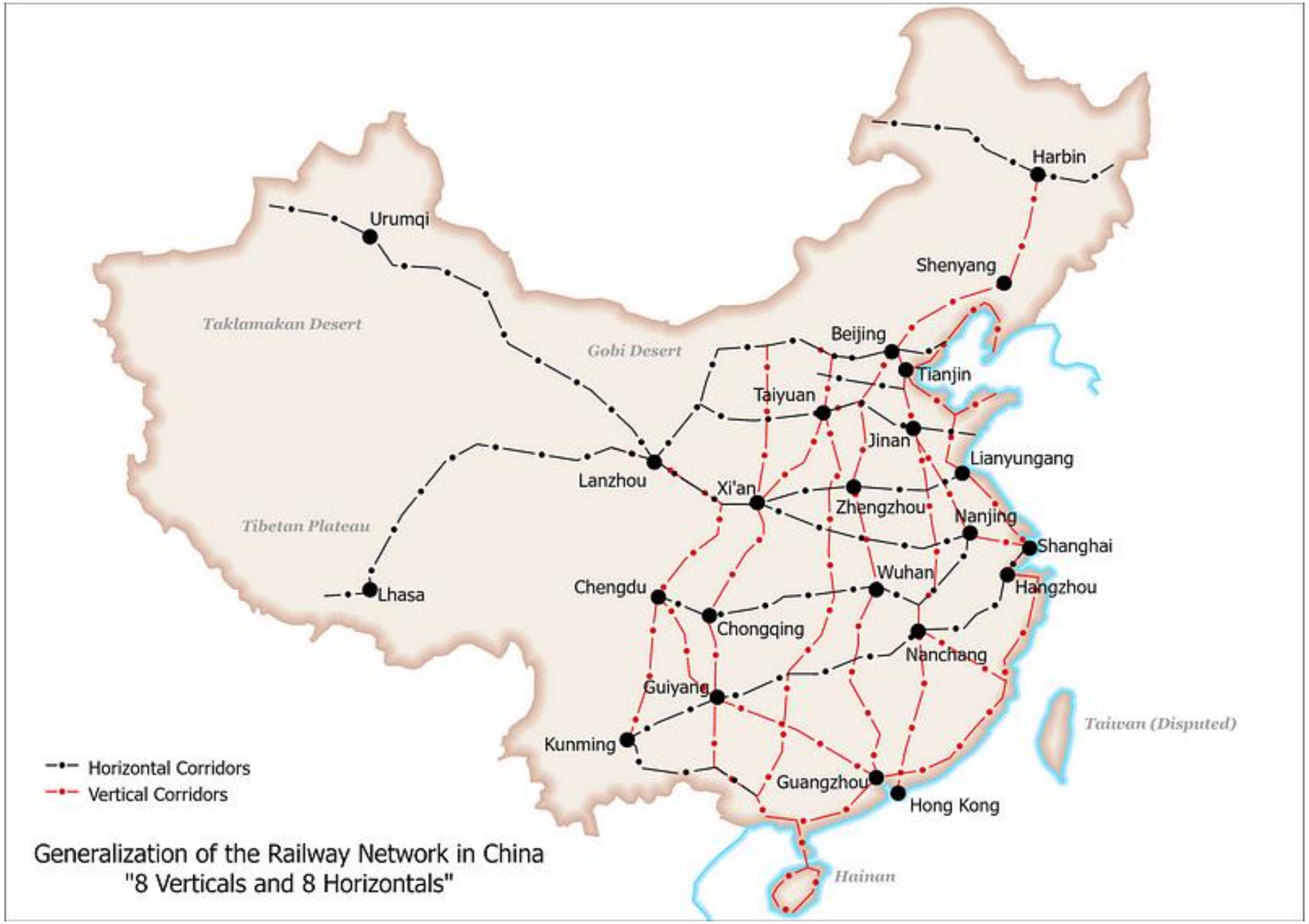
The odds are 30X higher of the virus spreading successfully, if the first case is in a big city.

That eliminates maybe half of the people in China. So the odds of Wuhan are 1.2%.

The odds could be higher. Wuhan is a major hub in the railway network. It’s also a major hub in the wildlife trade. A large quantity of animals and animal products were shipped through Wuhan.

SARS started in the 14th largest city, Covid started in the 9th largest.

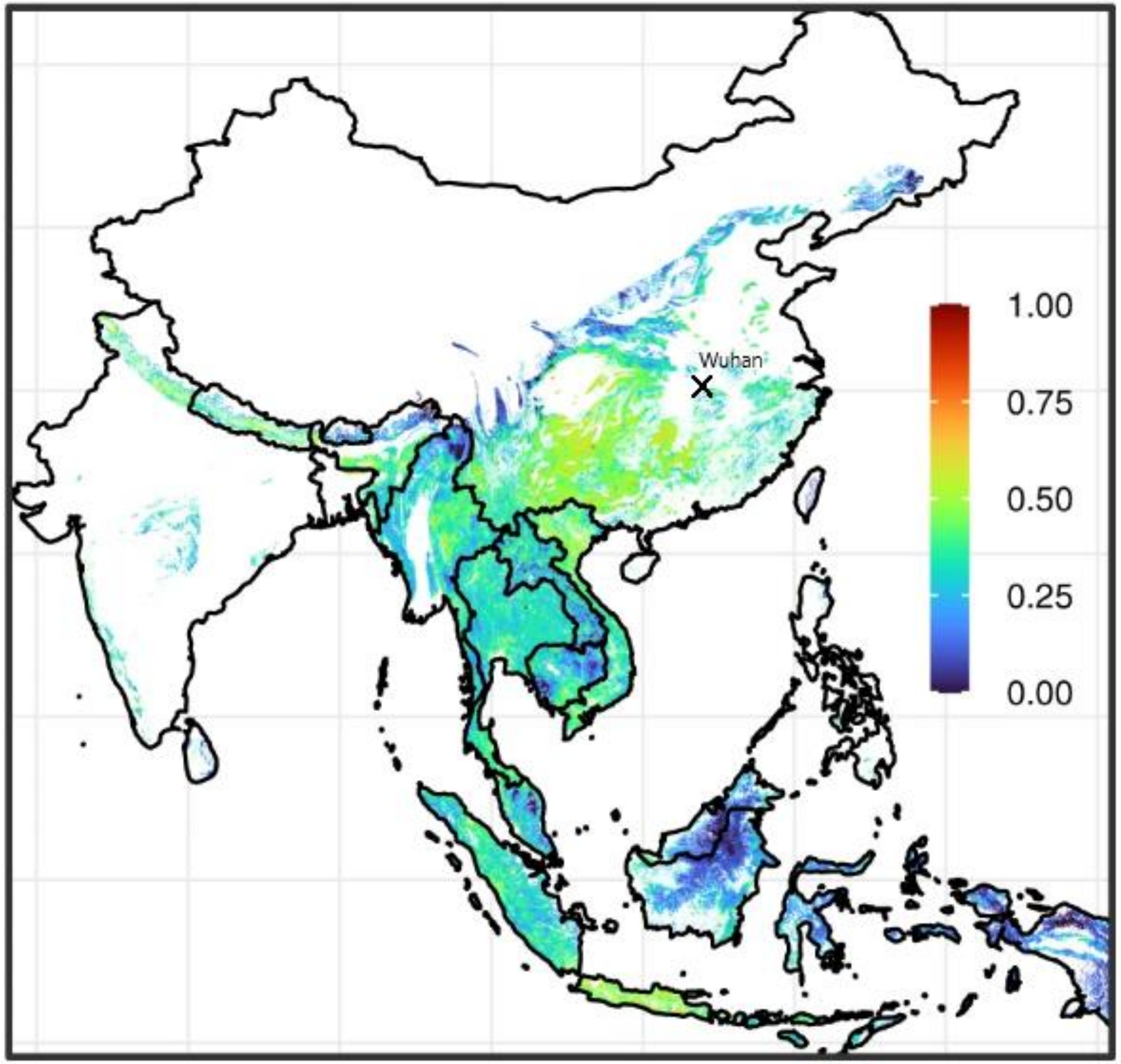
If you need a really big city to cause a pandemic, in the top 20, then the odds of Wuhan might be 5%.



Generalization of the Railway Network in China
"8 Verticals and 8 Horizontals"

There aren't as many bats in northern China.

Also, more people eat wildlife in the south.



If we exclude northern China, the odds double again.

Farming in Hubei may have been different

After the SARS pandemic, Guangdong province shut down civet farms.

Hubei did not.

On Hubei farms, wild civets were trapped and put together with farmed civets, introducing new vectors.

That could be the reason why SARS started there.

Hubei will not ban civet cats for the time being

NEWS.SOHU.COM January 6, 2004 09:14 Changjiang Daily

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Guangdong Province began to close all wild animal markets in the province yesterday, and took action to kill civet cats that are farmed and sold in the provincial market. The reporter learned from the Wuhan Forestry Bureau yesterday that Hubei has no plans to follow up.

The relevant person in charge of the Municipal Forestry Bureau said that they had already inquired about the Hubei Provincial Forestry Bureau on the matter, but the province has not yet taken follow-up measures, "it will be done in accordance with the unified requirements of the State Forestry Administration."

Coincidentally, the Wuhan Evergreen Wildlife Trading Market was completed yesterday and began to attract investment. This market is the only professional market for wildlife management in Central China. According to the deployment of relevant departments, the scattered wildlife operators in the city will be regulated and concentrated in this market.

Image from Jon Ploug, from article source

Animal traders have the most exposure to SARS family viruses

3% of villagers near Yunnan caves had SARS antibodies. Spillovers are common, with tens or hundreds of thousands of people infected with these viruses every year. Most of the time people don't transmit the viruses.

After SARS, 13% of animal traders had antibodies, and 70% of the traders that worked with civets had antibodies.

Viruses often jump better via an intermediate host.

The most likely person in China to catch a new SARS-related virus isn't a villager.

It's an animal trader working with SARS susceptible species, or someone purchasing those animals.

For it to start a pandemic, this would have to be in a big city.

And it would happen in central or southern China.

	SARS	vs	Covid-19
Started in:	14th largest city		9th largest city
Closest bat virus found:	Yunnan (1,300 km away)		Yunnan (1,600 km) or Laos (2,200 km)
Closest bat virus:	96%		96.8%
Closest recombinant ancestor:	98.6%		98.8%
Found at:	markets selling civets + raccoon dogs		market selling civets + raccoon dogs
Intermediate animals from:	possibly Hubei farms		possibly Hubei farms
Closest virus in intermediate host:	99.8%		-----
Intermediate host:	Found 6 months later		Not found.

Why was the intermediate host found for SARS and not Covid?

The host for SARS was found six months later, in markets and farms that were still open.

With Covid, people didn't have months to search.

The Wuhan market was shut down December 31st, live animals were never tested. Samples were taken from frozen goods and from stray animals.

Hubei farms were shut down January 23rd, animals were released or killed without much testing.

Wuhan went into lockdown January 23rd.

The rest of China went into lockdown in February.

Farms across China were closed February 24th and tens of millions of animals were killed.

China did test 80,000+ animals for Covid, but that was unrelated livestock and poultry.
They only tested about 600 animals from farms related to the market.

For comparison, see this study during SARS, where scientists sampled 1,100 civets from farms supplying an infected Guangdong market. Zero of those farmed civets tested positive. Tracing viruses is harder than Rootclaim thinks.

In summary:

The start of Covid looks very similar to the start of SARS.

There are many ways that a natural virus could get to Wuhan.

The odds of Wuhan vs another city are probably in the 2% to 10% range.

But we still can’t rule out a lab leak, because we haven’t found the intermediate host.

What are the odds of a lab leak?

SARS leaked from labs several times.

Smallpox has leaked from labs.

These are usually small incidents, but a flu pandemic in 1977 may have been caused by some kind of lab (perhaps a vaccine trial, rather than a lab leak).

It's possible we've had one research triggered pandemic in prior history and many natural pandemics.

Natural pandemics are much more common.

Labs tend to leak known viruses, not novel viruses

Lab leaks are usually obvious – they start with infected researchers.

Even if you didn’t know who was infected, you could tell the lab was the source because the virus would be the same as what they were studying.

For the 1977 flu, the key evidence is that it was genetically similar to the 1950 flu, with so few mutations that it looked like it might have been frozen in the years in-between.

Covid is a novel virus.

It’s only 80% similar to SARS.

It’s 96% similar to the closest bat virus held in a lab. That’s still a large distance, it would take 40 years for evolution to close that 4% gap.

There’s no known virus where we can say, “you could turn this into Covid”.

The lab would need a secret virus to start with.

There has been one novel virus detected as part of lab accident

There’s been one lab related novel virus outbreak, in the case of Marburg.

Vaccine labs imported primates from Uganda for an experiment. The animals had the Marburg virus.
It spread to lab employees, transmission outside the lab was limited.

That’s a zoonotic spillover, but it’s related to lab activities.

Novel viruses are much more likely to be found with natural origins, not through lab accidents.

There has never been a gain of function lab leak

My opponent says that SARS-CoV-2 was created through gain of function research and then leaked.

That’s never happened in history, so it’s hard to guess the odds from prior events.

You can calculate it by chaining together the odds. For instance:

Probability that covid was created from gain of function research =

Probability that the lab had a secret starting virus	**(? We’ll discuss at the second debate)**
*** Probability they created a virus that looks like this**	**(? second debate topic)**
*** Probability that it escaped the lab**	**(1 in 500 per lab, per year)**
*** Probability that it started a pandemic**	**(1 in 3)**
*** Probability the virus made it across town to the market without spreading elsewhere**	**(we’ll talk about this today)**
*** Probability the lab successfully hid all the evidence**	**(? Depends on the quality of the cover-up and the sleuths)**

By the end of this debate, I will put numbers on all these factors, to show that a lab origin is very unlikely.

What are the odds there would be a lab leak theory?

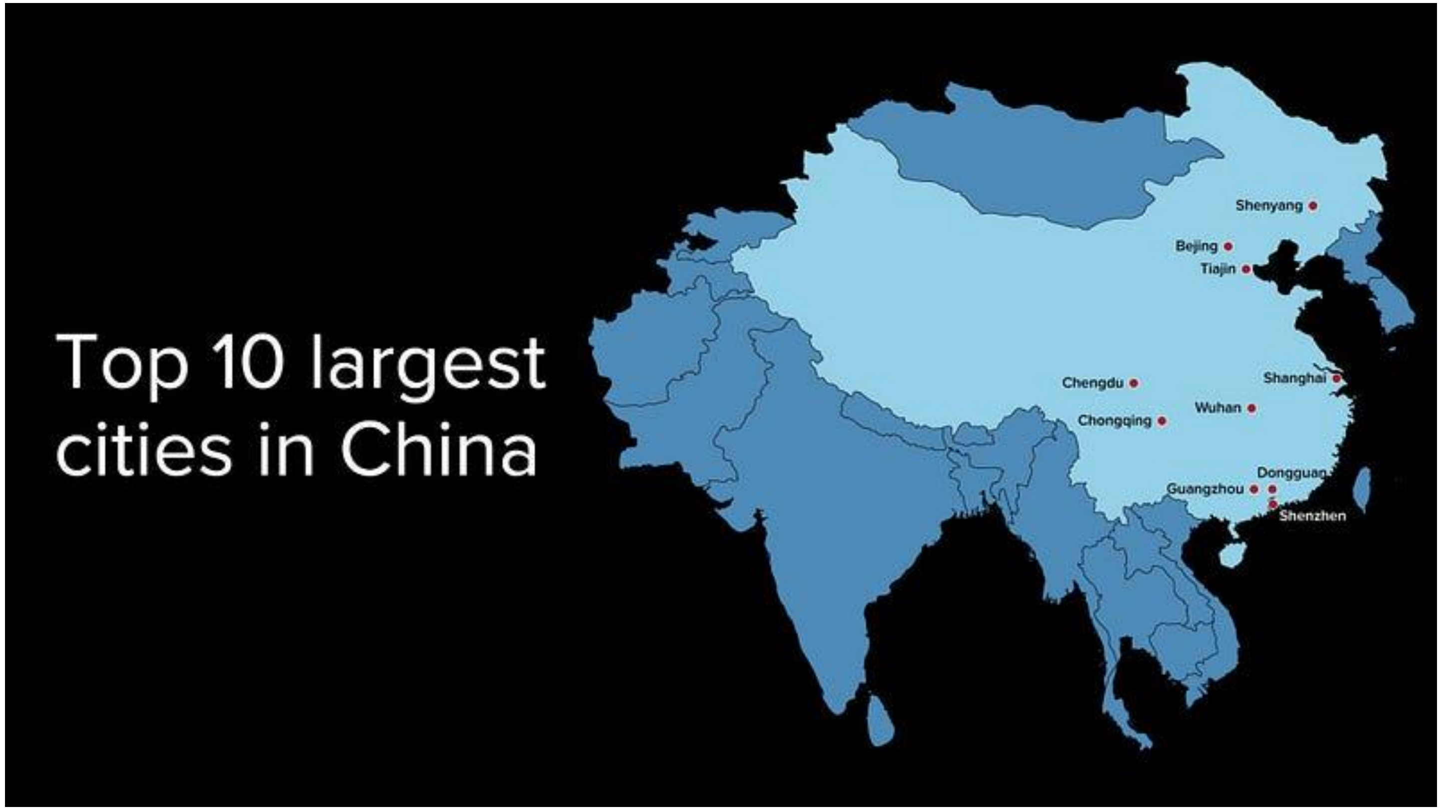
Some people ask: “What are the odds that the pandemic would start in the city with the only BSL-4 lab in China?”

That’s not true. There are two BSL-4 labs in China. One is in Wuhan, one in Harbin (the 15th largest city).
The Harbin lab has done gain of function research on flu viruses.

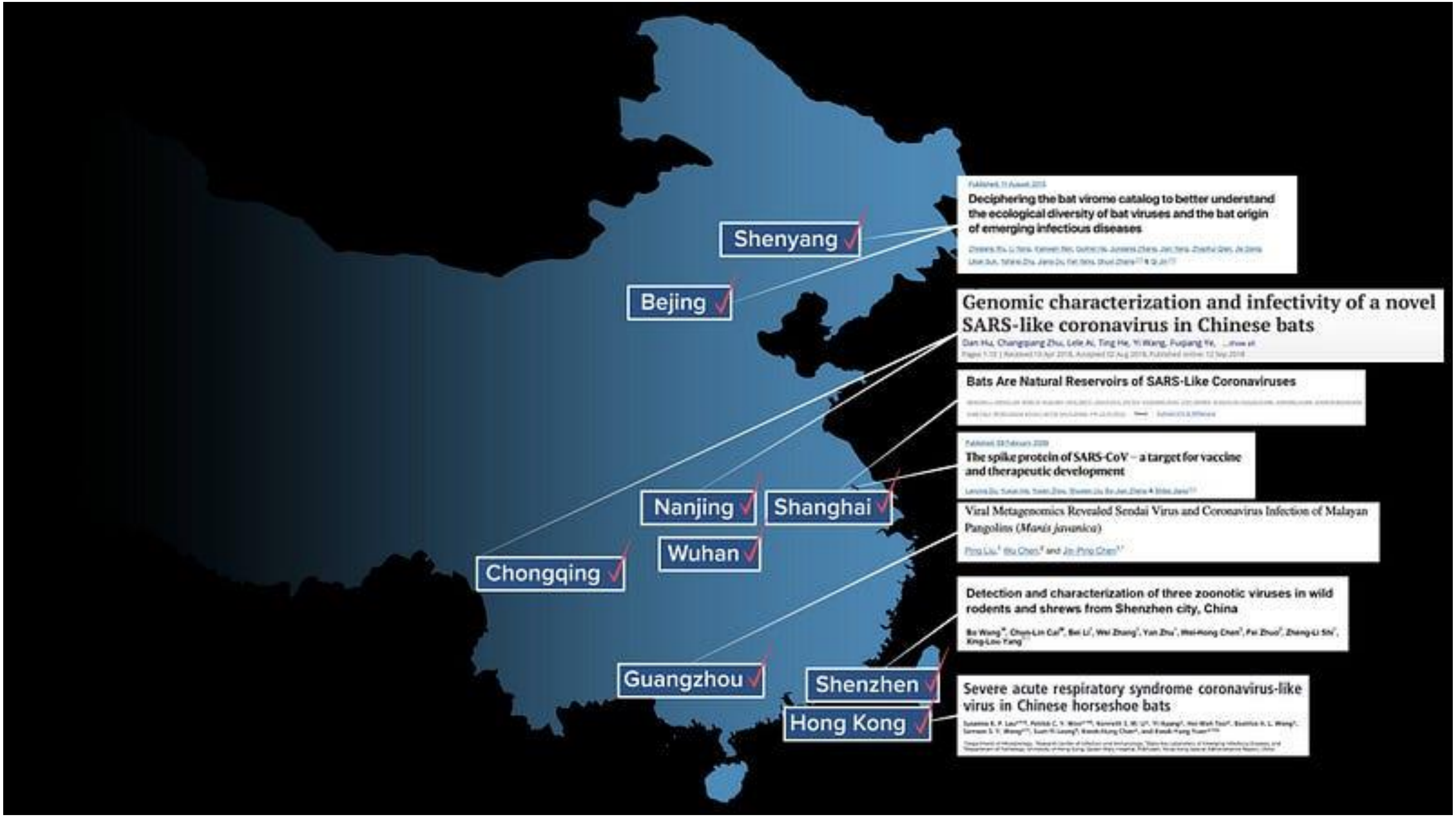
But it’s also irrelevant, because the theories go on to say that the Wuhan lab was reckless and did dangerous research at BSL-2 or BSL-3.

Maybe the question should be: “what are the odds that the pandemic started in a city with a BSL-2 or BSL-3 lab?”

Wuhan is one of the 10 largest cities in China:



At least 7 of those cities have virology labs:



Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases

Genomic characterization and infectivity of a novel SARS-like coronavirus in Chinese bats

Dan Hu, Changqiang Zhu, Lele Ai, Ting He, Yi Wang, Fuqiang Ye, …show all

Bats Are Natural Reservoirs of SARS-Like Coronaviruses

The spike protein of SARS-CoV – a target for vaccine and therapeutic development

Viral Metagenomics Revealed Sendai Virus and Coronavirus Infection of Malayan Pangolins (*Manis javanica*)

Ping Liu, Wu Chen, and Jin-Ping Chen

Detection and characterization of three zoonotic viruses in wild rodents and shrews from Shenzhen city, China

Bo Wang, Chun-Lin Cai, Bei Li, Wei Zhang, Yan Zhu, Wei-Hong Chen, Pei Zhou, Zheng-Li Shi, Xing-Lou Yang

Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats

Graphic From Michael Worobey

If this happened in Beijing, you could blame Qi Jin at the Institute for Pathogen Biology.
Qi Jin's group sampled hundreds of bats throughout China, including from the "Mojiang Mine".

Some labs in Beijing worked with EcoHealth Alliance.

One lab in Beijing inserted furin cleavage sites into coronaviruses.

If this happened in Guangzhou, you could blame Jin-Ping Chen who also worked with EcoHealth Alliance.
You might look at the 2019 work they'd done on pangolin coronaviruses.

In fact, DRASTIC has already created theories about a lab in Guangzhou that went to the "Mojiang Mine".
One member points to scientist Libiao Zhang, and calls him "the largest bat samples collector for WIV".
Another member says she wonders if Covid was made in a Guangdong lab.

If Covid began in Nanjing, you could talk about the recent publication of the first SARS2-like virus there (ZC45)
by a Chinese military hospital. In 2020, lab leak theorist Li Meng Yan claimed that ZC45 was
used to create SARS-CoV-2. She could still make the same theory if the virus started in Nanjing.

There are more than 100 BSL-3 labs in China.

You could make some lab leak theory for almost any city in China

This is also not the first lab leak theory in history

The HIV pandemic had several lab origin theories.

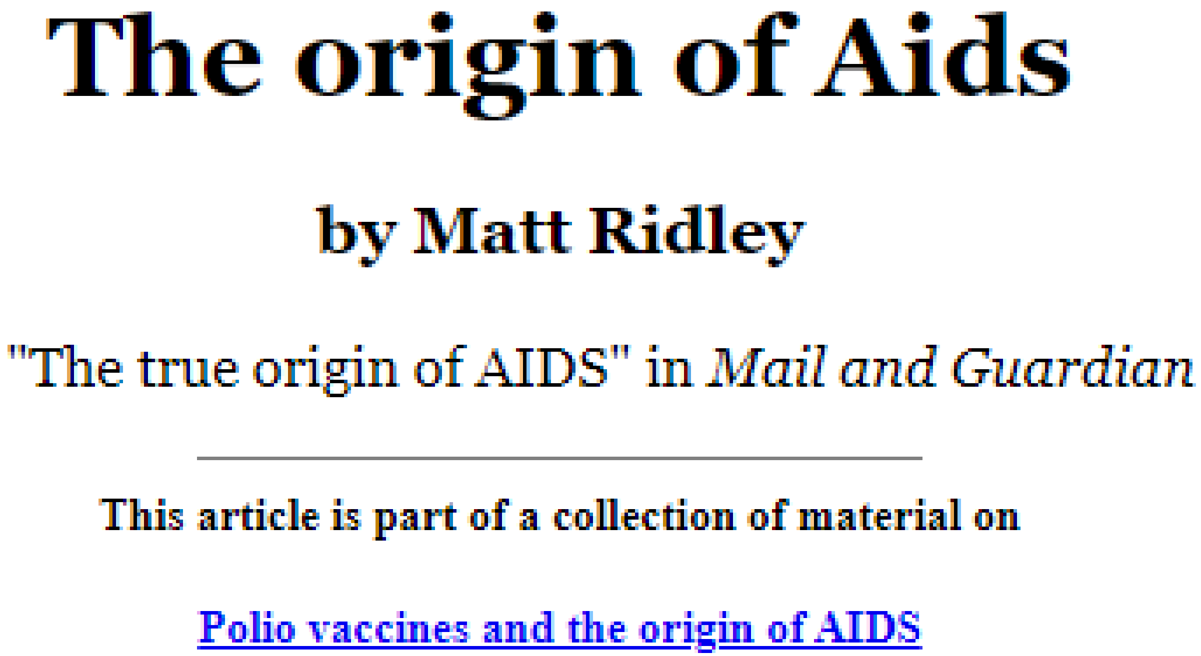
One theory said HIV was created at Fort Detrick, by splicing together two other viruses, Visna and HTLV-1.

Another theory blamed the smallpox vaccination campaign.

A third said it was lab created by government scientists and introduced through the Hepatitis B vaccine.

Perhaps the most popular theory blamed the oral polio vaccine, which was grown in cultures of chimpanzee kidney cells.

Some people that promoted HIV lab theories are writing today’s Covid lab leak theories:



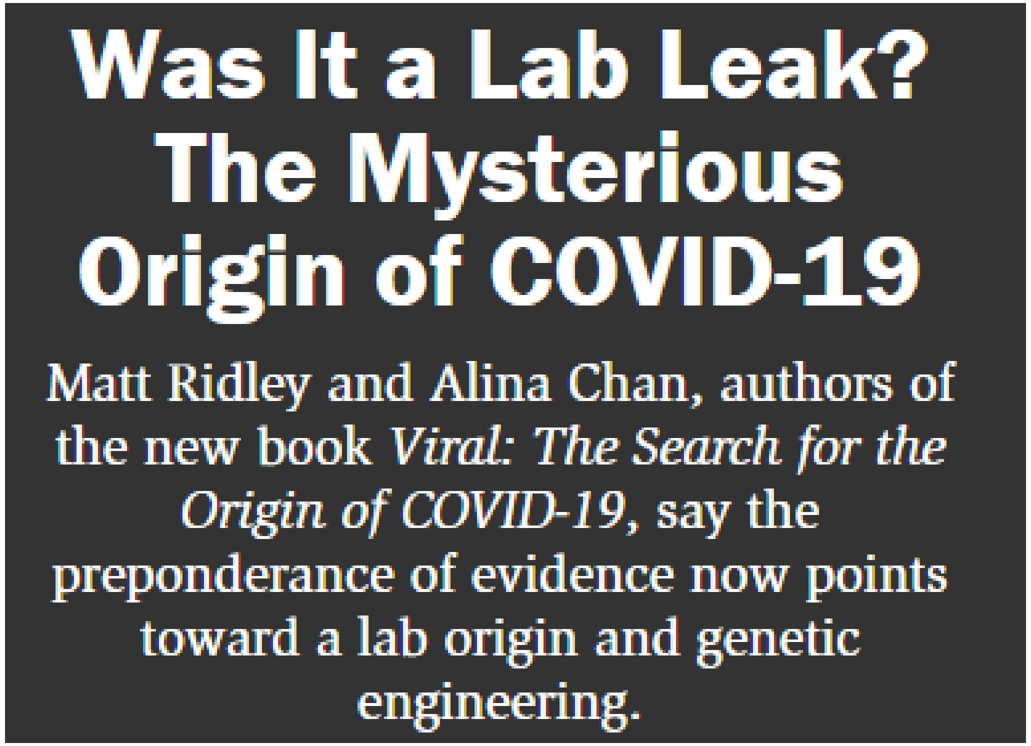
The origin of Aids

by Matt Ridley

"The true origin of AIDS" in *Mail and Guardian*

This article is part of a collection of material on

Polio vaccines and the origin of AIDS



Was It a Lab Leak? The Mysterious Origin of COVID-19

Matt Ridley and Alina Chan, authors of the new book *Viral: The Search for the Origin of COVID-19*, say the preponderance of evidence now points toward a lab origin and genetic engineering.

There were also lab leak theories for Ebola, for Monkeypox, and for Omicron.

Even Lyme disease had a lab leak theory – people said it was from the Plum Island Animal Disease Center, which did tick experiments done there from the 1950s to 1970s.

It was later proven that Lyme disease existed before the lab did.

The 1918 Spanish flu was too early for lab leak theories.

But there was still a theory that pandemic was linked to the use of aspirin produced by the German company Bayer.

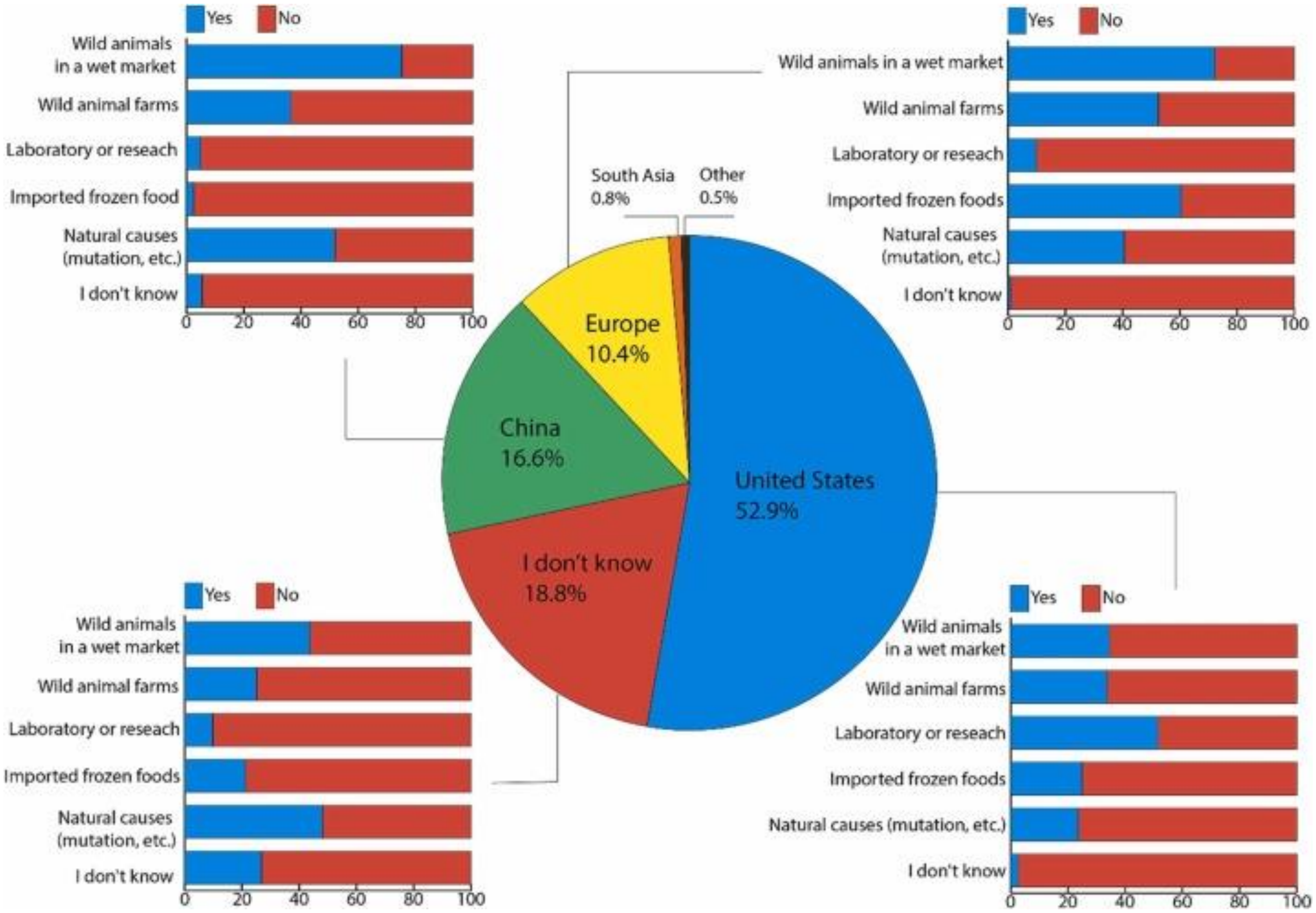
There was also a fringe theory that the Spanish flu was spread around the world by German submarines.

The 1918 virus was most widely known as “Spanish flu”, but it had a lot of names.

In Spain, it was “the French flu”. In Brazil, it was the “German flu”. In Poland it was the “Bolshevik disease”. In Senegal it was “the Brazilian flu.” Every country nicknamed the virus after a political opponent.

In America today, Covid is the China virus.
In China, it’s the American virus.

A [survey of 1,000 people in China](#) asked where they thought that Covid comes from. The majority said it comes from the United States:



US bioweapon theory:

This is a popular theory in China and also in some fringe US media.

China and Iran were the first countries that got hit.

If we are free to blame the Chinese lab without much evidence, it’s also possible to blame US labs without much evidence.

You can find headlines about US labs that sound just as suspicious as Chinese labs. Here’s a [2019 New York Times article]:

Deadly Germ Research Is Shut Down at Army Lab Over Safety Concerns

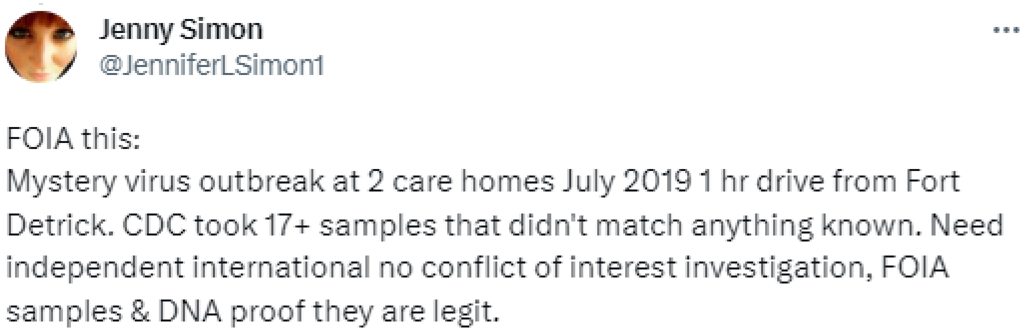
Problems with disposal of dangerous materials led the government to suspend research at the military’s leading biodefense center.

Denise Braun prepared to demonstrate lab work during a media tour at the Army Medical Research Institute of Infectious Diseases in Fort Detrick, Md., in 2011. Patrick Semansky/Associated Press

By Denise Grady

Aug. 5, 2019

You can also find mysterious disease outbreaks near that lab:



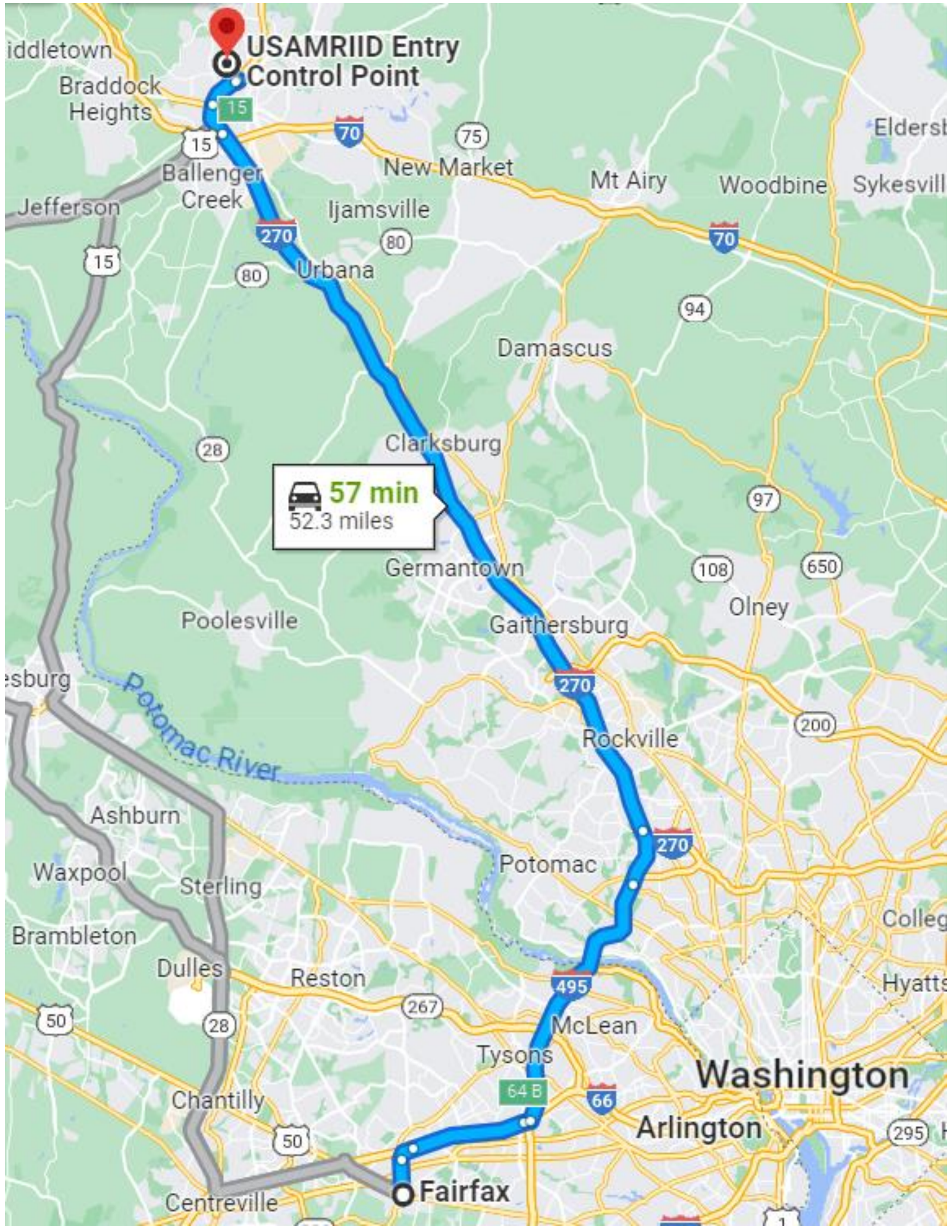
Jenny Simon
@JenniferLSimon1

FOIA this:
Mystery virus outbreak at 2 care homes July 2019 1 hr drive from Fort Detrick. CDC took 17+ samples that didn't match anything known. Need independent international no conflict of interest investigation, FOIA samples & DNA proof they are legit.

Third person has died after respiratory illness outbreak at Greenspring Village, Fairfax officials say

CDC has tested 17 samples but has so far failed to identify the cause.

By Fredrick Kunkle
July 17, 2019 at 5:43 p.m. EDT



Lab leak theories are popular

Some people like conspiracy theories.

Some people are xenophobic.

Most people just want explanations for tragic events – it’s more appealing to blame a person.

Covid turned out to be the worst pandemic in 100 years.

The odds are 100% that there would be conspiracy theories of where it came from.

None of those lab theories panned out for previous viruses.

That should give us a good guess that Covid is not a lab leak.

But it’s not proof.

Scientists have better technology today, maybe this could be the first time they started a novel pandemic.

We still have to evaluate the evidence.

Which lab leak theory?

Before I get into the evidence, I want to point out that there isn’t one lab leak theory, there are dozens.

The different theories disagree on how the virus was created.

The theories disagree with each other on basic details like the month that the virus leaked or even which lab it leaked from.

As we go through the evidence, we should be able to see which lab leak theories can be discarded.

I want to lay out a few of the major ones.

Robert Redfield thinks there was a lab leak in September:

But then you also have headlines saying that a lab leak happened in November

This can’t just be time lag – people claim the database went offline on September 12th.

It’s not going to take 2 months for the first people to end up in the hospital.

THE WALL STREET JOURNAL.

◆ WSJ NEWS EXCLUSIVE | WORLD

Intelligence on Sick Staff at Wuhan Lab Fuels Debate on Covid-19 Origin

Report says researchers went to hospital in November 2019, shortly before confirmed outbreak; adds to calls for probe of whether virus escaped lab

A World Health Organization-led team investigating the origins of the Covid-19 pandemic visited the Wuhan Institute of Virology on Feb. 3.

PHOTO: HECTOR RETAMAL/AGENCE FRANCE-PRESSE/GETTY IMAGES

By Michael R. Gordon, Warren P. Strobel and Drew Hinshaw

May 23, 2021 2:57 pm ET

The US government does not have a single theory.

The House GOP report claims that covid leaked from the Wuhan Institute of Virology in September 2019, then spread around the world in October through the Wuhan military games.

The senate GOP report says that covid started between October and November.

The Department of Energy thinks covid might be a lab leak, but they point to the Wuhan CDC, a different lab.

Biden's intelligence report couldn't decide on the origins, most intelligence agencies voted covid was natural.

None of these reports seem to know anything about those "3 sick WIV researchers".
That WSJ article cites "anonymous government sources".

Outside the government, it’s no clearer

Some people blame another lab, the Wuhan Institute of Biological Products.

One theory points to an October leak because of “cell phone records” or “roadblocks outside the lab”.

Vanity Fair and Propublica, theorized a lab accident around November 12th, 2019, based on a “secret language of Chinese officials”

Many Chinese speakers disagreed.

This could line up with the “3 sick WIV workers”, but it contradicts the September theories.

Propublica later walked back those claims, based on US intelligence reports that disagreed.

COVID-19 Origins: Investigating a “Complex and Grave Situation” Inside a Wuhan Lab

The Wuhan Institute of Virology, the cutting-edge biotech facility at the center of swirling suspicions about the pandemic’s onset, was far more troubled than previously known, explosive documents unearthed by a Senate research team reveal. Following the trail of evidence, *Vanity Fair* and ProPublica provide the clearest picture yet of a laboratory institute in crisis.

BY KATHERINE EBAN AND JEFF KAO

OCTOBER 28, 2022

Researcher Toy Reid sits before a timeline chronicling the lead-up to the pandemic at the Hart Senate Office Building in Washington, DC. PHOTOGRAPH BY MARK PETERSON/ REDUX

“A Secret Language of Chinese Officialdom”

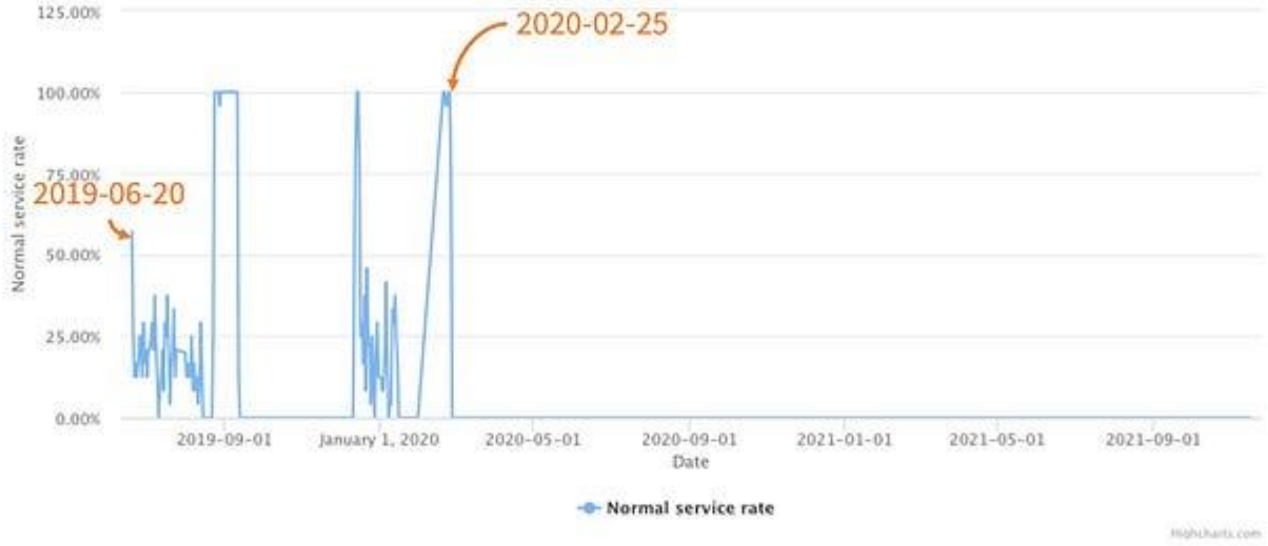
These theories can’t all be true.

September theories are the most unlikely.

The virus wasn’t noticed until December.

Covid is highly contagious, it would be all over the world by December if it started in September.

The database going down in September is probably not even true, website monitoring shows it was hard to access before September and accessible again through February 2020.



http://msis.csdb.cn, for 野生动物携带病毒病原特色数据库, accessed 2021-11-17

Database [monitoring graph from Flo Debarre]

Lab leak theories also disagree on how the virus was made.

Some say covid is a bat virus with a furin cleavage site added.
or it's a chimera combining bat and pangolin viruses.
or it was created synthetically by stitching together multiple segments of RNA.
or it was created by serial passaging in ferrets.
or by serial passaging in transgenic mice.
or by serial passaging in cells.
or it has HIV genes inserted.
or it was developed as a self-spreading vaccine against other coronaviruses.
or that Moderna patented the virus 3 years before the pandemic.
There's also a theory that it was a natural virus harvested in a mineshaft back in 2012, in which case it doesn't need gain of function research, because it was already 50% fatal.
There's also that theory that Covid was made in a US lab and released in China. That theory is popular in China. It's also promoted by Ron Unz in the US.

Again, it's not possible for all these theories to be correct.

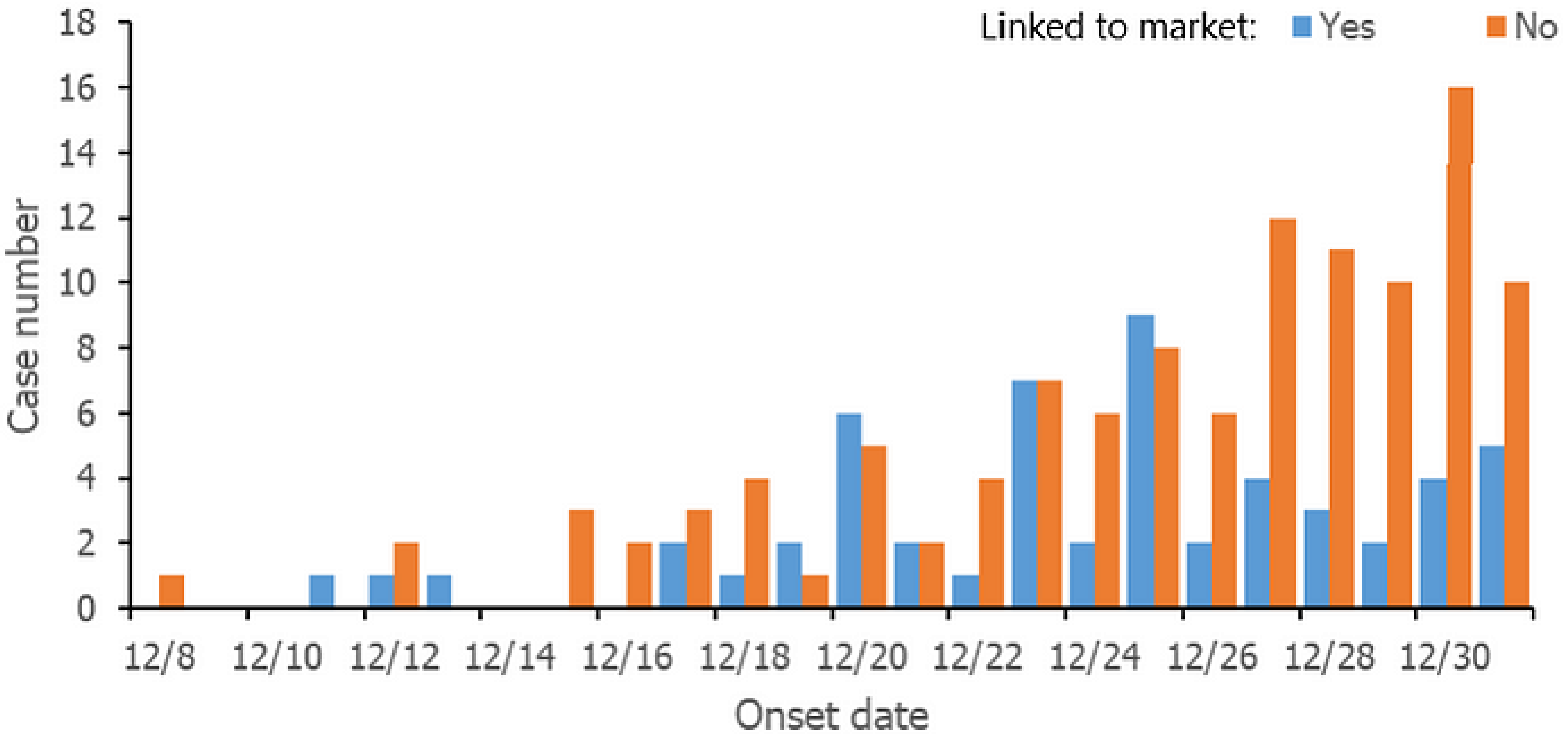
Even if a lab leak happened, we still need to figure out which theory is true.

We have scientific reasons to prove why many of these theories are false.

Data on when covid started.

When covid started:

There were 174 confirmed covid cases in Wuhan, in December 2019:



Graph from the WHO report

The earliest listed case was December 8th.

This man (Accountant Chen) was not connected to the Huanan market, and he lived across town, closer to the lab than to the market.

Back in 2020, I thought the market origin was suspect, for this reason – if the earliest case was not at the market, how do we know it started there?

Two DRASTIC researchers later concluded that Chen had actually gotten sick on December 16th, this was just a recording error.

Michael Worobey came to the same conclusion, he went over the case and found this man didn't actually have covid at first, he had a dental emergency. 8 days later, he got covid.

The actual first known case was a shrimp vendor at the market named Wei Guixian, on December 10th.

3 of the first 5 cases were vendors at the market.

Two of the first 5 are not vendors.

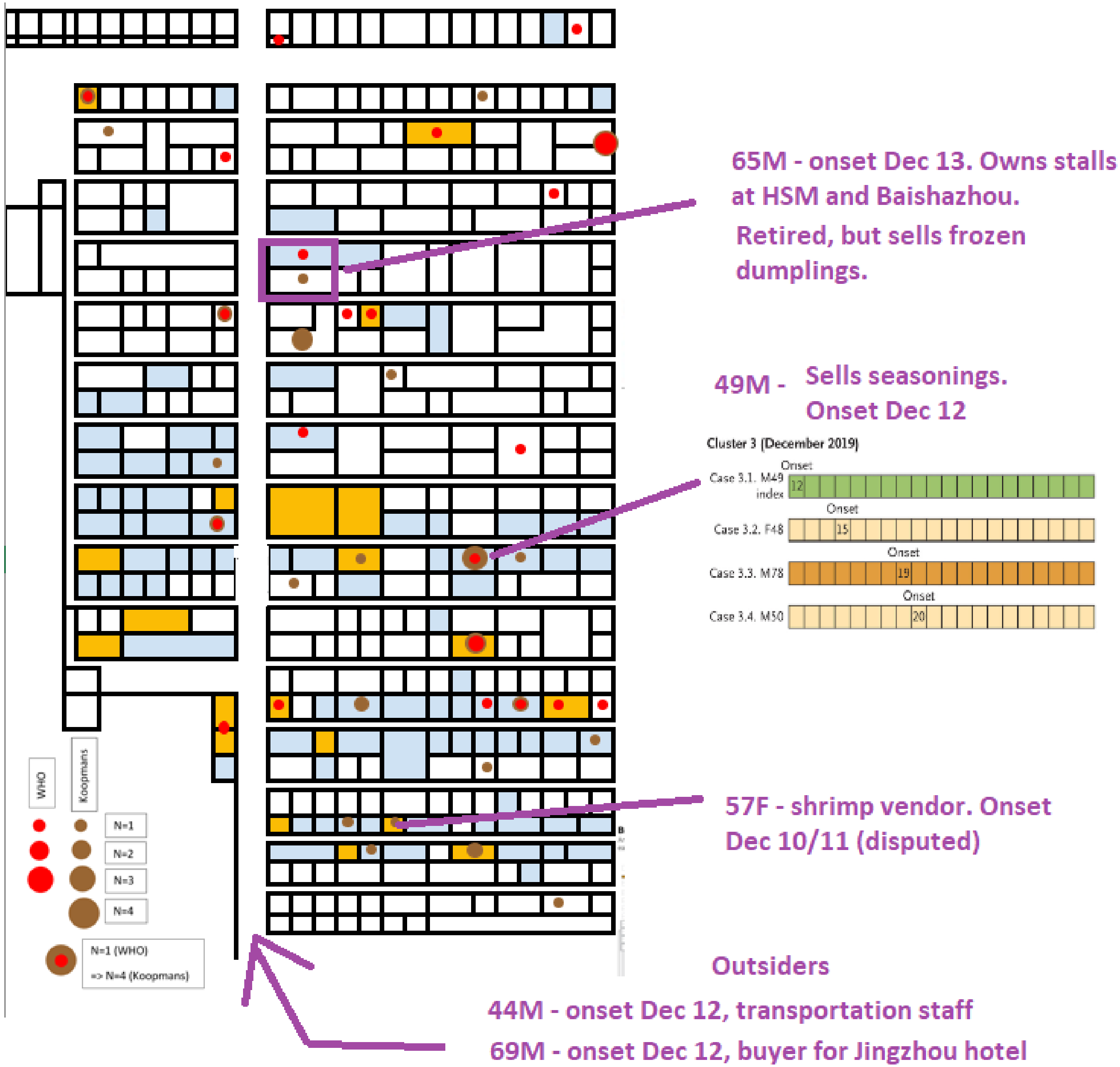
One of those two is “transportation staff” at the market, so he doesn’t have a stall but he’s still working there.

The other one is a buyer from a hotel, so he’s a repeat visitor, likely infected on a previous visit.

Those 2 are listed as December 12th onset.

Then there are vendor cases on the 12th and 13th.

Image source: [Early cases map] from DRASTIC member TheEngineer2.



65M - onset Dec 13. Owns stalls at HSM and Baishazhou.
Retired, but sells frozen dumplings.

49M - Sells seasonings.
Onset Dec 12

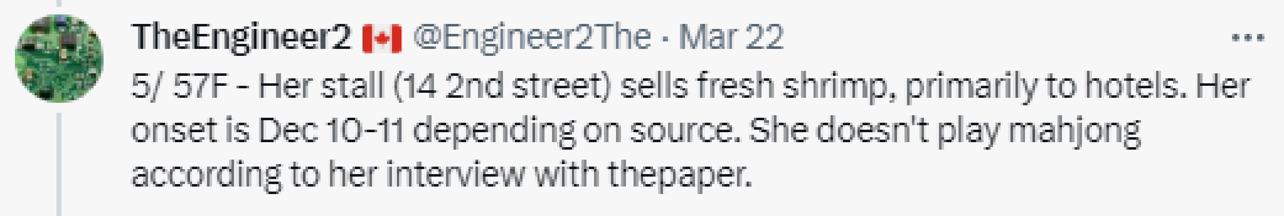
57F - shrimp vendor. Onset Dec 10/11 (disputed)

Outsiders

44M - onset Dec 12, transportation staff
69M - onset Dec 12, buyer for Jingzhou hotel

The two visitors might be connected to the first case

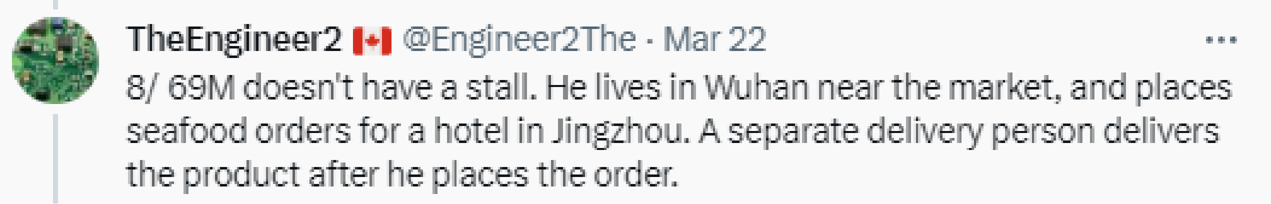
Wei Guixian sells shrimp to hotels:



TheEngineer2 🇨🇦 @Engineer2The · Mar 22

5/ 57F - Her stall (14 2nd street) sells fresh shrimp, primarily to hotels. Her onset is Dec 10-11 depending on source. She doesn't play mahjong according to her interview with thepaper.

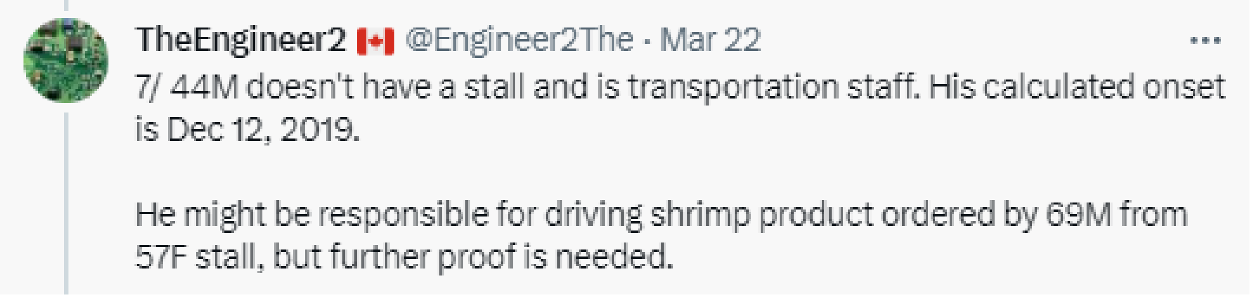
69M buys seafood for his hotel:



TheEngineer2 🇨🇦 @Engineer2The · Mar 22

8/ 69M doesn't have a stall. He lives in Wuhan near the market, and places seafood orders for a hotel in Jingzhou. A separate delivery person delivers the product after he places the order.

and 44M may deliver them:



TheEngineer2 🇨🇦 @Engineer2The · Mar 22

7/ 44M doesn't have a stall and is transportation staff. His calculated onset is Dec 12, 2019.

He might be responsible for driving shrimp product ordered by 69M from 57F stall, but further proof is needed.

This paper describes the case.

The WSJ article on Wei says she got sick December 10th.

Some people say this Chinese video calls her onset December 11th, but I think it sounds more like the 10th.

I had someone translate the video and also found 2 other translations.

The timeline is: she started feeling sick on December 10th then had a fever on December 11th and sought help.

That makes sense, it matches my own experience with covid:
One day I knew I was sick. The next day, the bad fever started.

Wei Guixian lives very close to the market.

That's as opposed to the December 16th case across town (accountant Chen), who commutes to work and thinks he may have been infected on the subway.

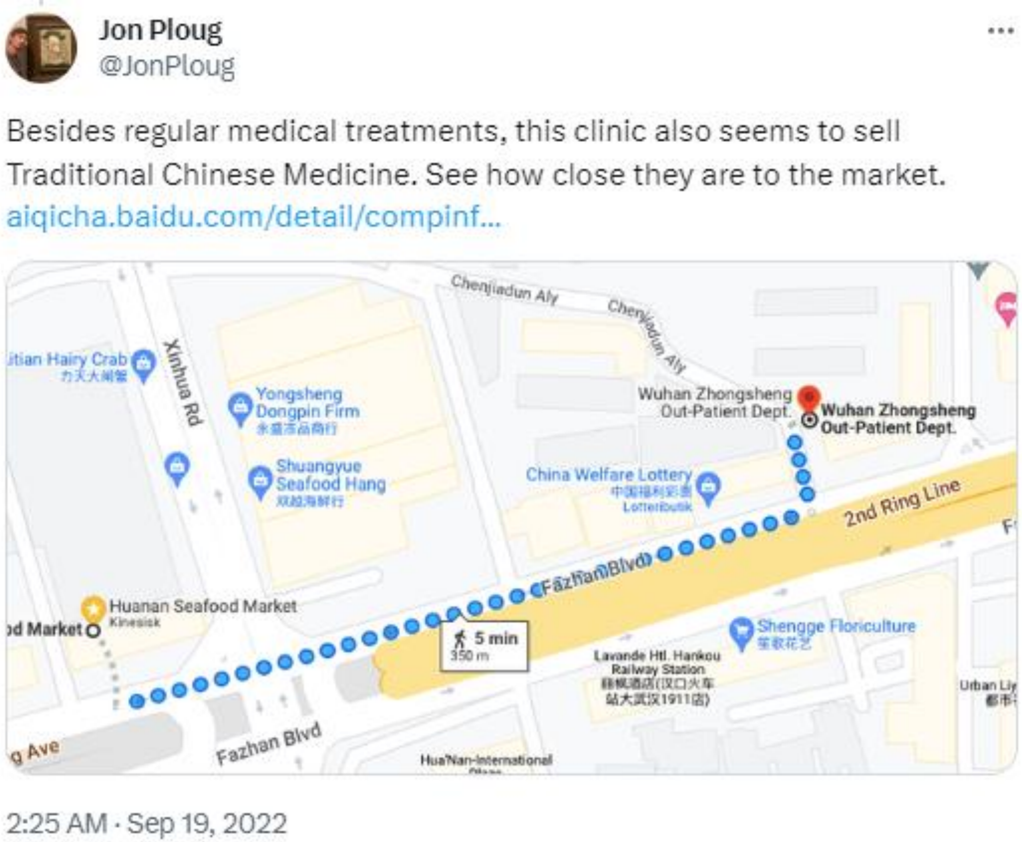
Wei doesn't do much outside work. She doesn't play mahjong.

How did Wei get sick?

> "Looking back, Ms. Wei thinks she might have been infected via the toilet she shared with the wild meat sellers and others on the market's west side."

Wei Guixian was first treated at a clinic very near the market.

It seems clear she brought Covid to the clinic, not the other way around.



Jon Ploug
@JonPloug

Besides regular medical treatments, this clinic also seems to sell Traditional Chinese Medicine. See how close they are to the market. aiqicha.baidu.com/detail/compinf...

2:25 AM · Sep 19, 2022

TheEngineer2 🇨🇦
@Engineer2The

😃Glad you brought it up. This clinic is the one that 57F shrimp vendor visited on Dec 11, 2019. She brought SARS2 into the clinic, not the other way around. By the end of December all workers (2 doctors and 2 nurses) were sick and they closed the doors.

2:03 PM · Sep 22, 2022

The second hospital she went to, on December 16th, was Xiehe hospital.

The WSJ article quotes some doctors talking about other early Huanan market patients:

> "Zhang Jinnong, the head of Xiehe Hospital's emergency department, said he doesn't recall treating Ms. Wei, but remembers the first Hua'nan patients coming in between Dec. 10 and 16."

> "When Ms. Wei came around three days later, she was barely able to move, but remembers one doctor surnamed Kong telling her, around Dec. 21, that two other workers from Hua'nan market were at Tongji Hospital, another major one in Wuhan."

The location of Tongji and Xiehe hospitals (yellow stars), relative to Huanan market

Did we only find these early market cases because of a biased search?

If Covid was all over Wuhan by early December, and you randomly picked a case, the odds would be very low that they'd work at Huanan market (~1,000 workers out of ~10 million people = 1 in 10,000 chance). The odds of 5 early market cases are impossibly low, if Covid was everywhere.

Several hospitals independently found early cases from the market, it was often 50% or more of their patients. This was all before the market connection was announced, on December 29th.

Those hospitals included:

Xiehe (union) hospital

Tongji hospital

Hubei Provincial Hospital of Integrated Chinese and Western Medicine

Wuhan Central hospital.

Zhongnan hospital, near the WIV.

The market connection was discovered by doctors in these hospitals, not by some market surveillance system.


Dr. Zhang Jixian

A 2021 paper by Michael Worobey analyzed the early case search, to look for ascertainment bias.

On December 27th, 2019, Doctor Zhang Jixian had 2 patients with pneumonia, a 63 year old man and woman. Both had suspicious lung scans.

She had experience with SARS cases, 20 years prior, and suspected a similar virus.

She ordered a lung scan for their son, who wasn't ill. He still showed the same lung abnormalities on the scan. That proved human to human transmission.

The family had no known link to the market. But, over the next 2 days, she had 4 more covid patients, and all were linked to the market.

She talked to colleagues at 2 other hospitals. Both had Huanan linked patients. At Wuhan central, 4 out of 7 were market linked.

By Dec. 29th, the link between Covid and the market was known.

Of cases identified before that date, > 50% had a link to the market.

It was later discovered that Zhang's first two patients lived only 2 kilometers from the market.

It’s the same story at other hospitals.

Take Zhongnan hospital, right next to the Wuhan lab.

On December 31st, the hospital VP ordered a search for pneumonia cases with an unknown etiology.

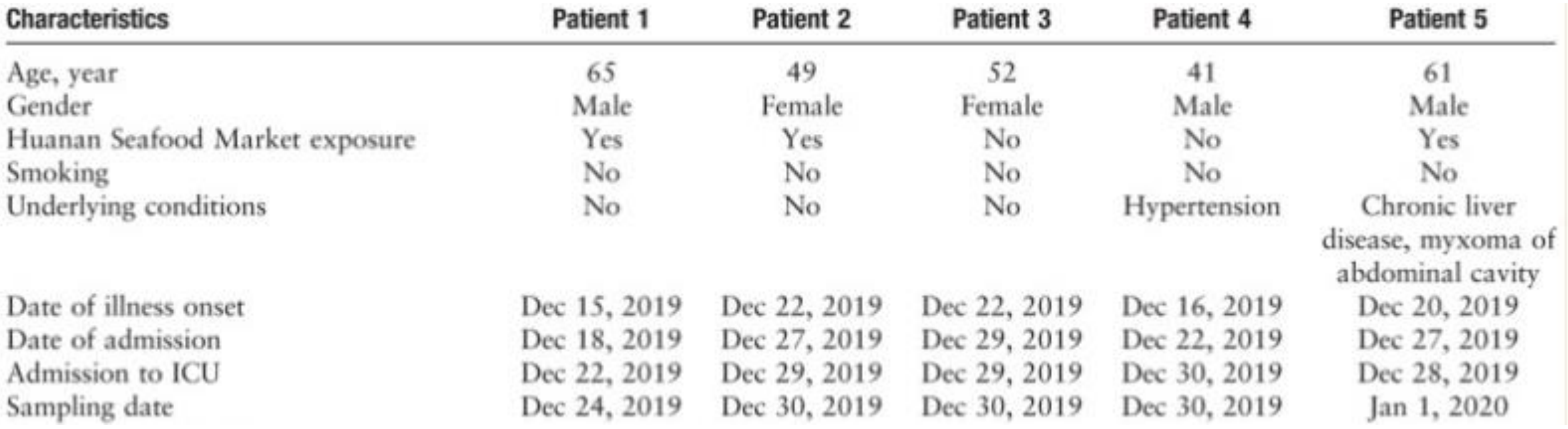
They found 2 cases.

One worked at the Huanan market.

The second had friends who worked at the market, who had visited his home.

The first lab that samples were sent to is called Vision medical.

Here are their earliest samples:



Characteristics	Patient 1	Patient 2	Patient 3	Patient 4	Patient 5
Age, year	65	49	52	41	61
Gender	Male	Female	Female	Male	Male
Huanan Seafood Market exposure	Yes	Yes	No	No	Yes
Smoking	No	No	No	No	No
Underlying conditions	No	No	No	Hypertension	Chronic liver disease, myxoma of abdominal cavity
Date of illness onset	Dec 15, 2019	Dec 22, 2019	Dec 22, 2019	Dec 16, 2019	Dec 20, 2019
Date of admission	Dec 18, 2019	Dec 27, 2019	Dec 29, 2019	Dec 22, 2019	Dec 27, 2019
Admission to ICU	Dec 22, 2019	Dec 29, 2019	Dec 29, 2019	Dec 30, 2019	Dec 28, 2019
Sampling date	Dec 24, 2019	Dec 30, 2019	Dec 30, 2019	Dec 30, 2019	Jan 1, 2020

3 of the first 5, including the earliest one, were market linked. All were hospitalized before December 29th.

Again, that makes perfect sense if covid started at the market.

All these places finding ~50% market linked patients is extremely unlikely if the virus was all over Wuhan.

We don’t have full ascertainment of market cases

Wei Guixian is just the first known case, she’s not patient zero

Contact tracing is easy for highly deadly diseases, it’s harder for milder diseases.

MERS is easy to trace, at 30% lethal. SARS is a little bit harder, at 10%.

Covid was maybe 0.6% lethal, with the earliest strain.

When you get covid, you don’t always know how you got it.

Some people are asymptomatic. Some have a mild case, some go to the hospital.

The hospitalization rate varies. It could be 5%. Could be higher.

If these 5 patients are the first 5 hospitalized, are there really 100 cases by then? Or maybe less because there was some retrospective scrutiny of the market, so the ratio is different.

Genetic models predict < 25 cases, as of December 10th (with 50% confidence) or < 100 cases (95% confidence).

Is patient zero actually a wildlife trader at the market?

It seems likely.

Maybe they have a milder case, because of prior exposure to these diseases.

In the first SARS pandemic, 70% of civet traders had SARS antibodies.

The wildlife traders might also be highly inclined to lie about illness, to avoid punishment.

Patient zero could also be an adjacent vendor.

China could have tested everyone at the market for antibodies, but they either never did or never published that study.

They could have interviewed all the wildlife traders about illness history, the exact animals they were selling, where the animals came from. They did not do that or publish that.

The index cases for SARS didn’t all have animal contact, either:

Table 6

Case series of index cases by municipality in SARS epidemic, Guangdong, China, November 2002–April 2003[a]

Case no.	City	Sex	Age	Occupation	Date of onset	Animal contact	Secondary transmission
Case 1	Foshan	M	45	Administrator and village leader	Nov 16, 2002	Yes	Yes
Case 2	Heyuan	M	34	Restaurant chef	Dec 10, 2002	Unknown	Yes
Case 3	Jiangmen	M	26	Factory worker	Dec 21, 2002	No	No
Case 4	Zhongshan	M	30	Restaurant chef	Dec 26, 2002	Yes	Yes
Case 5	Guangzhou	M	49	Office worker	Jan 2, 2003	No	Yes
Case 6	Shenzhen	M	46	Office worker	Jan 15, 2003	No	Yes
Case 7	Zhaoqing	F	39	Market vendor	Jan 17, 2003	Probably	Yes

Open in a separate window

[a] SARS, severe acute respiratory syndrome; M, male; F, female.

None of the first 7 index cases are animal traders.

1 is a market vendor, not a trader. (just like covid)
She worked at a market but did not sell animals.

2 are restaurant chefs.

4 aren’t market or restaurant linked at all.

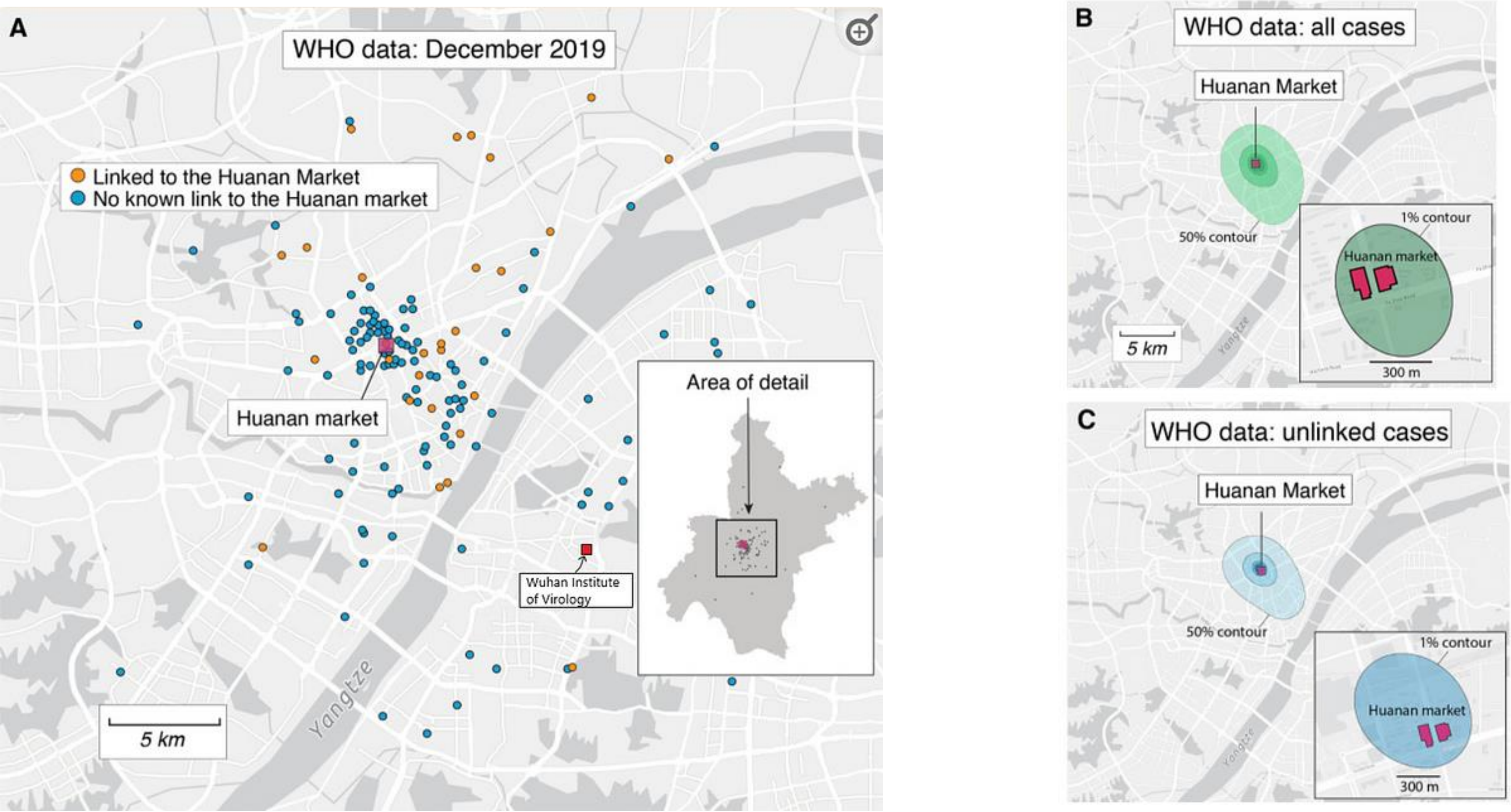
Only 1 of these 7 index cases had known contact with civets (that’s case #4).

Table from Xu et al, 2004

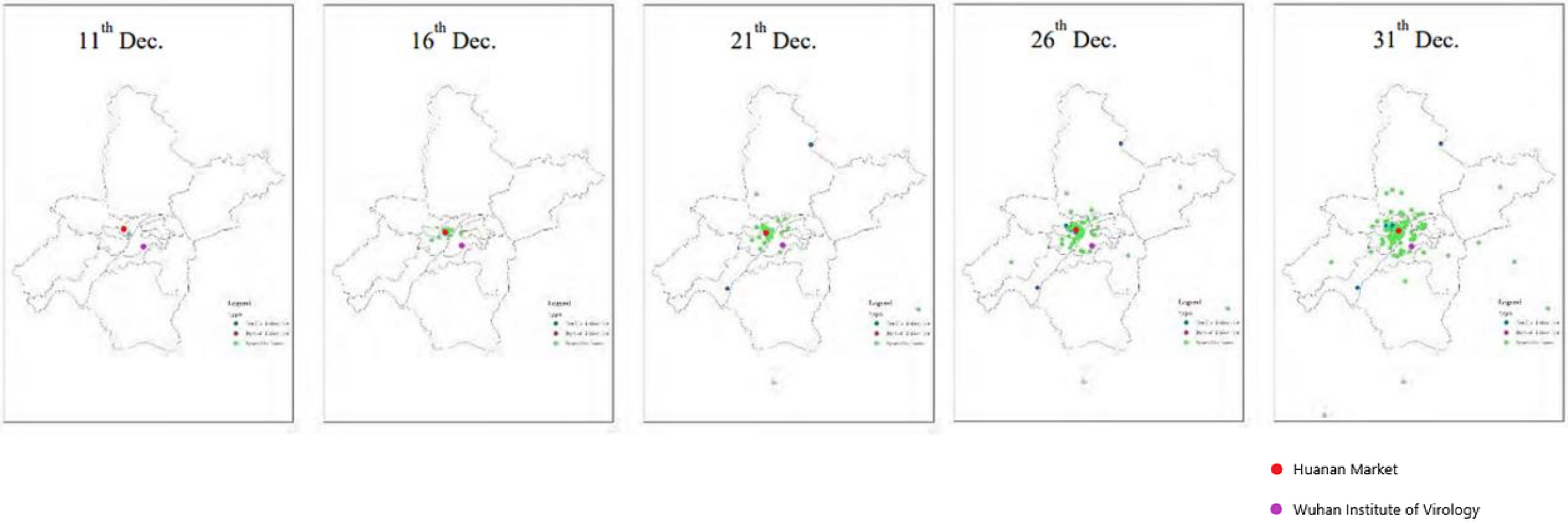
Data on where covid started

Where covid started:

A paper from June 2022, with Michael Worobey as the lead author, mapped the earliest covid cases in Wuhan. Many cases are linked to the market. Even the unlinked cases are centered on the market.

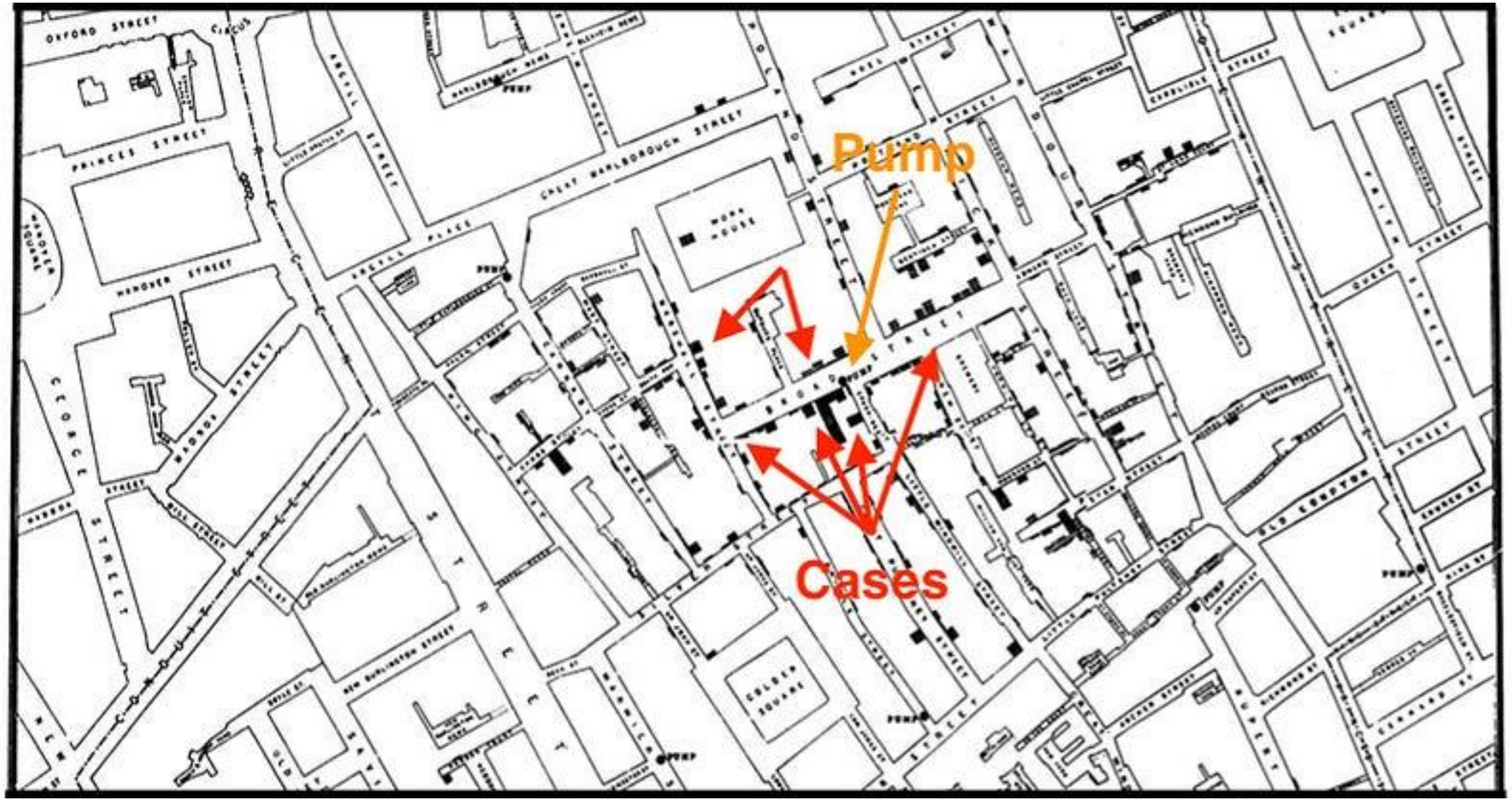


Cases spread out from the market over time:



This approach has been used before.

Here’s a map from 1854, from a Cholera outbreak in London. John Snow mapped the cases and found the infected water pump:



There were two early strains of covid

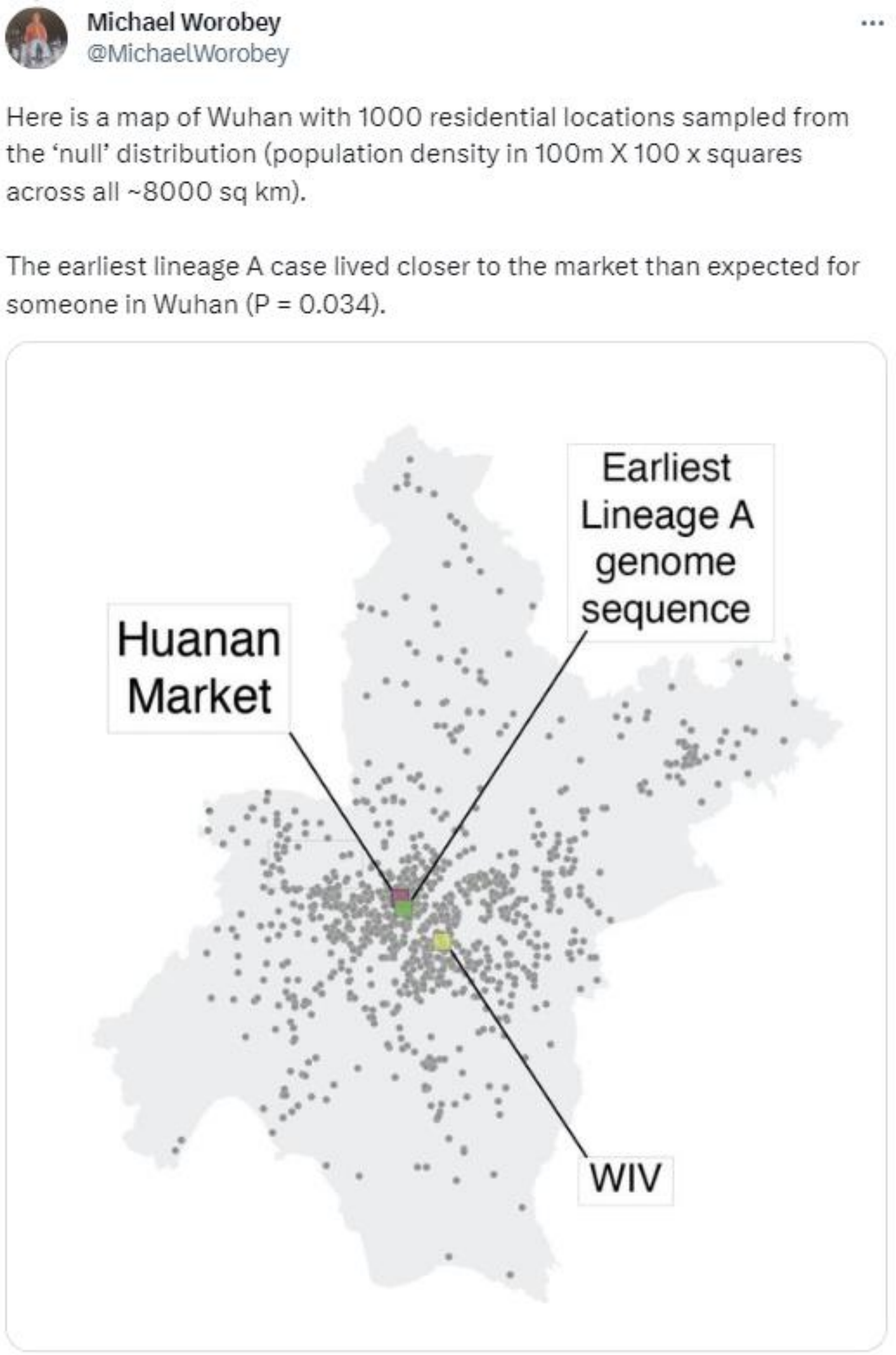
The earliest lineage B case is at the market, on December 10th. All the market cases which were sequenced were lineage B.

The earliest lineage A case came later, they lived 2 km from the market.

The other known December A case stayed at a hotel next to the market for 5 days before getting sick. The odds are very low that the 2 earliest A cases would be so close ($P = 0.001$), if lineage A was not associated with the market.

Both lineage A and B were found during sampling of the market.

All subsequent covid cases can be traced back to these strains.



Michael Worobey
@MichaelWorobey

Here is a map of Wuhan with 1000 residential locations sampled from the 'null' distribution (population density in 100m X 100 x squares across all ~8000 sq km).

The earliest lineage A case lived closer to the market than expected for someone in Wuhan ($P = 0.034$).

Possible reasons why the cases are centered on the market, and all early cases were seen at the market.

1. The market is the origin of the pandemic.

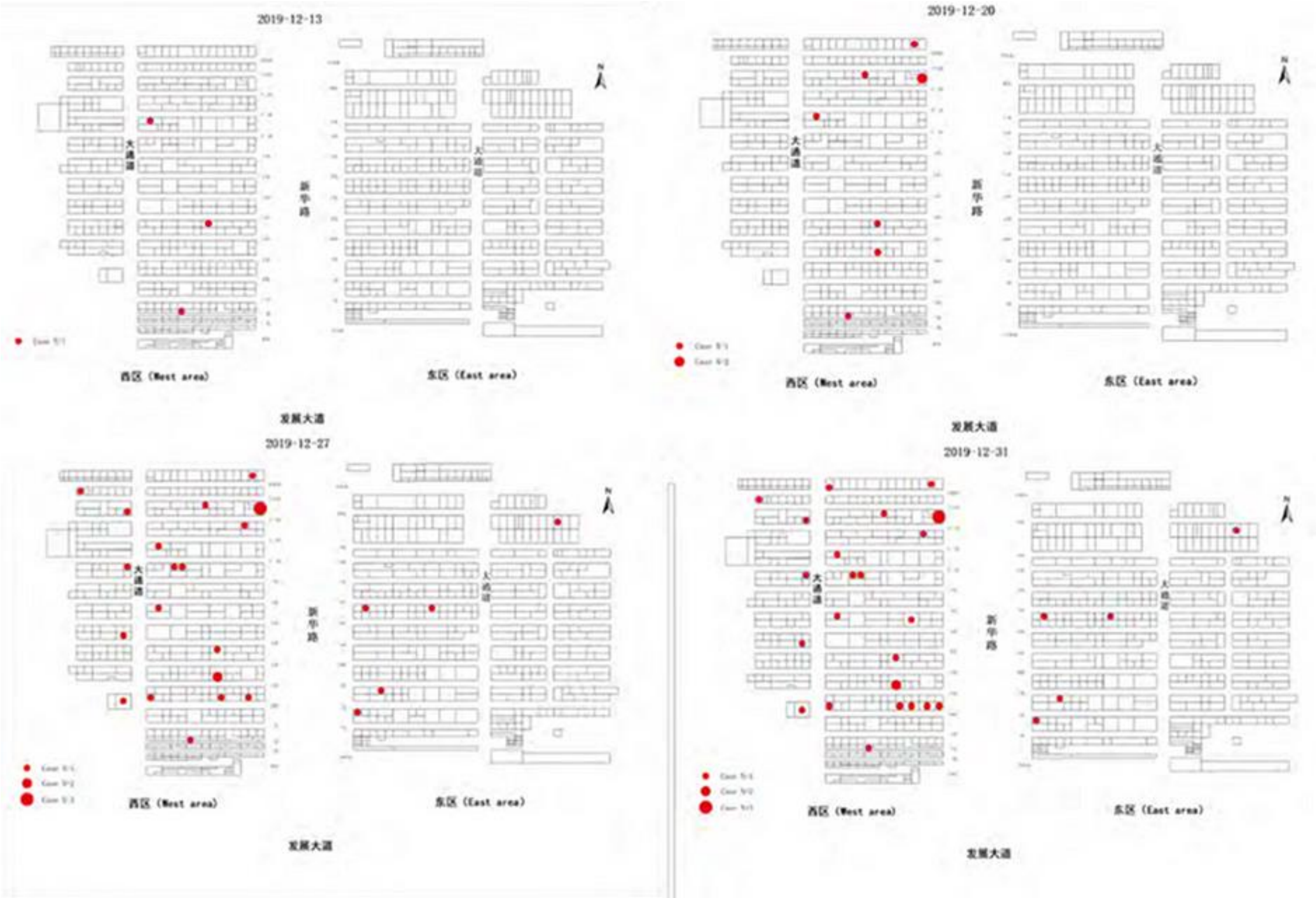
2. The market is not the origin, but it’s the first superspreading event.

3. The data is biased, because China was only looking for cases associated with the market.

4. China lied about the case locations.

5. Something else near the market is actually the origin.

Was the market just a superspreading event?

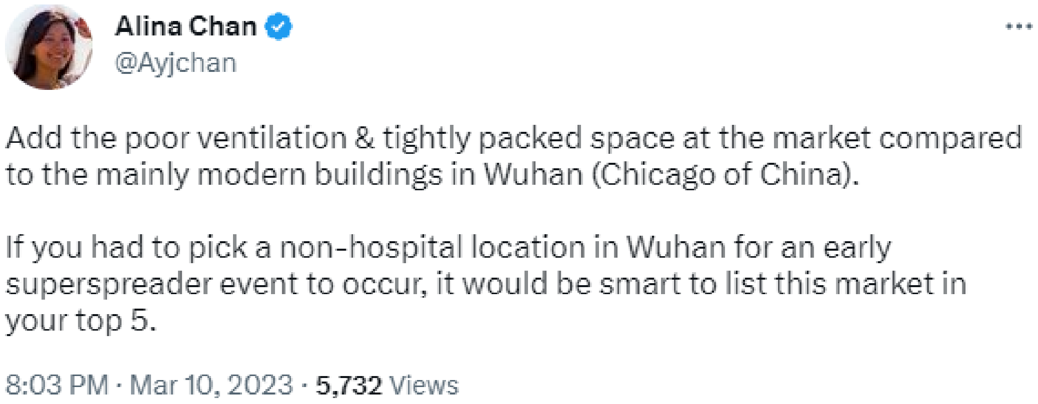


Case location map from the WHO report. I've added shop 2-14. These case maps show spread but are now a subset of all known cases. See Marion Koopman's case map, for most complete map.

Is the market a likely place for a random outbreak?

Lab leak theorists say yes.

Data says no.



Alina Chan
@Ayjchan

Add the poor ventilation & tightly packed space at the market compared to the mainly modern buildings in Wuhan (Chicago of China).

If you had to pick a non-hospital location in Wuhan for an early superspreader event to occur, it would be smart to list this market in your top 5.

8:03 PM · Mar 10, 2023 · 5,732 Views

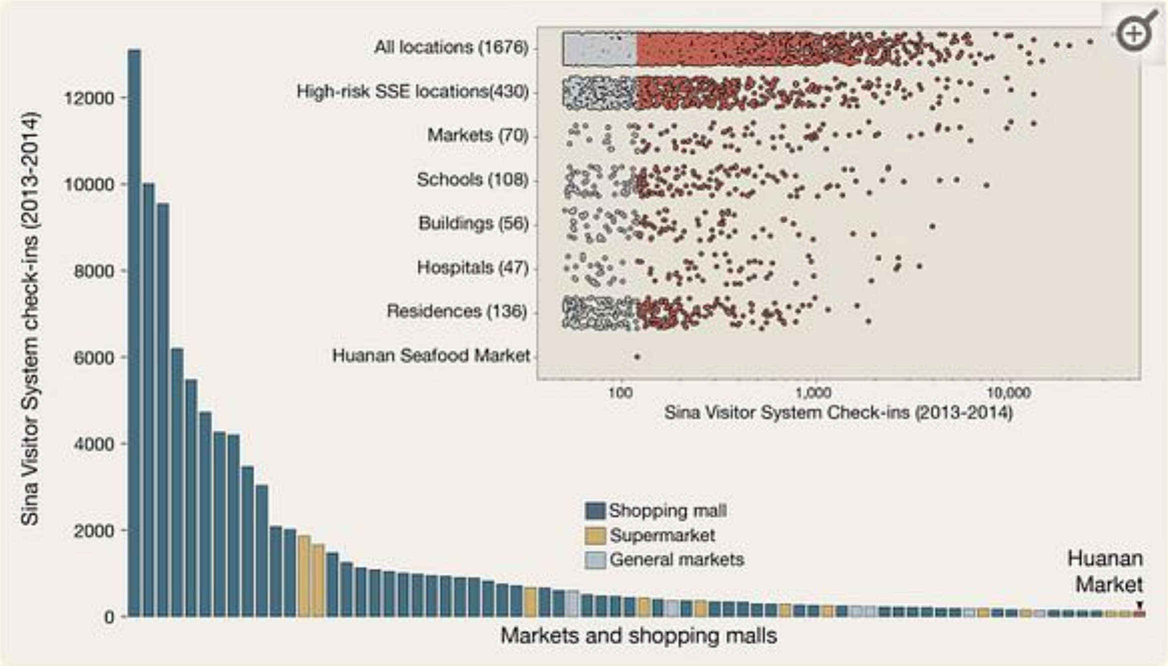


Fig. 3.

Visitors to locations throughout Wuhan.

Number of social media check-ins in the Sina Visitor System from 2013-2014 as shared by (33). Number of visitors to individual markets throughout the city are shown in comparison to the Huanan market. Inset: the total number of check-ins to all individual locations across the city of Wuhan, grouped by category. Locations with more than 50 visitor check-ins are shown, and the locations which received more check-ins than the Huanan market in the same period are shown in red.

There are 1,677 places in Wuhan that see higher traffic than the market.

Weighted by traffic, the odds that this would be the first cluster are 1 in 10,000.

But there are only 4 wet markets in Wuhan selling wild animals.

There are 20 shops at all those markets, selling wild animals. The Huanan market has 10 of them.

It’s the single most likely place in Wuhan for a natural virus to emerge.

Was the search for cases biased?

This is another common objection to the Worobey paper:

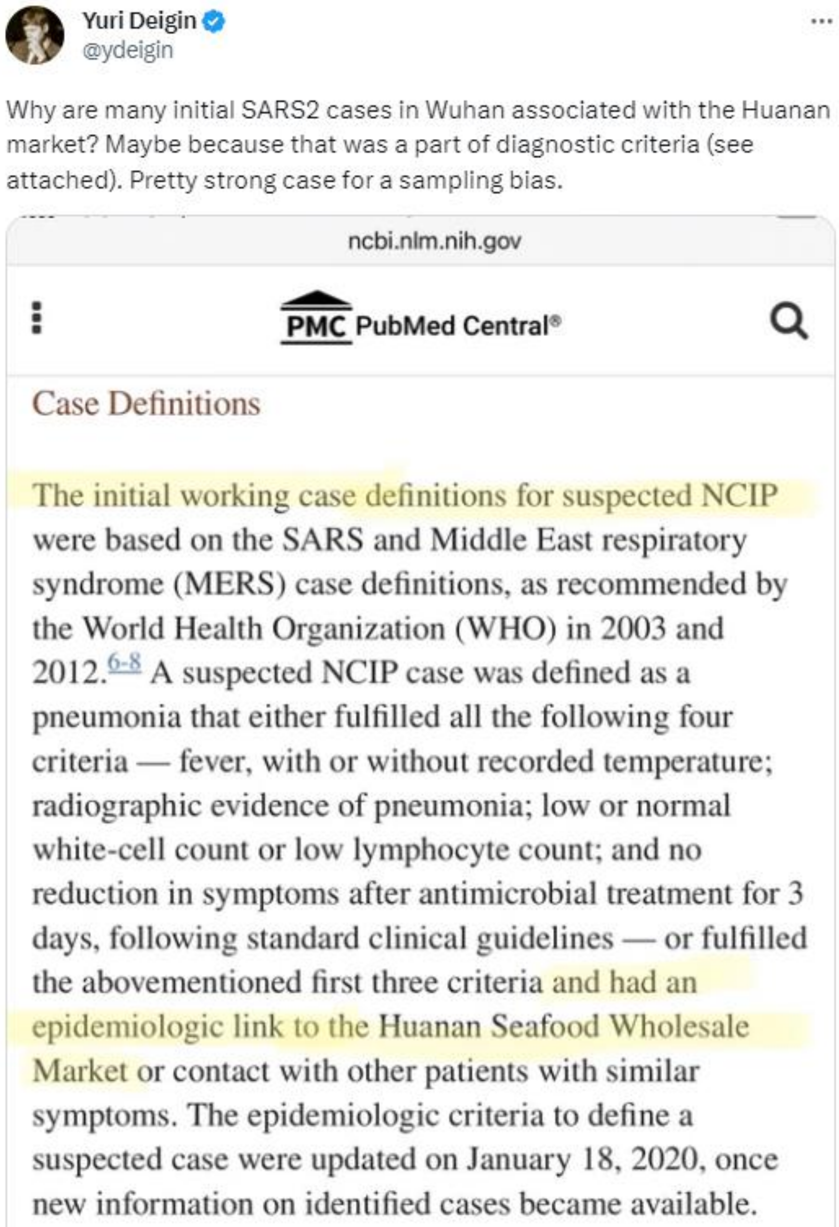
Alina Chan @Ayjchan

Case study of selection bias misleading scientists:

Wuhan investigators only searched for early cases linked to or living near the market because human-human transmission was not recognized.

Western scientists say early cases clustering around the market mean it's ground zero.

4:06 PM · Mar 1, 2023 · **52.7K** Views



Yuri Deigin @ydeigin

Why are many initial SARS2 cases in Wuhan associated with the Huanan market? Maybe because that was a part of diagnostic criteria (see attached). Pretty strong case for a sampling bias.

Case Definitions

The initial working case definitions for suspected NCIP were based on the SARS and Middle East respiratory syndrome (MERS) case definitions, as recommended by the World Health Organization (WHO) in 2003 and 2012.[6-8] A suspected NCIP case was defined as a pneumonia that either fulfilled all the following four criteria — fever, with or without recorded temperature; radiographic evidence of pneumonia; low or normal white-cell count or low lymphocyte count; and no reduction in symptoms after antimicrobial treatment for 3 days, following standard clinical guidelines — or fulfilled the abovementioned first three criteria and had an epidemiologic link to the Huanan Seafood Wholesale Market or contact with other patients with similar symptoms. The epidemiologic criteria to define a suspected case were updated on January 18, 2020, once new information on identified cases became available.

We've already seen that the case searches found mostly market linked cases at first, before the link was known.
After that, the searches found more unlinked cases.

Dec 31st (data from 3 hospitals) 16 December cases, 62% linked to market

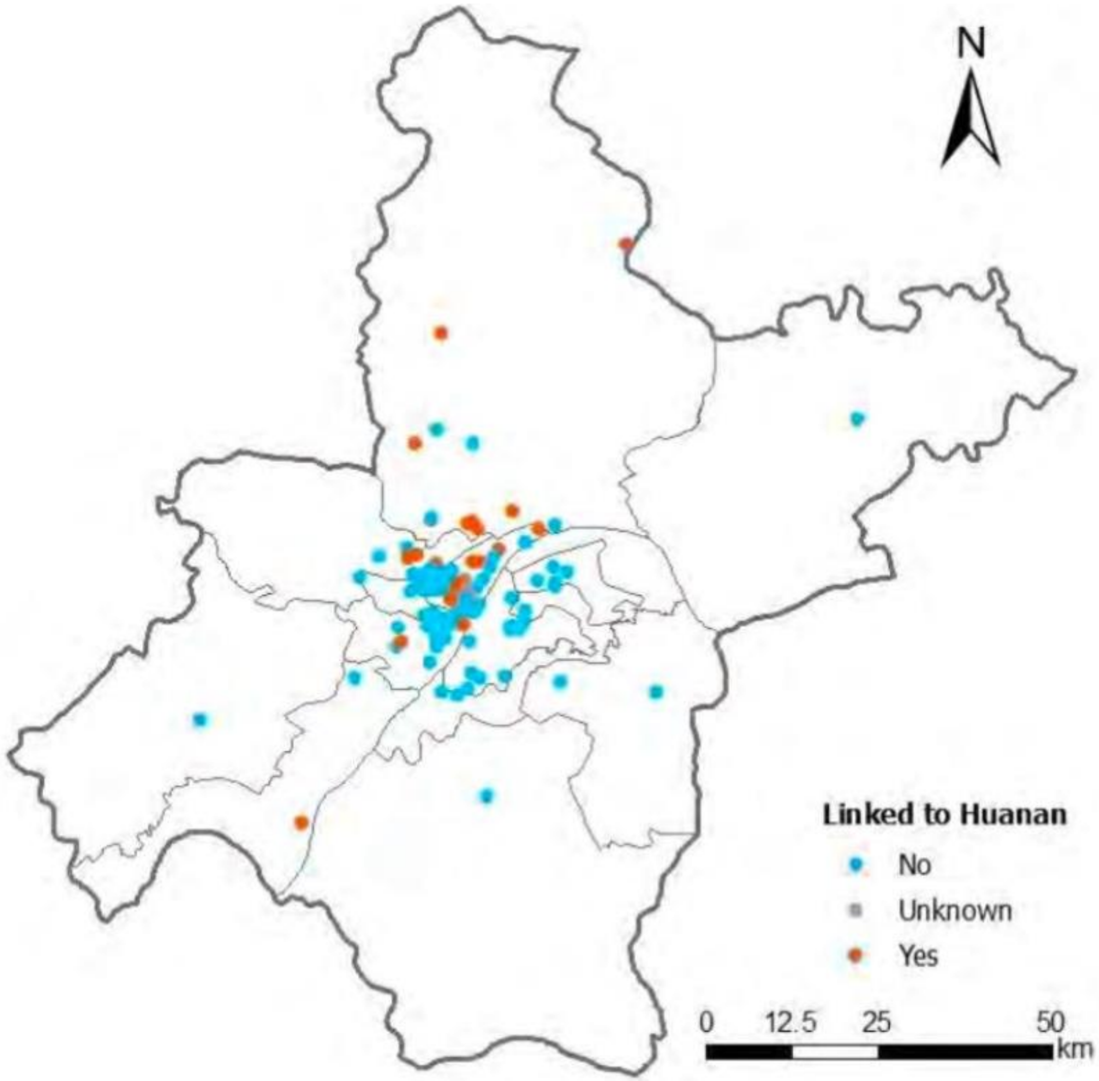
Jan 2nd data (Huang et al 2020) 40 December cases, 68% linked to market

Jan 22nd data (Li et al 2020) 47 December cases, 55% linked to market

WHO report: 174 December cases, 33% linked to market.

127 of these 174 were added after January 18th, in a retrospective search. That's after China had recognized human to human transmission and also dropped the link to the market in case searches.

The search mostly found people with no link to the market and found a few people who lived far away from it.
It’s unclear how a biased case search could find those.
The search was done in hospitals, not going door to door.



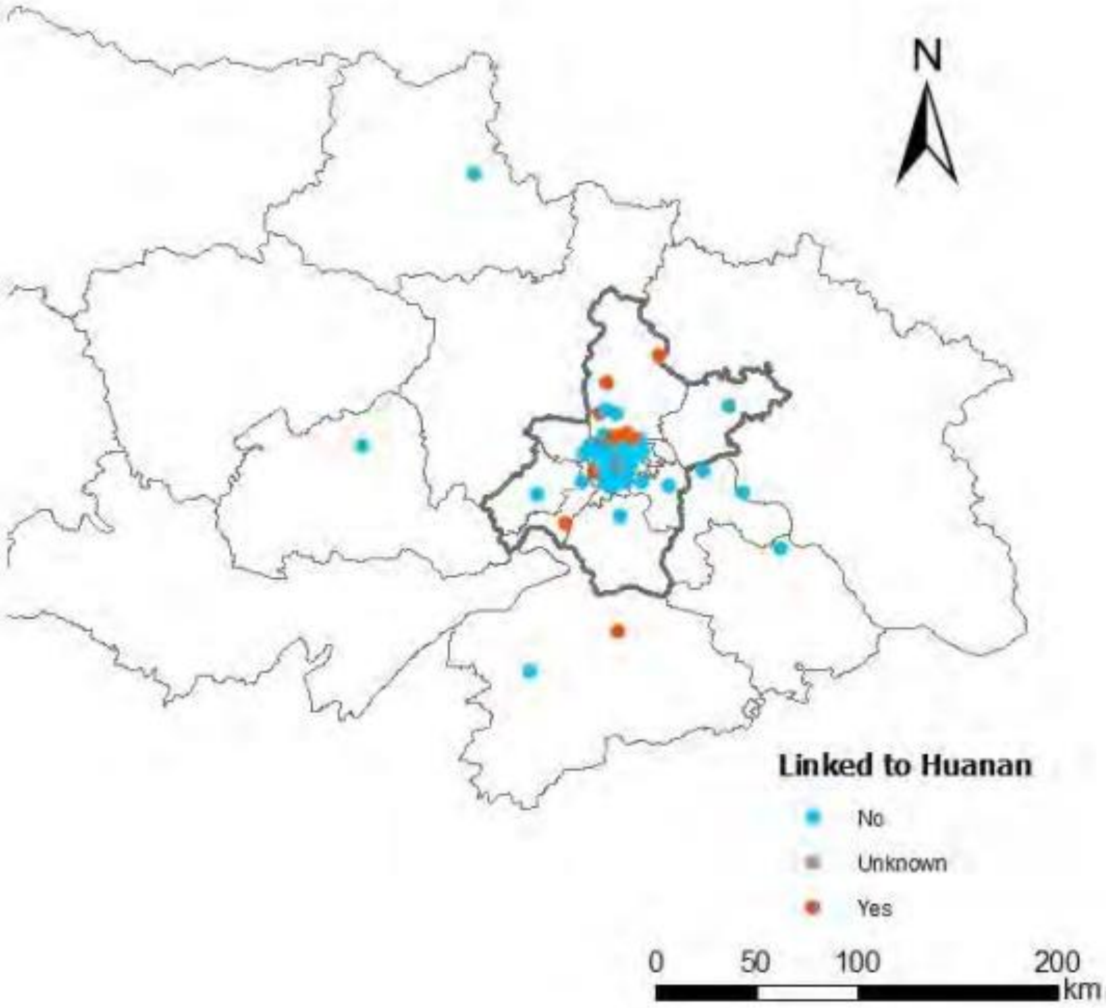
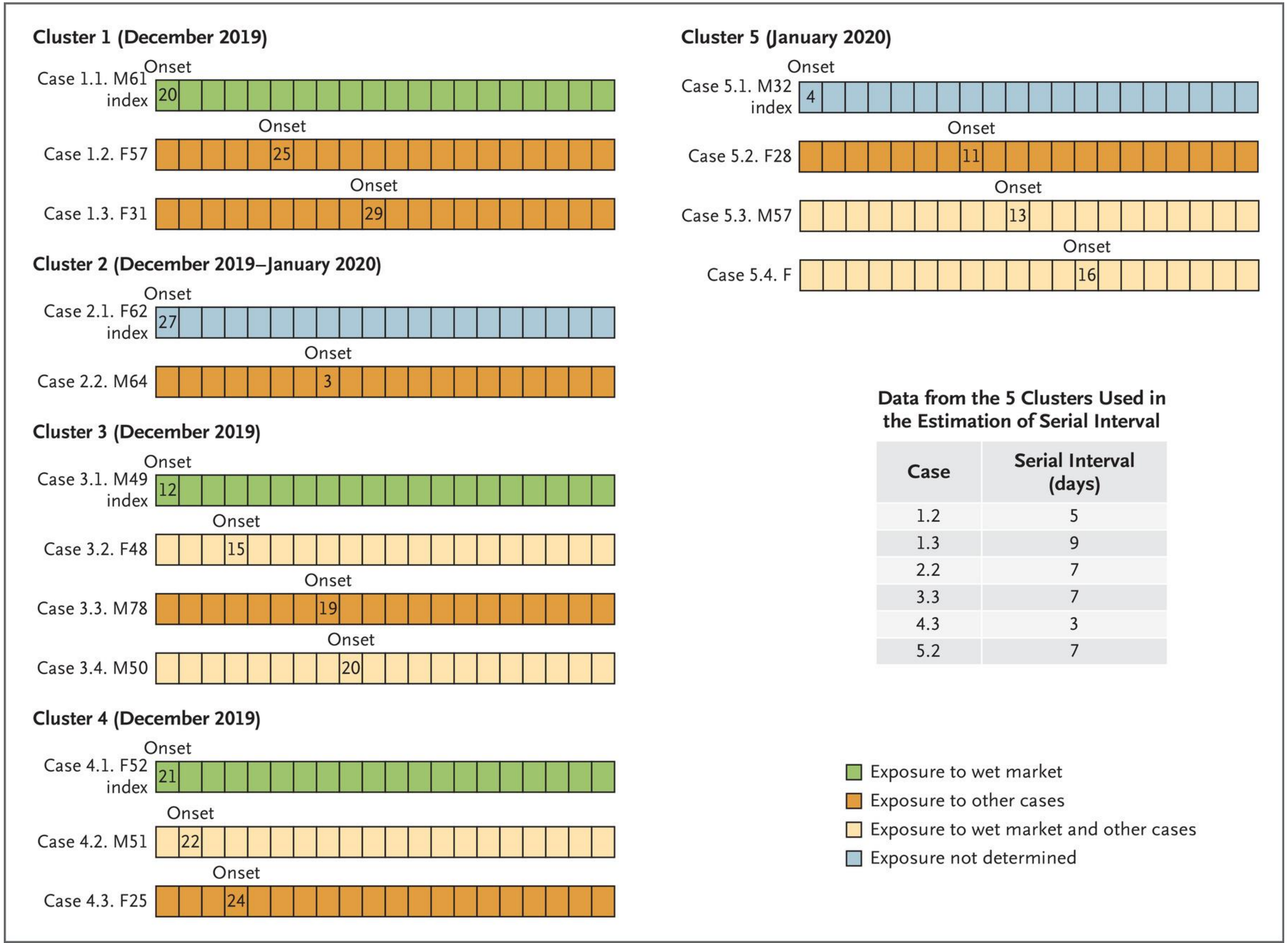


Fig. 3. Spatial distribution of the 174 cases by home address.

The first 3 patient clusters described were caused by a patient with wet market exposure infecting other people. Again, that makes sense for a market origin, it would be another unlikely coincidence otherwise.



Data from the 5 Clusters Used in the Estimation of Serial Interval

Case	Serial Interval (days)
1.2	5
1.3	9
2.2	7
3.3	7
4.3	3
5.2	7

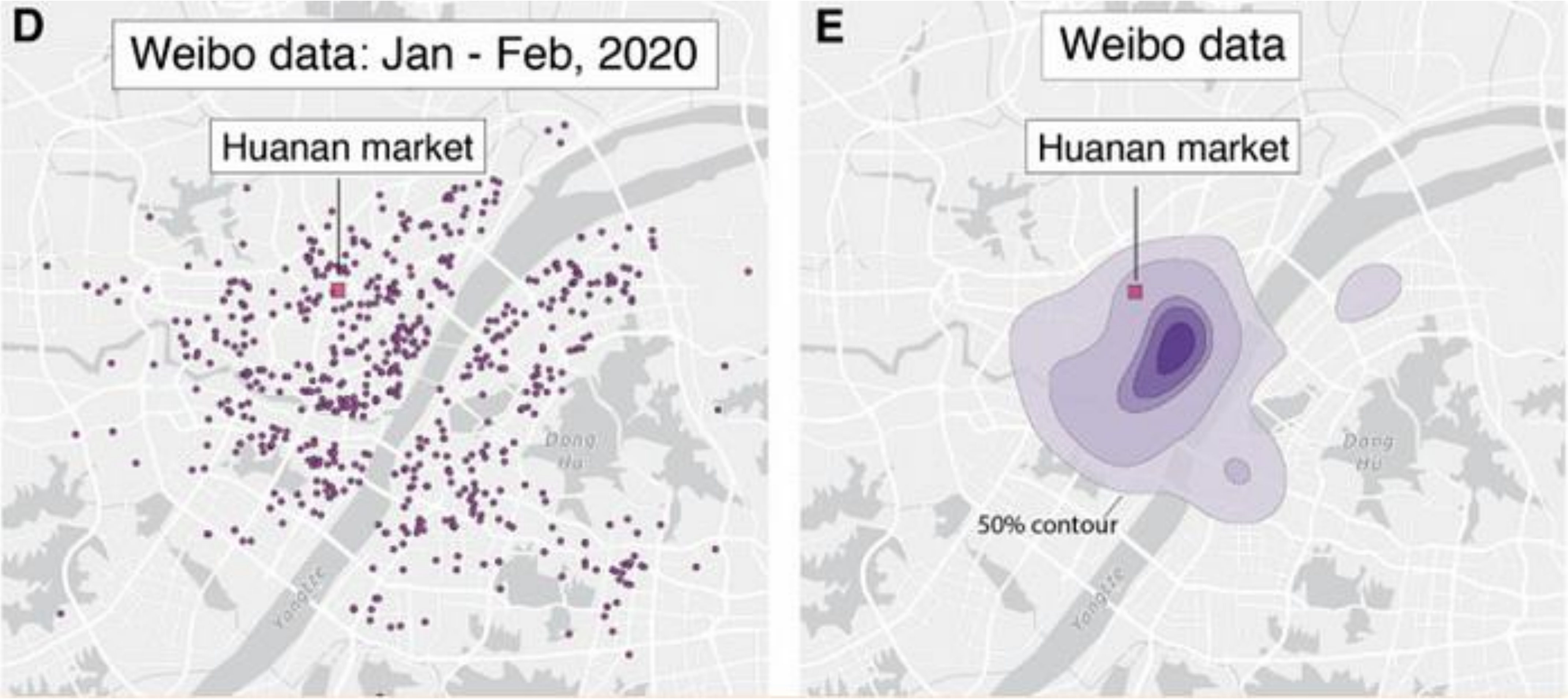
We have a few other data sources to check against

We have data from a Weibo app from January-February 2020.

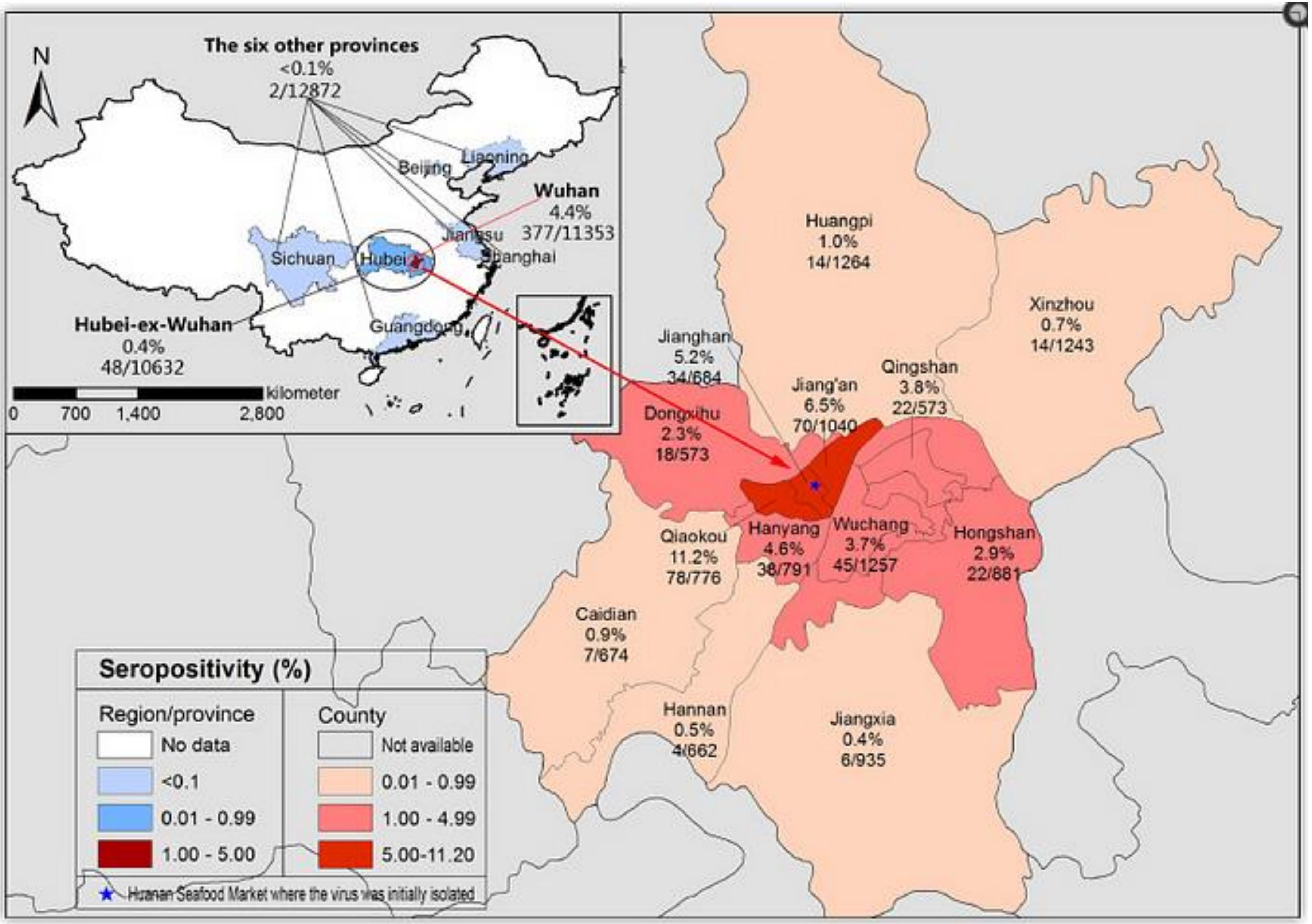
Cases are now centered more towards the center of town.

They’re still centered on the north side of the river.

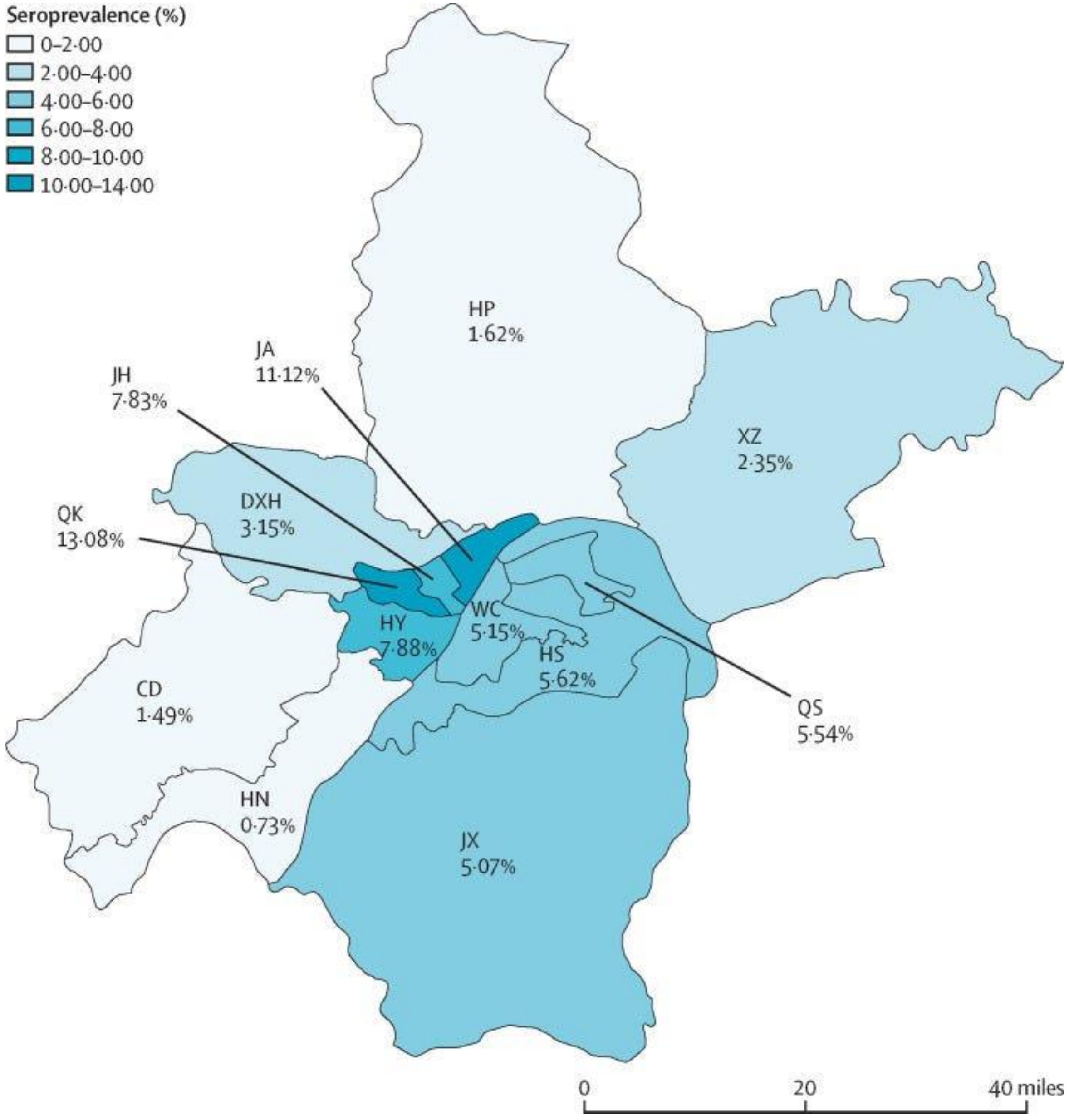
The Weibo data has at most 3 cases from 2019, so it can’t tell us where the virus started.



A Seroprevalence study, from April 2020, still puts most cases north of the river, near the market.



This was confirmed by a second seroprevalence study



Weekly excess mortality data from WHO report:

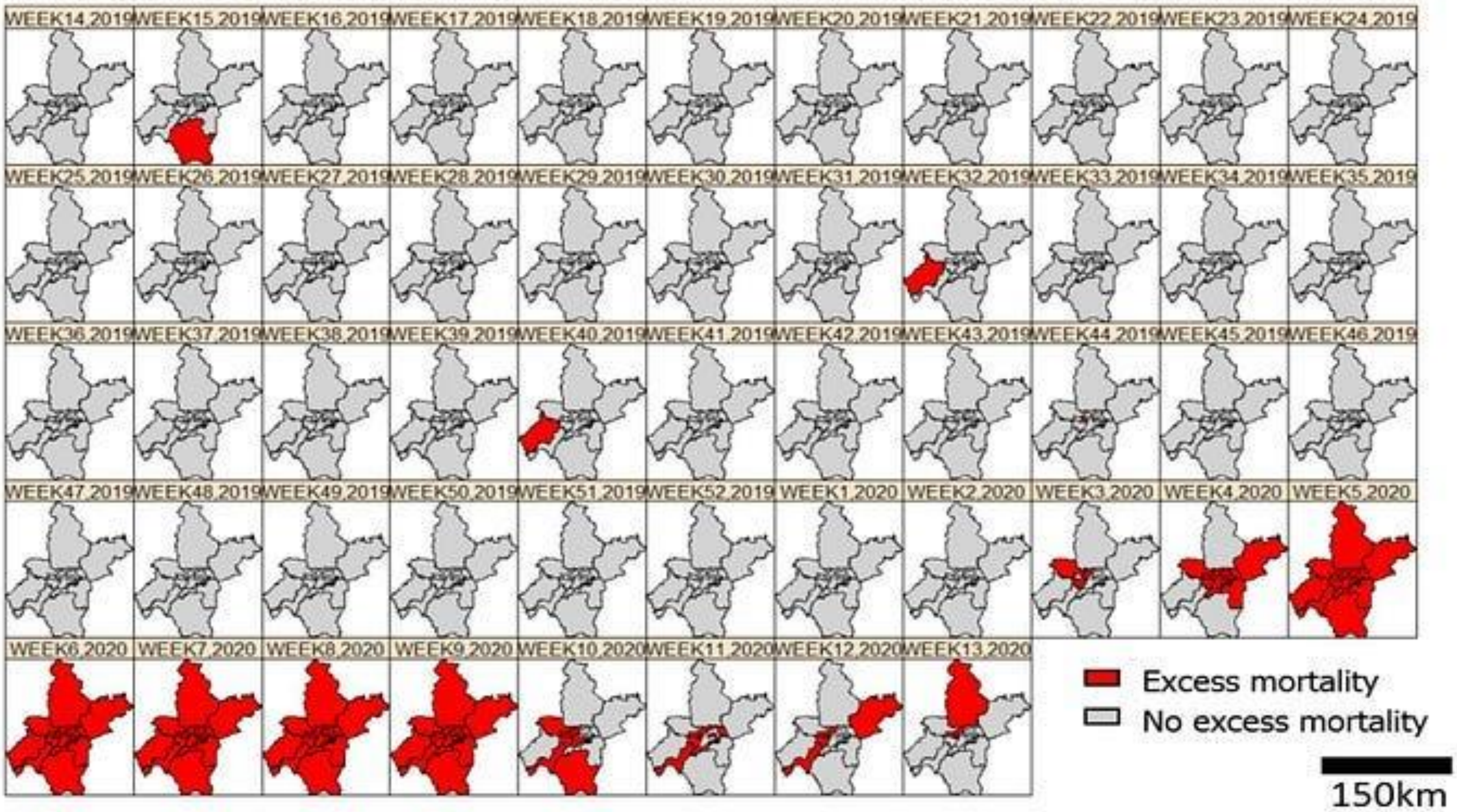
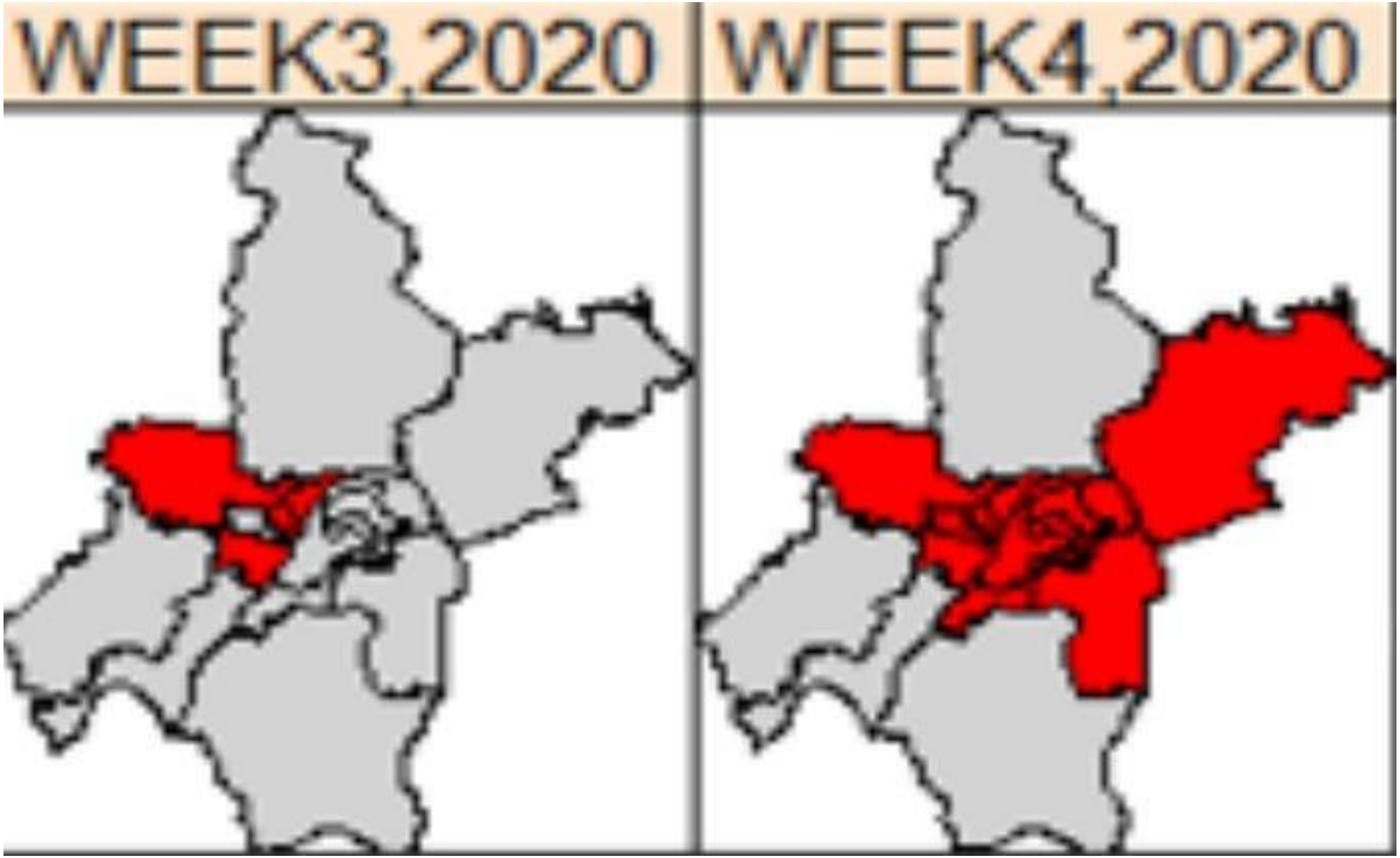


Fig. 21. Weekly excess mortality of pneumonia by districts in Wuhan, 2019-2020.

Excess mortality goes up on the north side of the river one week before the south side



Is China lying about the case locations?

Did they hide earlier cases?
Did they fake the later case locations to surround the market?

We have reports from before any cover-up would have started. We have those early market patients. One early whistleblower, doctor Li Wenliang, identified the wet market as ground zero of the epidemic in December. 7 out of 7 of the patients he reported were from the market. He went on to die from covid.

If China lied to make the market look like the source, you'd think the lie would be consistent.

At first, China said the market was the source of the outbreak. A few months later, they said it was not. In the 2021 WHO report, they said that there were no wild animals at the market. They now say the virus came into China on frozen food, or it was made in a US lab.

The data within the market points towards infected animals, but it's not perfect data. China could have faked that data to emphasize the animals. Or they could have faked it to remove the shops selling wild animals. They did neither.

It's worth keeping a list of everything China would have to lie about, for lab leak to be true.

Could something else nearby be the origin?

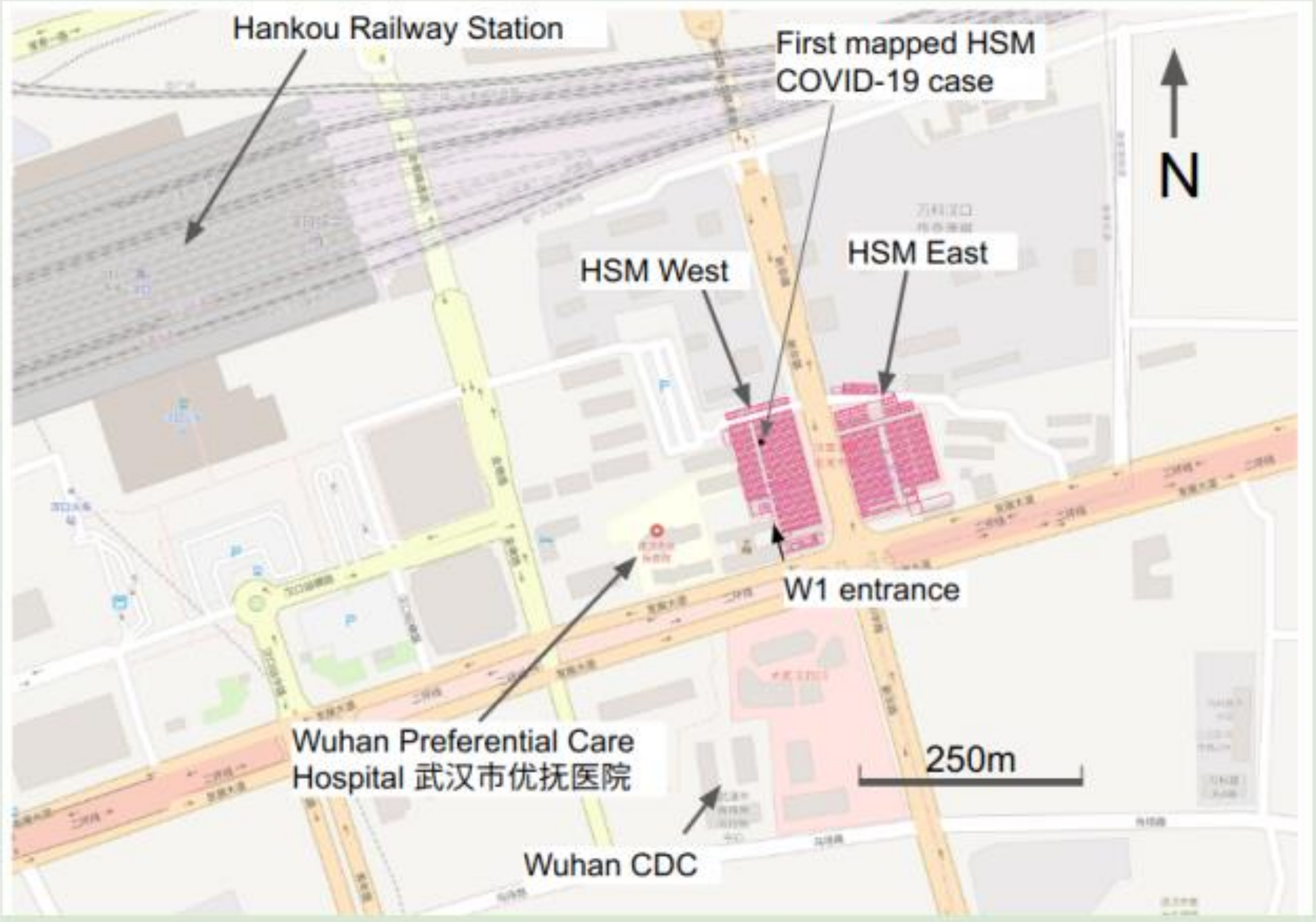


Fig. 1. Map of Huanan Seafood Market location in Wuhan, location of the Hankou railway station and Wuhan Preferential Care Hospital and Southwestern entrance 'W1'.

Wuhan CDC is very near the market, could it be the source of SARS-CoV-2?

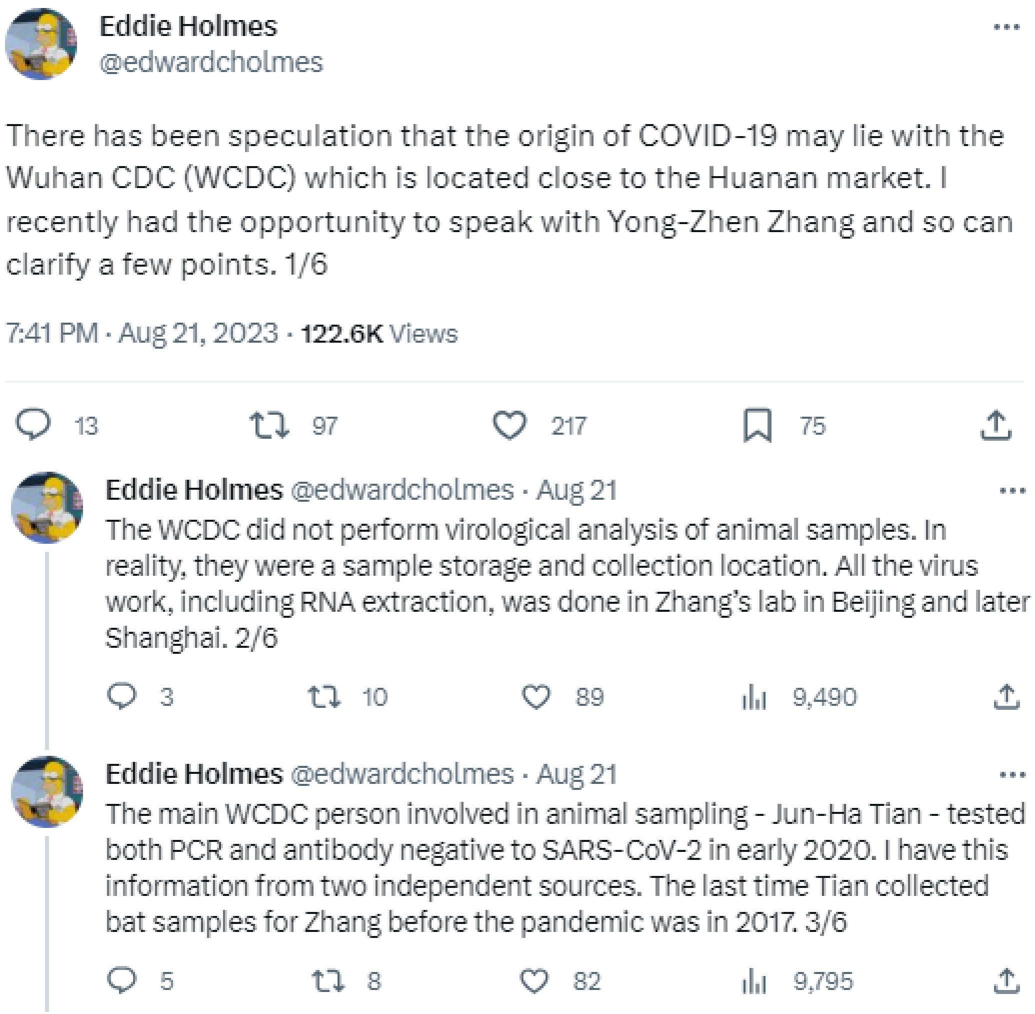
Wuhan CDC moved to that location around December 2nd. The move might be after Covid started.

No one was doing gain of function research there, this is mostly a lab for testing human diseases.

There was one researcher there, Dr Tian, who had a history of working with bats.

The number of animals at that lab was possibly zero and certainly lower than the number of animals at the market.

Eddie Holmes asked Chinese scientists for more information on the Wuhan CDC:



Eddie Holmes
@edwardcholmes

There has been speculation that the origin of COVID-19 may lie with the Wuhan CDC (WCDC) which is located close to the Huanan market. I recently had the opportunity to speak with Yong-Zhen Zhang and so can clarify a few points. 1/6

7:41 PM · Aug 21, 2023 · **122.6K** Views

13 97 217 75

Eddie Holmes @edwardcholmes · Aug 21
The WCDC did not perform virological analysis of animal samples. In reality, they were a sample storage and collection location. All the virus work, including RNA extraction, was done in Zhang's lab in Beijing and later Shanghai. 2/6

3 10 89 9,490

Eddie Holmes @edwardcholmes · Aug 21
The main WCDC person involved in animal sampling - Jun-Ha Tian - tested both PCR and antibody negative to SARS-CoV-2 in early 2020. I have this information from two independent sources. The last time Tian collected bat samples for Zhang before the pandemic was in 2017. 3/6

5 8 82 9,795

Eddie Holmes @edwardcholmes · Aug 21
There was no long-term storage of bat samples at the WCDC. As soon as a sufficient number were collected, whole animal carcasses were shipped to Yong-Zhen Zhang's lab in Beijing (later Shanghai). 4/6

1 7 77 8,339

Eddie Holmes @edwardcholmes · Aug 21
The WCDC moved to its new location close to the Huanan market in November 2019. NO bats were moved as part of this as none were on site. The only animal samples moved from the old to the new lab were from invertebrates. 5/6

1 8 82 9,094

Eddie Holmes @edwardcholmes · Aug 21
Interestingly, Zhang had a meeting of his research network in Guangzhou on December 7-8 2019. Collaborators - ID physicians - from Wuhan Central Hospital were in attendance. There was no talk of any COVID-like cases in Wuhan. 6/6

12 7 92 12.1K

In January 2020, Dr Tian went around Hubei,
sampling animals to look for Covid.

That’s a strange thing to do, if he started the pandemic.

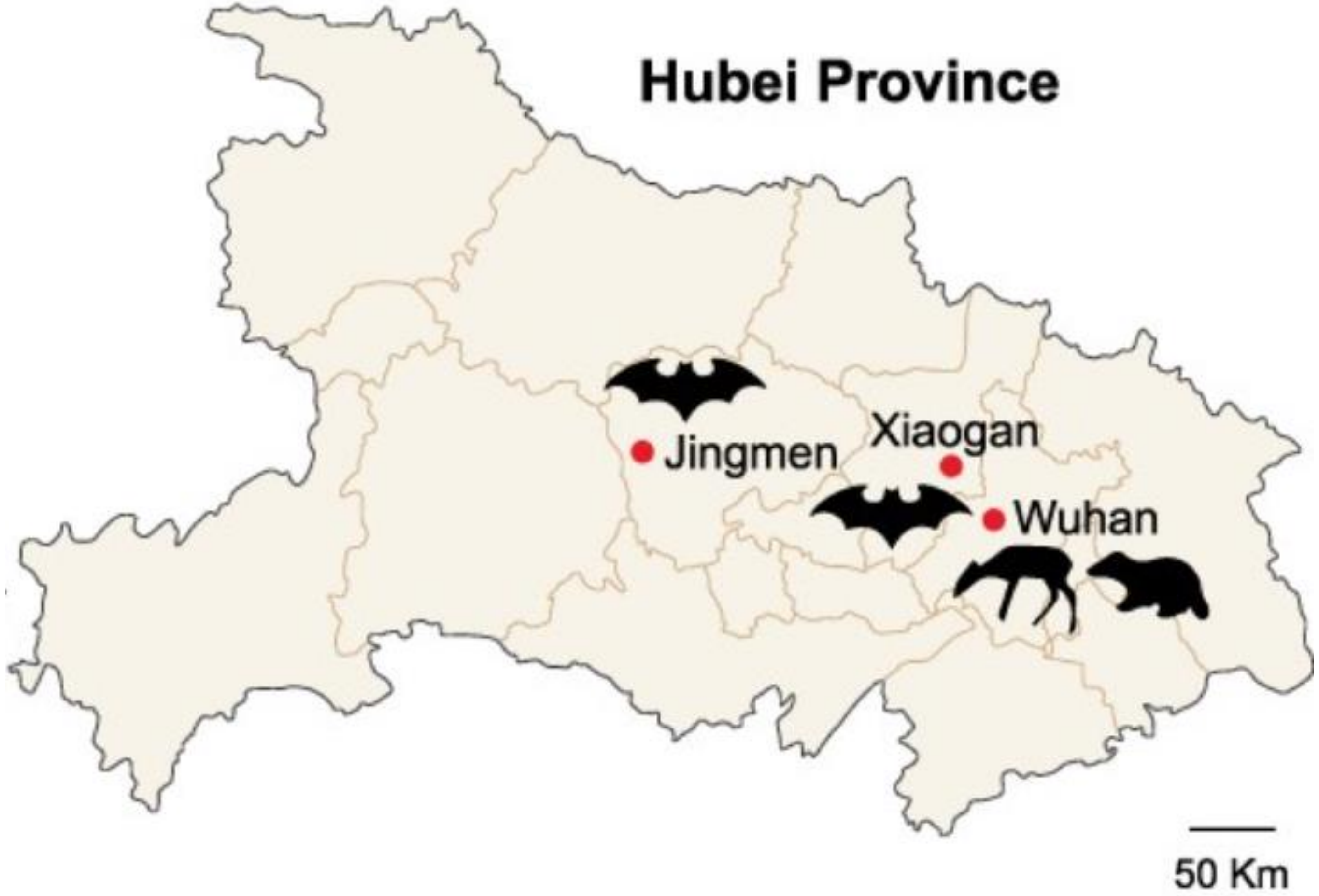
He found bats infected with two novel betacoronaviruses,
with 80-90% similarity to SARS-CoV-2,
depending on the segment of the genome.

Tian was not allowed to sample further west, in Enshi.

His study tested 15 wild raccoon dogs and found them
negative for Covid. Lab leak theorists often cite
the study to say that “no raccoon dogs in China
were naturally infected”.

It’s too small a sample to say that.

But it’s also weird to quote Tian’s research
if you think he started the pandemic.



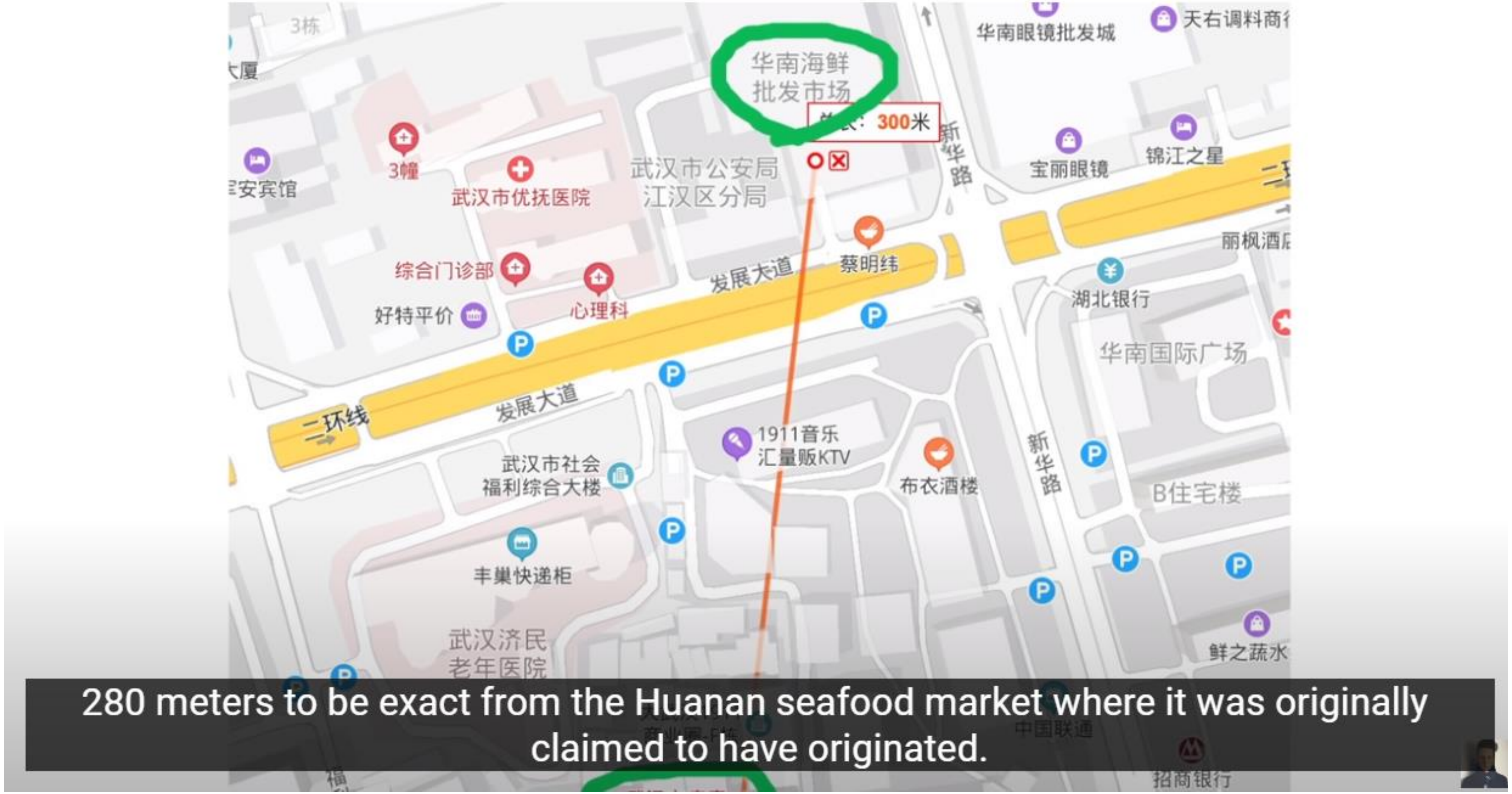
Some kind of accident at the Wuhan CDC is not 100% impossible, but it’s much less likely than a market origin.

Since this debate is between “gain of function research” and “natural origin”, this lab is mostly irrelevant,
the Wuhan CDC didn’t do gain of function research.

The Wuhan CDC mostly features a role in internet debates.

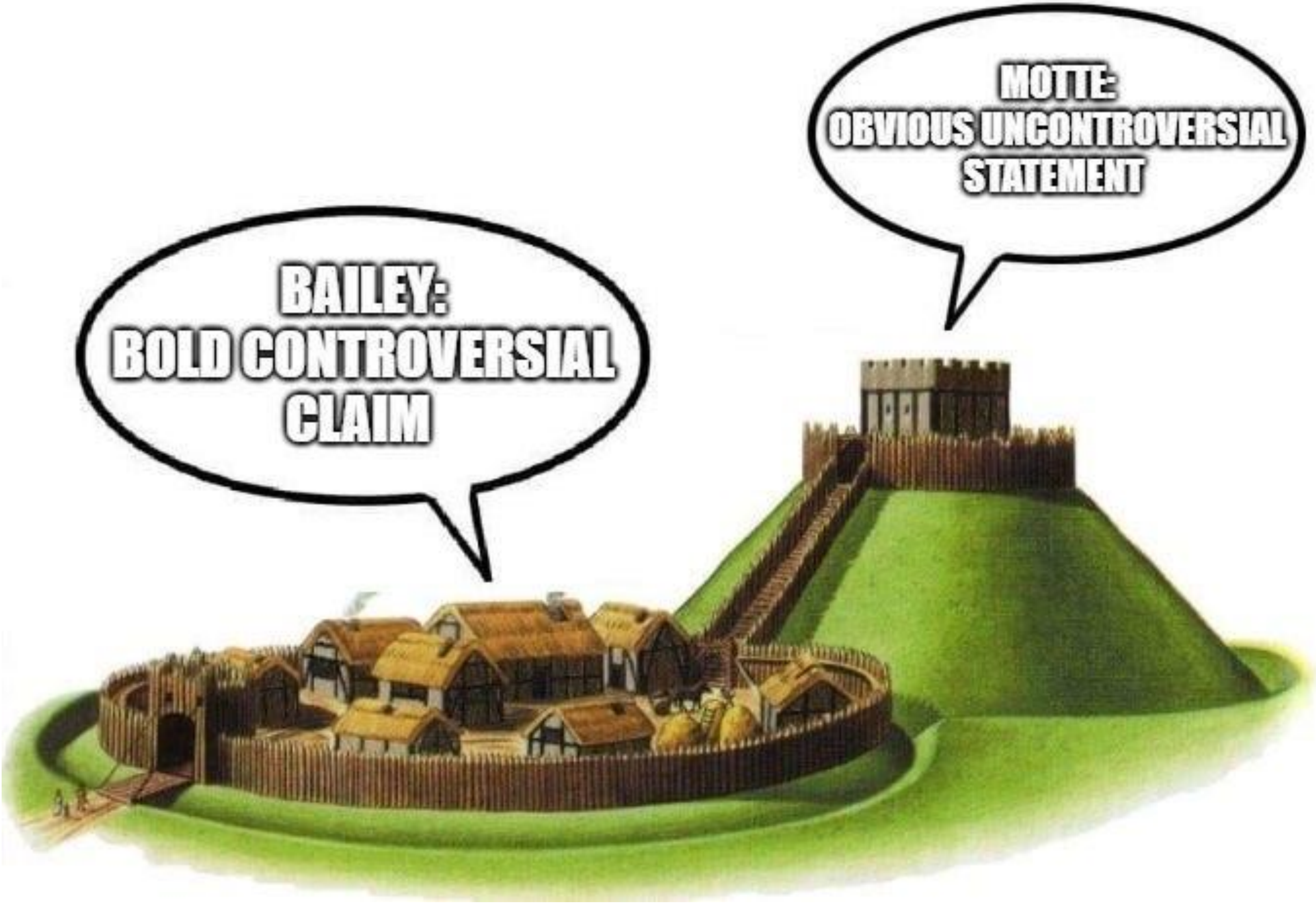
It’s mostly used as a bait and switch.

Here’s a popular 2020 video that talks about “the Wuhan lab” and uses details about the WIV, but then gives the location of the Wuhan CDC:

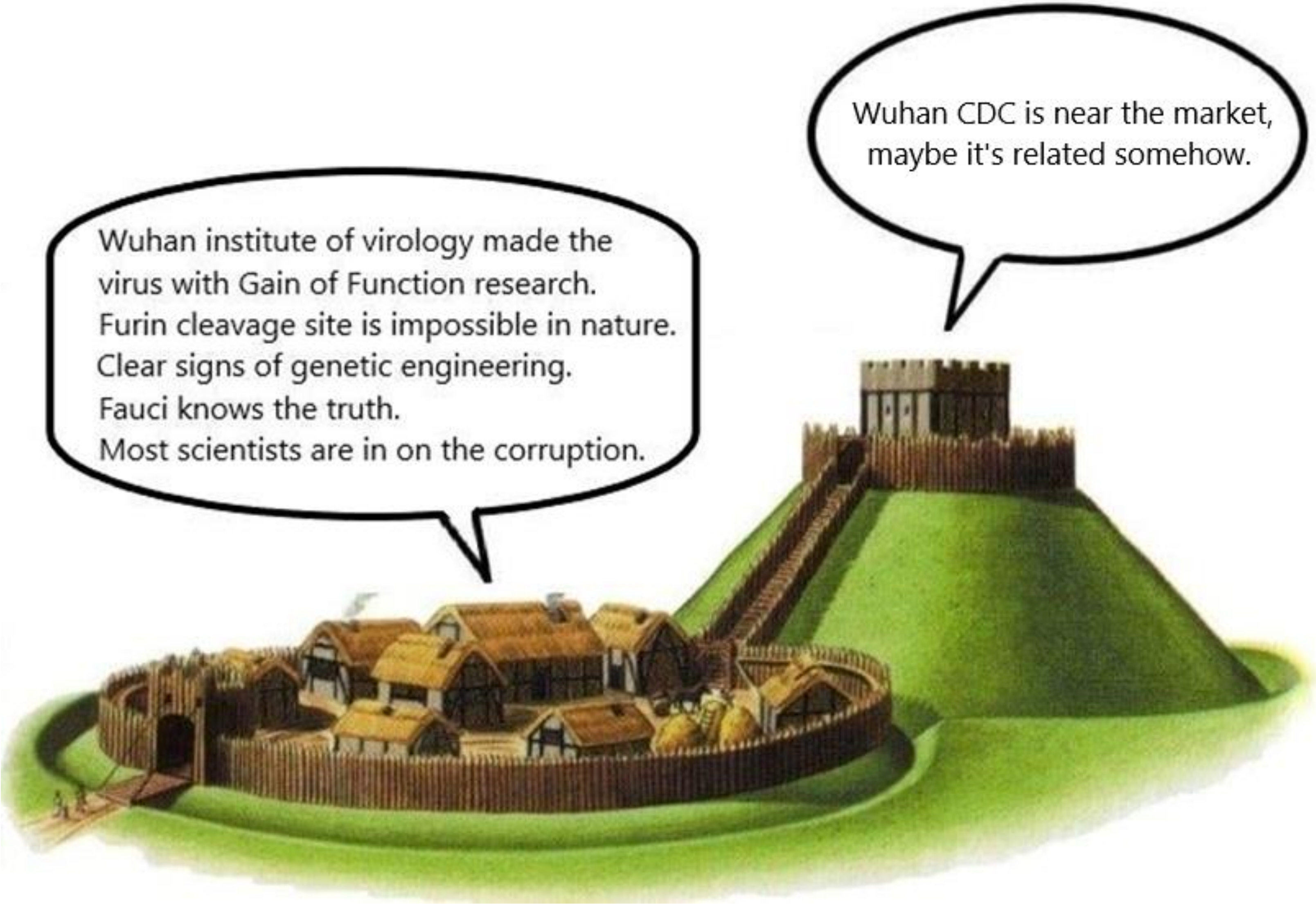


280 meters to be exact from the Huanan seafood market where it was originally claimed to have originated.

Other times, it’s a different kind of bait and switch.



Motte and Bailey: a common strategy for bad arguments


Wuhan institute of virology made the virus with Gain of Function research.
Furin cleavage site is impossible in nature.
Clear signs of genetic engineering.
Fauci knows the truth.
Most scientists are in on the corruption.
Wuhan CDC is near the market, maybe it's related somehow.

If you’re free to blame any BSL2/3 facility,
you can make lots of theories.

Those are all over Wuhan and other Chinese cities.

The WIV has 2 locations to choose from.

This map (from DRASTIC) shows 9 labs in one cropped area of Wuhan.

Another DRASTIC map has [11 locations marked](#).

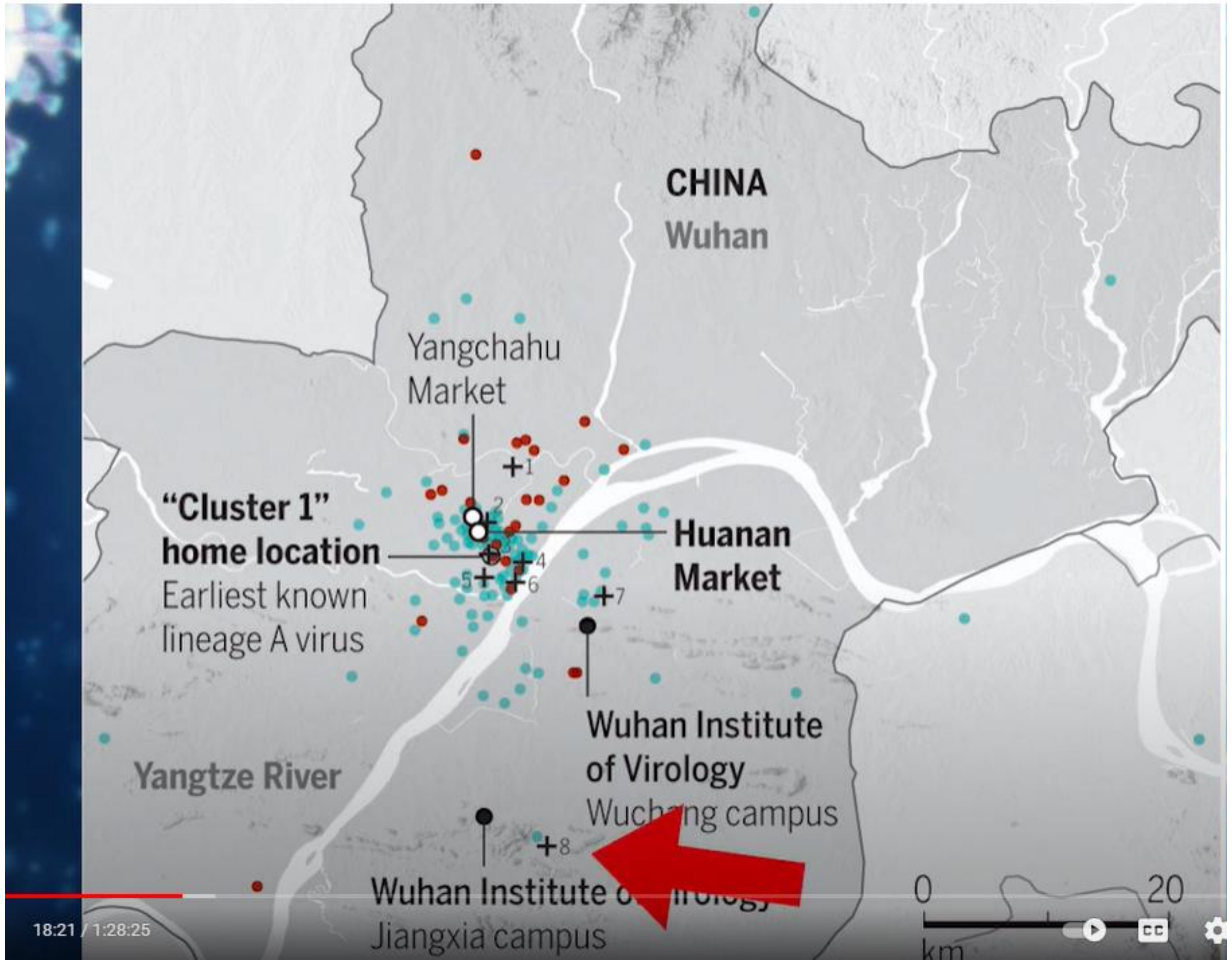
This map also shows the “subway line 2”, which goes near the WIV and also near the market.

If you’re free to use all subway lines and all labs, you can link many places to some lab.

Another theory blames the southern WIV campus, because one early case (not the earliest) lived near there.

DRASTIC looked at 100 bus lines and found one that connects Chen's neighborhood to the southern WIV.

If you have 3 labs to choose from (or 9), 6 subway lines, and 100 bus lines, you can say that any point in Wuhan is "connected to a lab".



What’s the second most likely place the virus started?

1. Virus started at the market

2. ???

3. Wuhan CDC

4. Wuhan Institute of Virology

The second most likely case is that covid started somewhere else in China.
If you assume there are lots of undetected early cases in Wuhan, then you don’t actually know it started in Wuhan.
Hankou railway station sees [60,000+ passengers per day]() or 1.8 million per month.
It [offers service]() to southern cities like Guangzhou.
One person could get infected elsewhere, take a train to Wuhan, visit the market.
Huanan market was number 1,677 on the list of most crowded places in Wuhan, Hankou station was number 3.
Compare 1.8 million travelers to ~60 people working on viruses at the WIV.

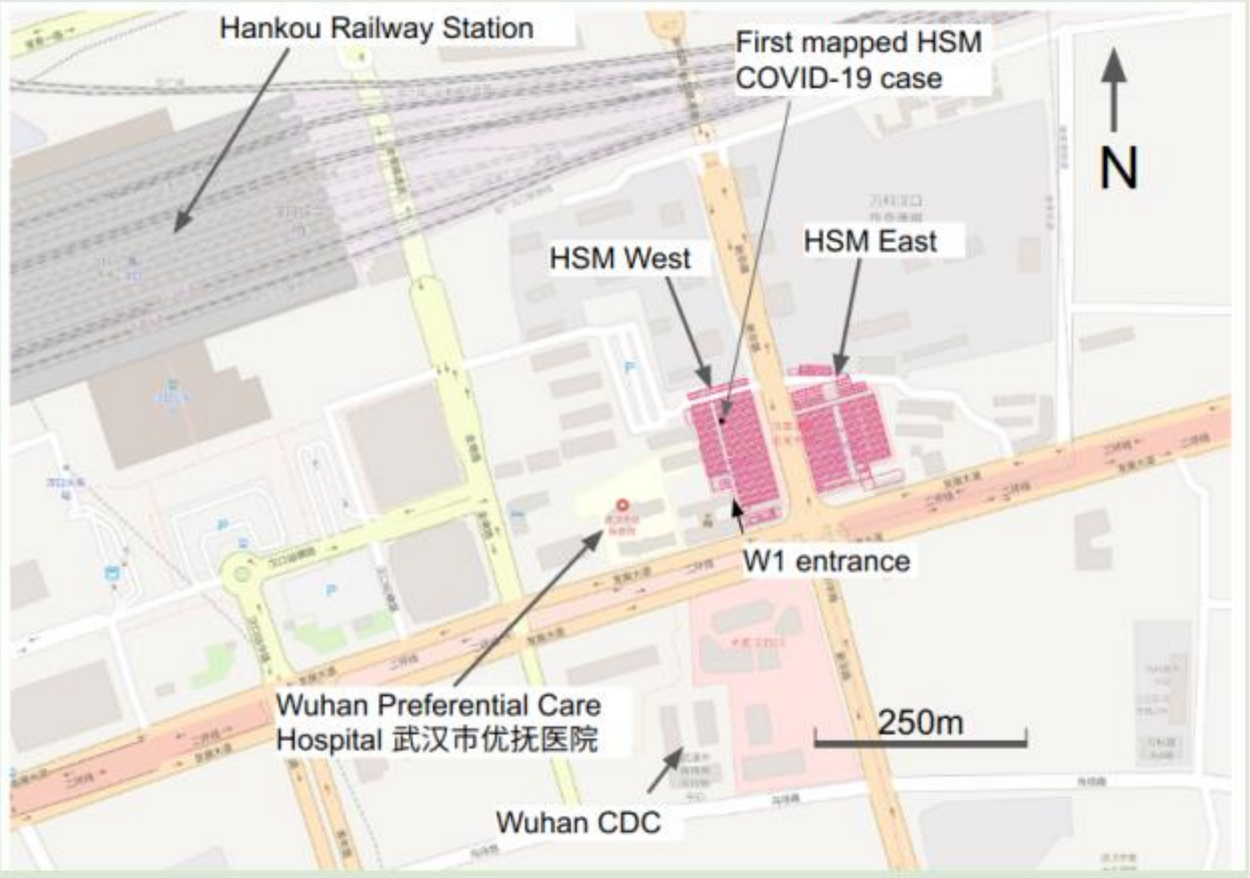


Fig. 1. Map of Huanan Seafood Market location in Wuhan, location of the Hankou railway station and Wuhan Preferential Care Hospital and Southwestern entrance ‘W1’.

What’s the second most likely place the virus started?

1. Virus started at the market from infected animals (the most likely scenario, by far)

2. It started elsewhere in China
    - brought to the market by an animal trader who got sick elsewhere
    - or it came into Wuhan via train

3. Wuhan CDC

4. Wuhan Institute of Virology

5. It came in on frozen food. (China favors this. It’s hard to place the odds, this could be #3).

6. An American lab.

Then there are things that definitely didn’t happen:

7. It came from outer space.

But someone still wrote a paper claiming that Covid came from outer space.

Searches for earlier cases

If you read earlier reports, you'll sometimes see cases listed on December 1st, 2nd, or 7th.
These were investigated in the WHO report and ruled out as covid cases:

"Three possible cases with disease onset on 1, 2 and 7 December 2019, respectively, were initially identified as potential cases in the retrospective case search and have been included in some published papers. Clinical review of these three cases by the Chinese expert team led to their exclusion as possible cases on the basis of the clinical features of their illness.

In the case with onset on 1 December, a 62-year-old man with past history of cerebrovascular disease was judged to have had a minor respiratory illness in early December, which responded to antibiotics. He developed a further illness with onset on 26 December 2019, which was later laboratory-confirmed to be COVID-19. This patient had no reported contact to the Huanan market, whereas his wife, who was admitted on 26 December with a COVID-19 compatible illness, reported close contact with the Huanan market. She was also later laboratory-confirmed to have COVID-19. This couple, together with their son, became part of the first recognized family cluster of COVID-19."

"In the second case, a 34-year-old woman with onset on 2 December 2019 was assessed to have had venous thromboembolic disease and subsequently pneumonia. She remained negative on SARS-CoV2 laboratory testing throughout a longer admission period ending in mid-February 2020.

In the third case, a 51-year-old man with onset on 7 December 2019 had symptoms of a cold and fever, and chest X-ray changes ("thickness of texture of both lungs and stripes"). His blood neutrophil count was raised and specific antibodies to Mycoplasma pneumoniae were detected. He responded well to antibiotics. Blood collected in April 2020 was reported negative for SARS-CoV-2-specific antibodies."

The WHO report describes a search for earlier cases.
Out of 76,000 hospital records, 92 sounded like they could possibly be covid.

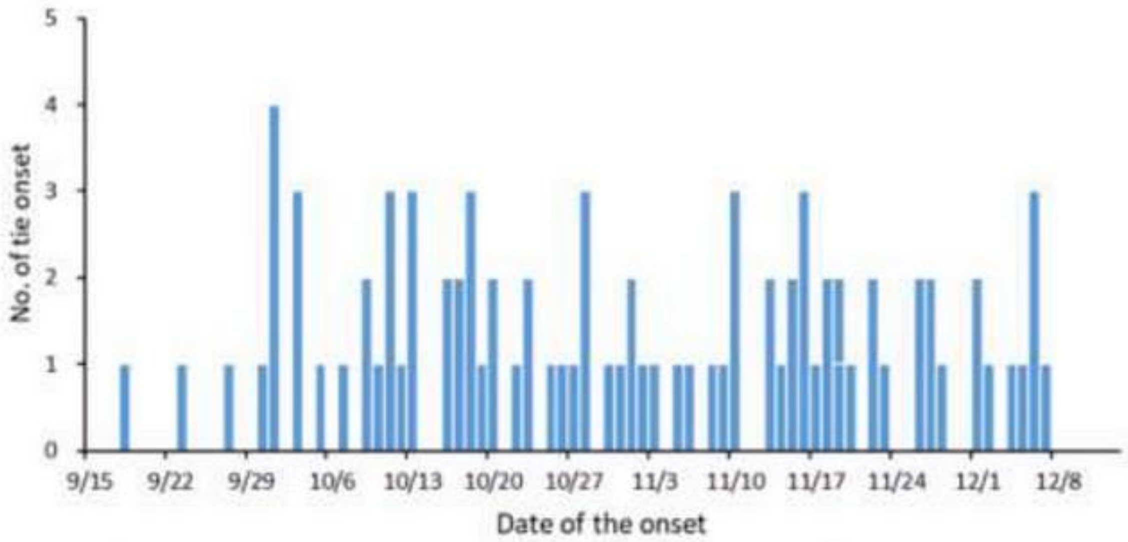


Fig. 27. Distribution of the 92 cases identified as potential cases of COVID-19 following review of the 76 253 episodes of illness presenting from 1 October to 10 December, by date of onset.

There was no trend, over time.
None of these patients formed clusters and there were no geographic trend.
They were tested for antibodies in 2021

> "The 92 cases were followed up in January 2021 and blood for SARS-CoV-2 serology collected from 67 of them (the remainder either having died, refused or were unobtainable). All 67 sera were reported to be SARS-CoV-2-specific antibody negative."

These probably weren't covid.

There are some media reports of other early cases:

South China Morning Post article lists a November 17th case.

Quotes an “anonymous Chinese government source”
Says there were 9 cases in November
Says there were 266 cases overall.
266 = 174+92, the same number of cases in the WHO report.
This might have been a preliminary government report, November cases were likely later ruled out, just like the early December cases.

British teacher (Connor Reed) living in Wuhan. Might have gotten sick November 25th.

Reported in a tabloid article (Dailymail)
Describes cold like symptoms for a week, followed by much worse fever and pneumonia
Says that he shopped at the seafood market, thinks he caught the virus there.
Claims his cat died from covid.
Likely just a tabloid story, but if accurate, that would just confirm the virus was at the market weeks before December 10th.

Tabloid article on May 29th, 2021 (during the spike of lab leak interest)

Claims there were unpublished November cases

references a Chinese article from 2/27/2020 (archive link)

describes Professor Yu Chuanhua looking at cases between September and November.

Chunhua called and retracted these cases before article was published:

> “Before going to press, Professor Yu Chuanhua told the Health Times reporter that the data of two patients with new corona pneumonia in November were entered incorrectly, and other data have yet to be verified one by one. When was the earliest onset time? Yu Chuanhua said, "We need to verify each one and investigate the relevant contact history before we can analyze it."

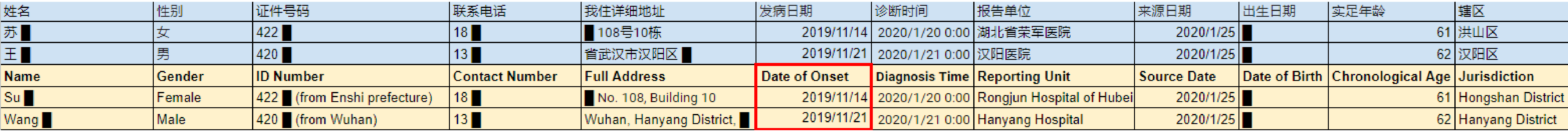
Chuanhua later published a paper saying there were no Covid cases before December

DRASTIC sleuths OCR’d a screenshot from the article.

“Date of Onset” is 2 months before “Diagnosis time”.

Looks like a data entry error and these should be January.

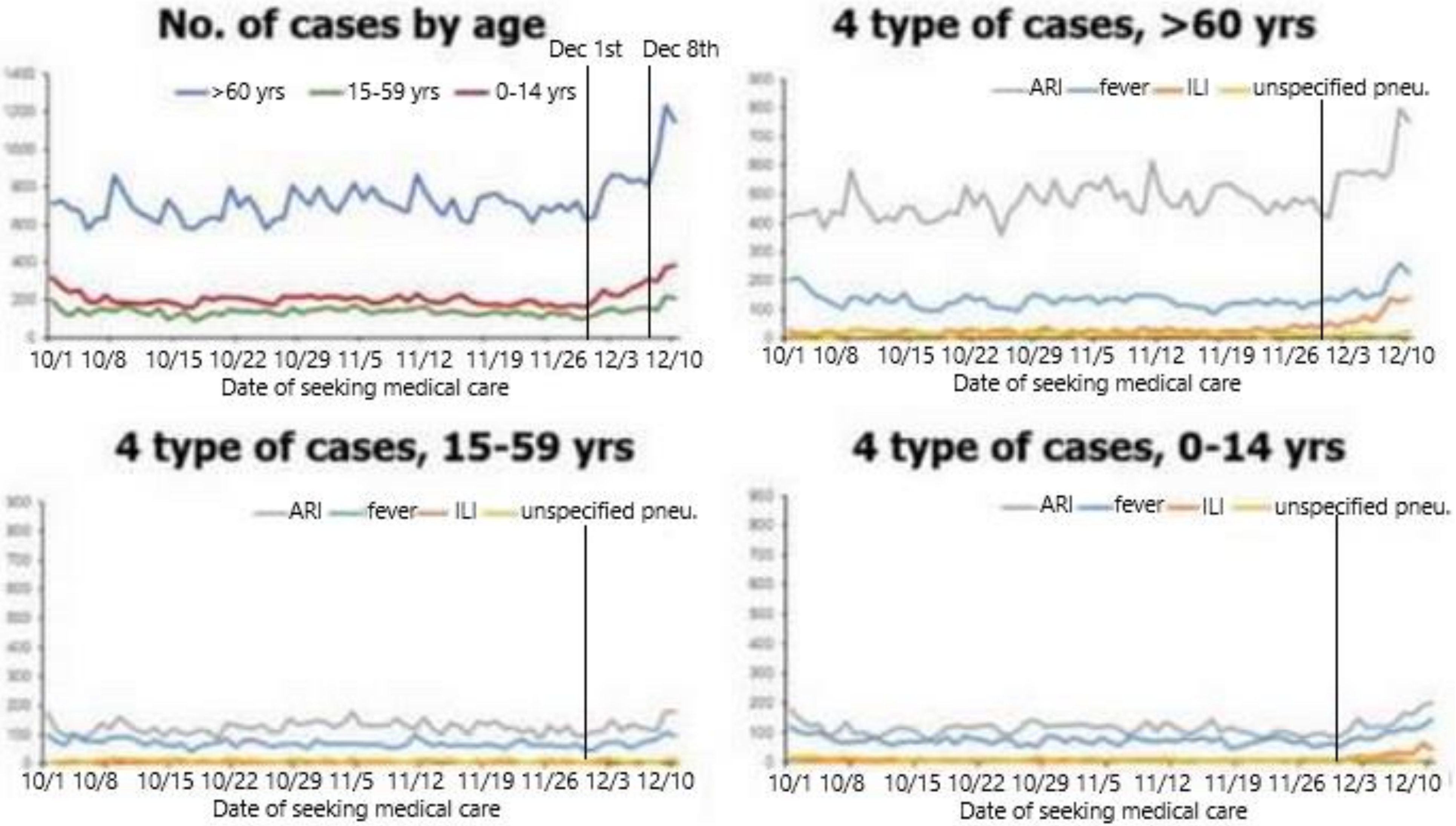
Some people in DRASTIC have decided these are early cases near the WIV.



姓名	性别	证件号码	联系电话	我住详细地址	发病日期	诊断时间	报告单位	来源日期	出生日期	实足年龄	辖区
苏 [redacted]	女	422 [redacted]	18 [redacted]	[redacted] 108号10栋	2019/11/14	2020/1/20 0:00	湖北省荣军医院	2020/1/25	[redacted]	61	洪山区
王 [redacted]	男	420 [redacted]	13 [redacted]	省武汉市汉阳区 [redacted]	2019/11/21	2020/1/21 0:00	汉阳医院	2020/1/25	[redacted]	62	汉阳区

Name	**Gender**	**ID Number**	**Contact Number**	**Full Address**	**Date of Onset**	**Diagnosis Time**	**Reporting Unit**	**Source Date**	**Date of Birth**	**Chronological Age**	**Jurisdiction**
Su [redacted]	Female	422 [redacted] (from Enshi prefecture)	18 [redacted]	[redacted] No. 108, Building 10	2019/11/14	2020/1/20 0:00	Rongjun Hospital of Hubei	2020/1/25	[redacted]	61	Hongshan District
Wang [redacted]	Male	420 [redacted] (from Wuhan)	13 [redacted]	Wuhan, Hanyang District, [redacted]	2019/11/21	2020/1/21 0:00	Hanyang Hospital	2020/1/25	[redacted]	62	Hanyang District

Wuhan hospital records show no uptick in illness before December 2019



No. of cases by age

4 type of cases, >60 yrs

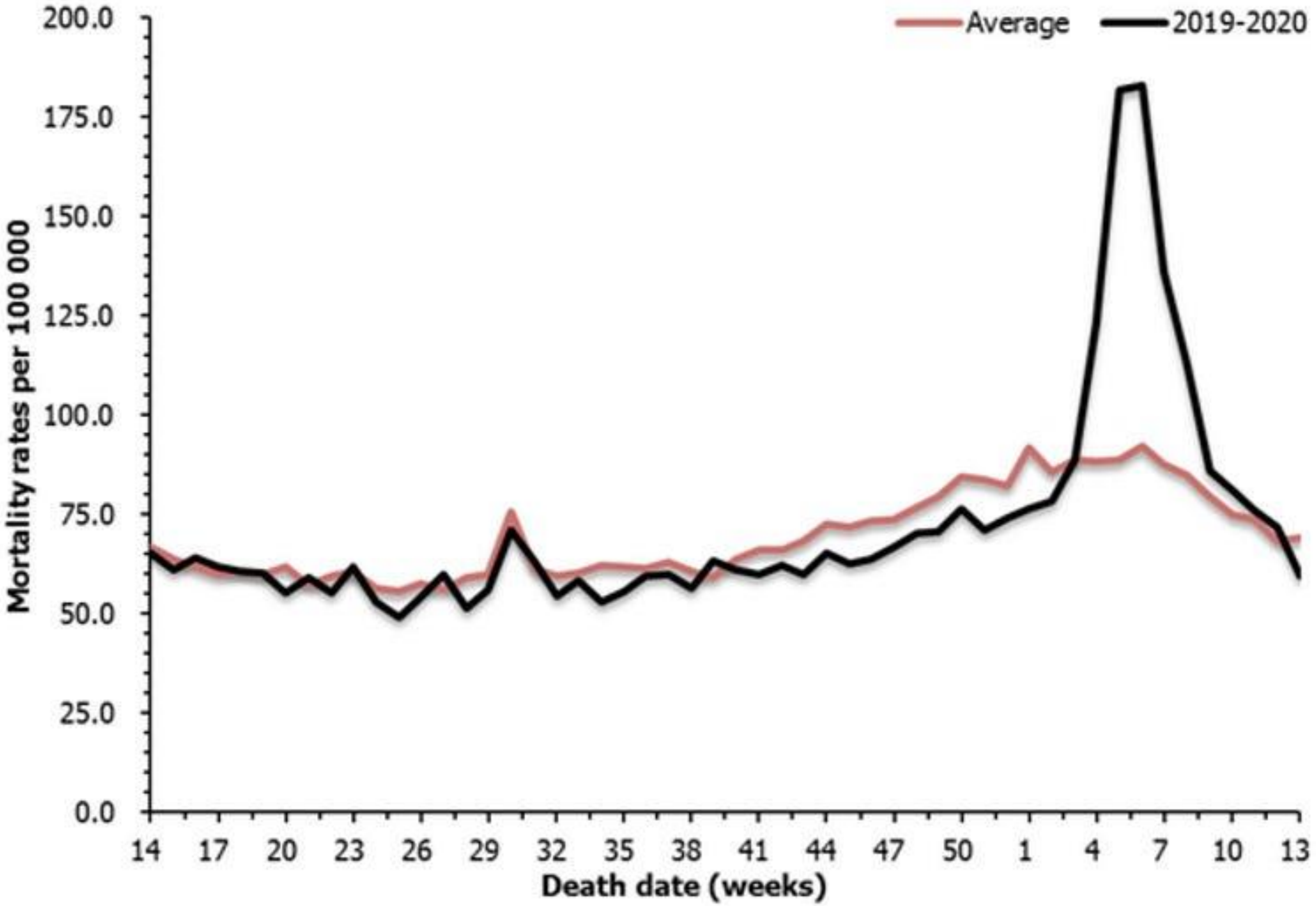
4 type of cases, 15-59 yrs

4 type of cases, 0-14 yrs

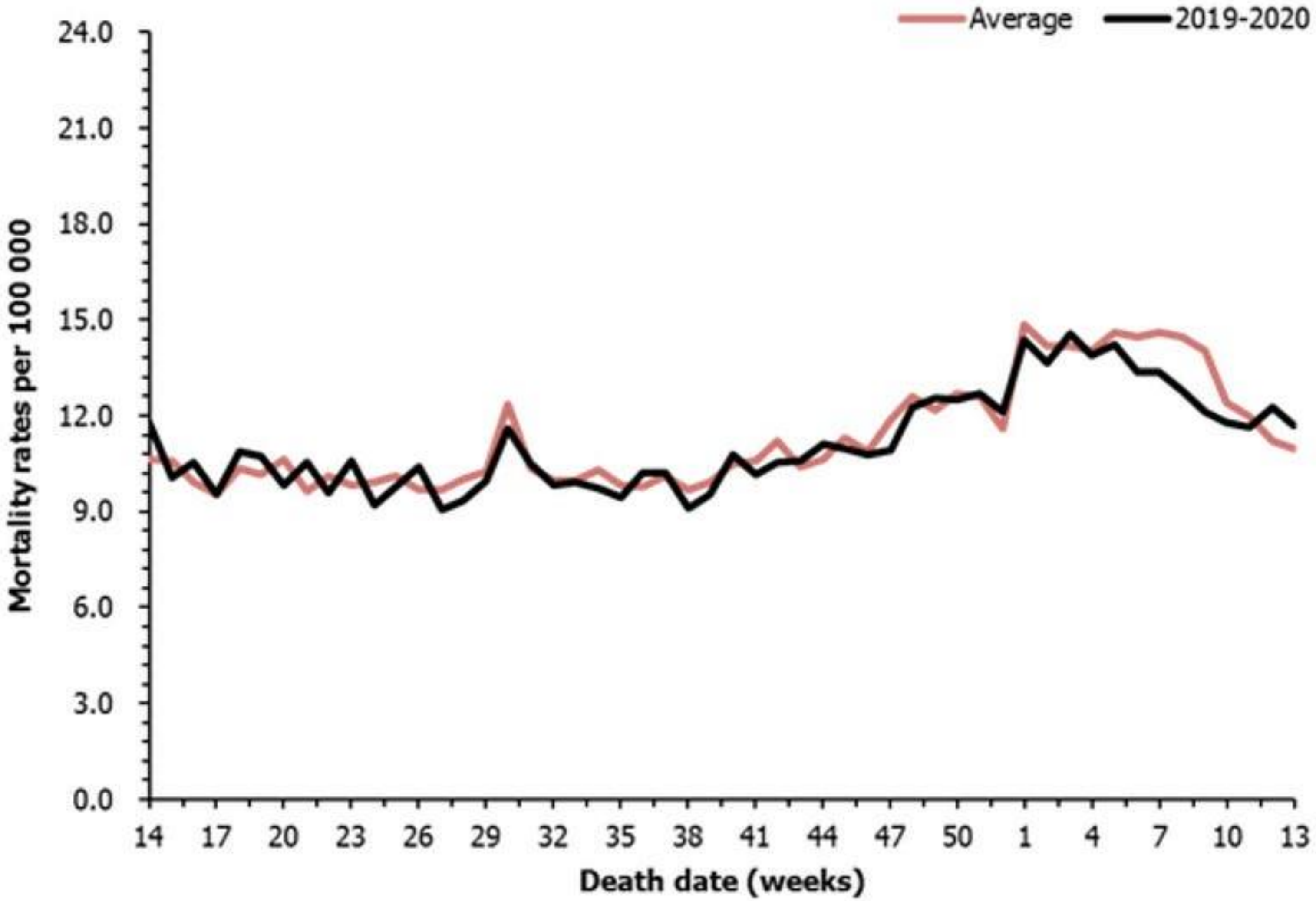
Fig. 26. Distribution of 76 253 episodes of illness identified in the retrospective review, 1 October – 10 December 2019; total by age group; diagnostic category by each age group.

Image source: WHO Report, page 48. ARI = acute respiratory infection. ILI = influenza like illness.

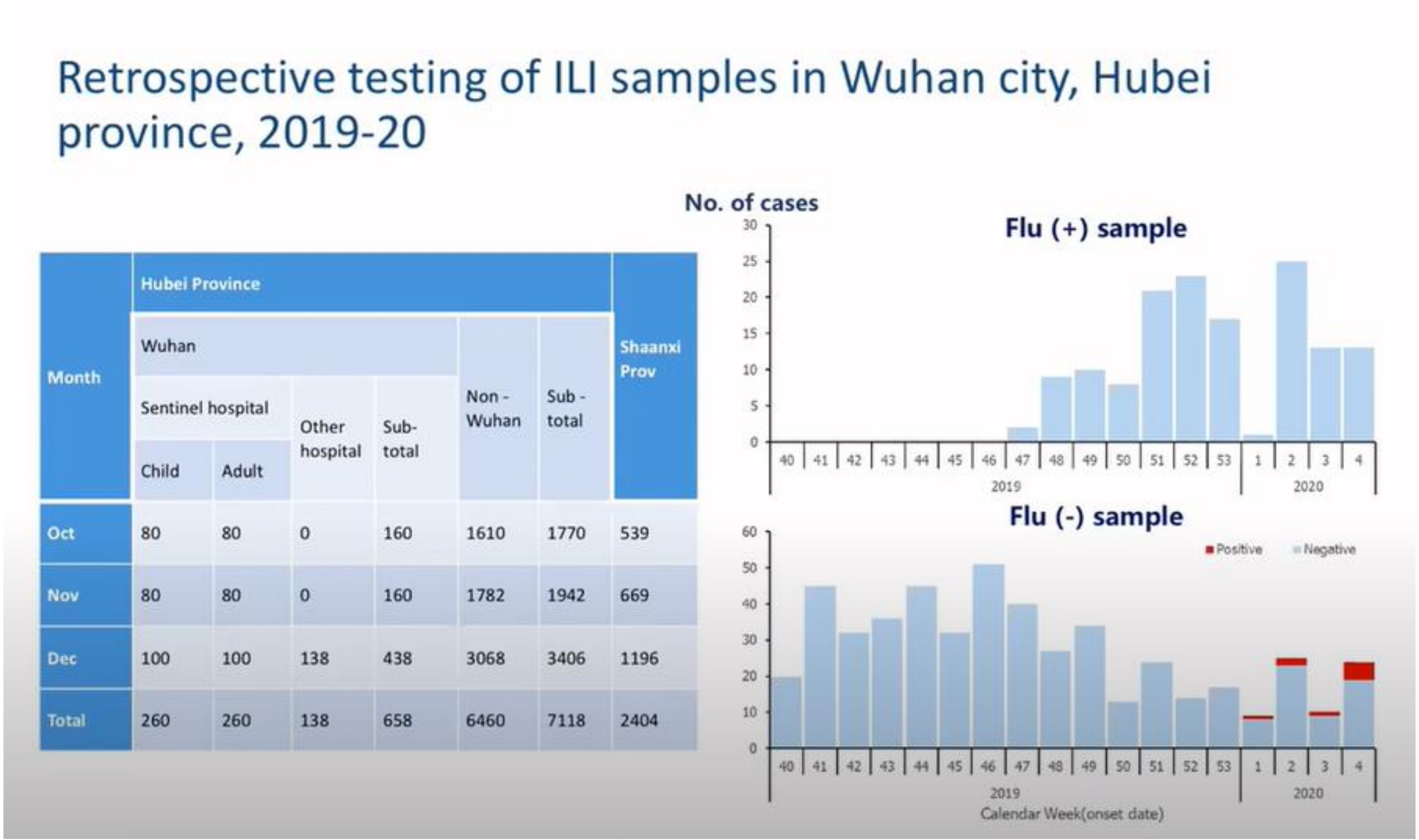
Excess deaths in Wuhan show no signal until 2020.



Excess deaths in Hubei province never show a signal:



WHO investigation tested hundreds of stored influenza like illness samples from Wuhan, and thousands from Hubei.



Retrospective testing of ILI samples in Wuhan city, Hubei province, 2019-20

Month	Hubei Province						Shaanxi Prov
	Wuhan				Non - Wuhan	Sub - total	
	Sentinel hospital		Other hospital	Sub-total			
	Child	Adult					
Oct	80	80	0	160	1610	1770	539
Nov	80	80	0	160	1782	1942	669
Dec	100	100	138	438	3068	3406	1196
Total	260	260	138	658	6460	7118	2404

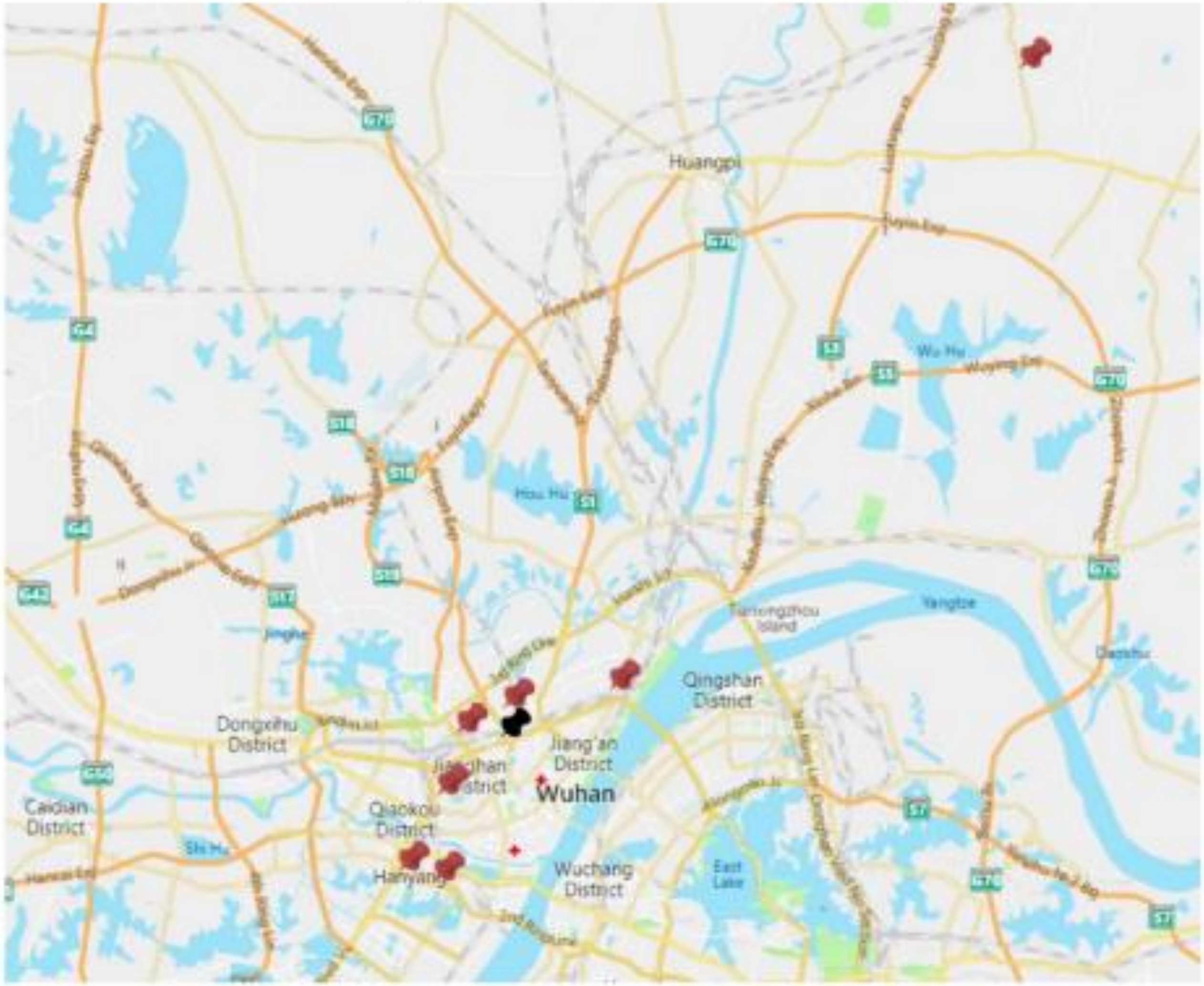
[Data from WHO report]

Retrospective throat swabs (early Jan 2020)

Another study tested 640 flu throat swabs,
from October 6th, 2019 to January 21st, 2020.

They found no positive tests in 2019, but
9 positive samples in January 2020.

All the positive cases lived on the North side of the river, most near the Huanan market.



Kong et al.
Nature Microbiology (2020)

Wuhan blood banks were tested

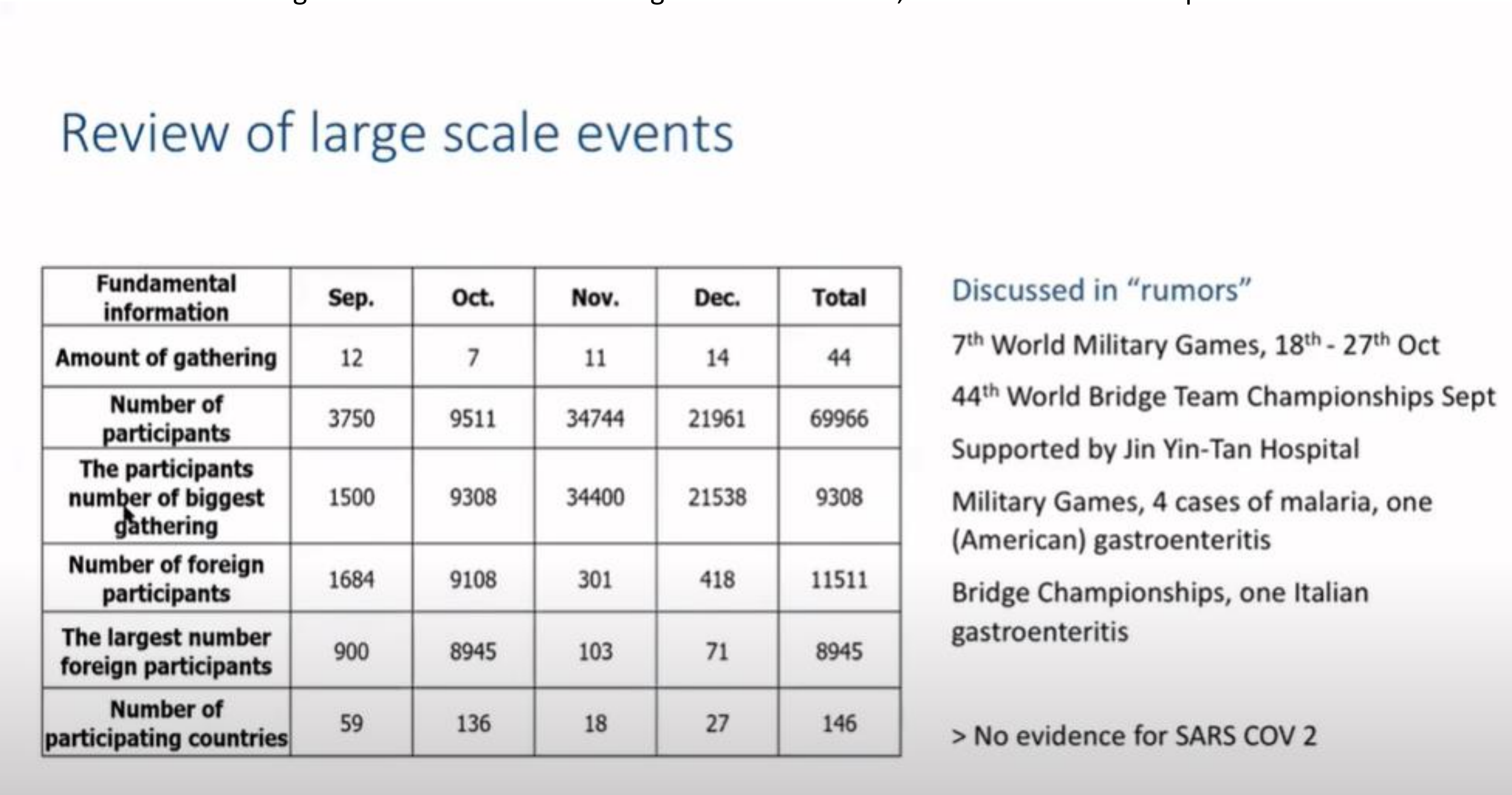
One study looked at 40,000 blood donor samples taken between September and December 2019.

None of them tested positive for covid antibodies.

That confirms the virus was not widely circulating around Wuhan before the outbreak at the market.

The first positive blood bank sample in Wuhan was found on January 5th, 2020.

The WHO team investigated medical records for large events in Wuhan, found no evidence of pneumonia outbreaks.



Review of large scale events

Fundamental information	Sep.	Oct.	Nov.	Dec.	Total
Amount of gathering	12	7	11	14	44
Number of participants	3750	9511	34744	21961	69966
The participants number of biggest gathering	1500	9308	34400	21538	9308
Number of foreign participants	1684	9108	301	418	11511
The largest number foreign participants	900	8945	103	71	8945
Number of participating countries	59	136	18	27	146

Discussed in “rumors”

7th World Military Games, 18th - 27th Oct

44th World Bridge Team Championships Sept

Supported by Jin Yin-Tan Hospital

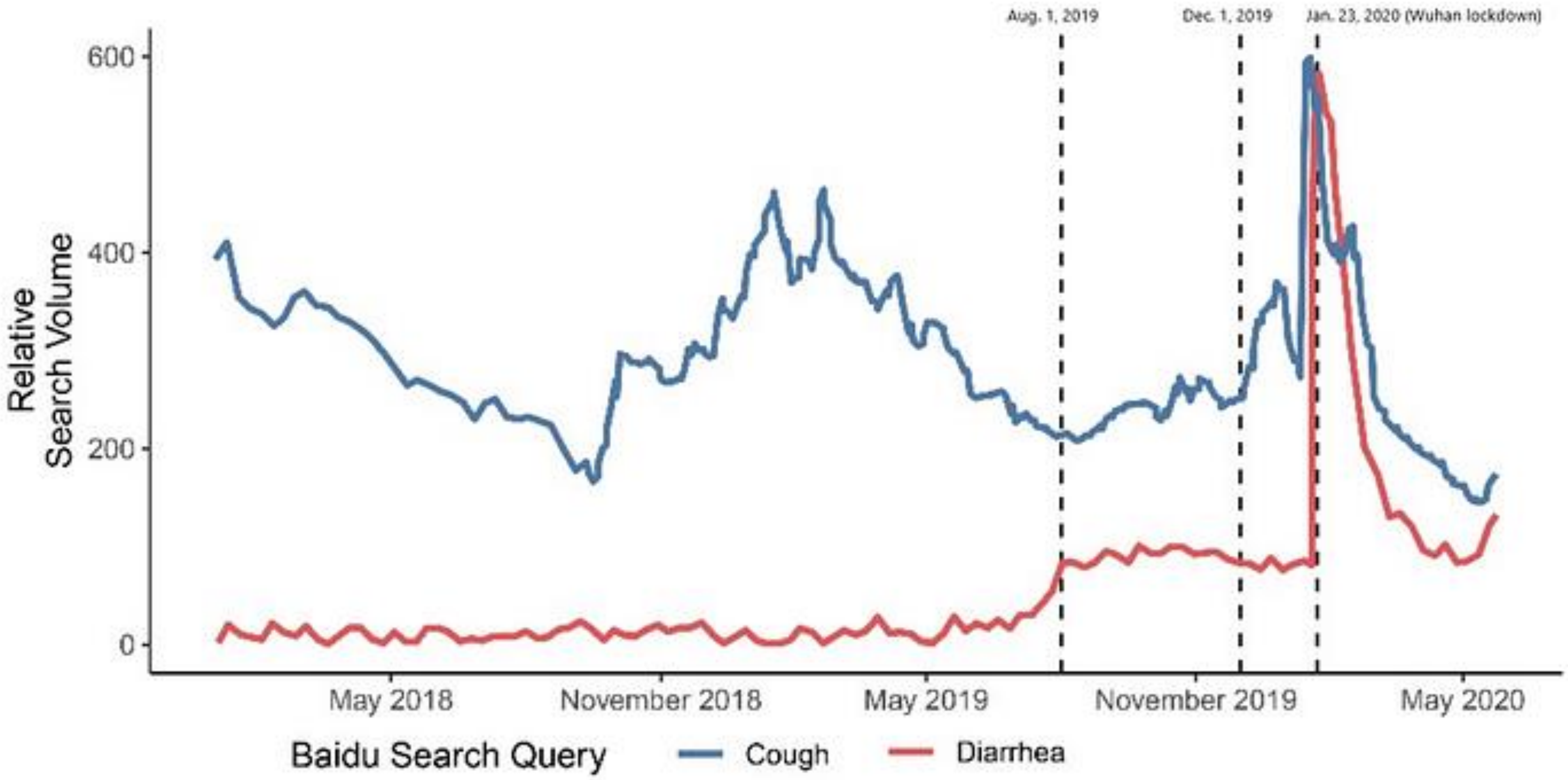
Military Games, 4 cases of malaria, one (American) gastroenteritis

Bridge Championships, one Italian gastroenteritis

> No evidence for SARS COV 2

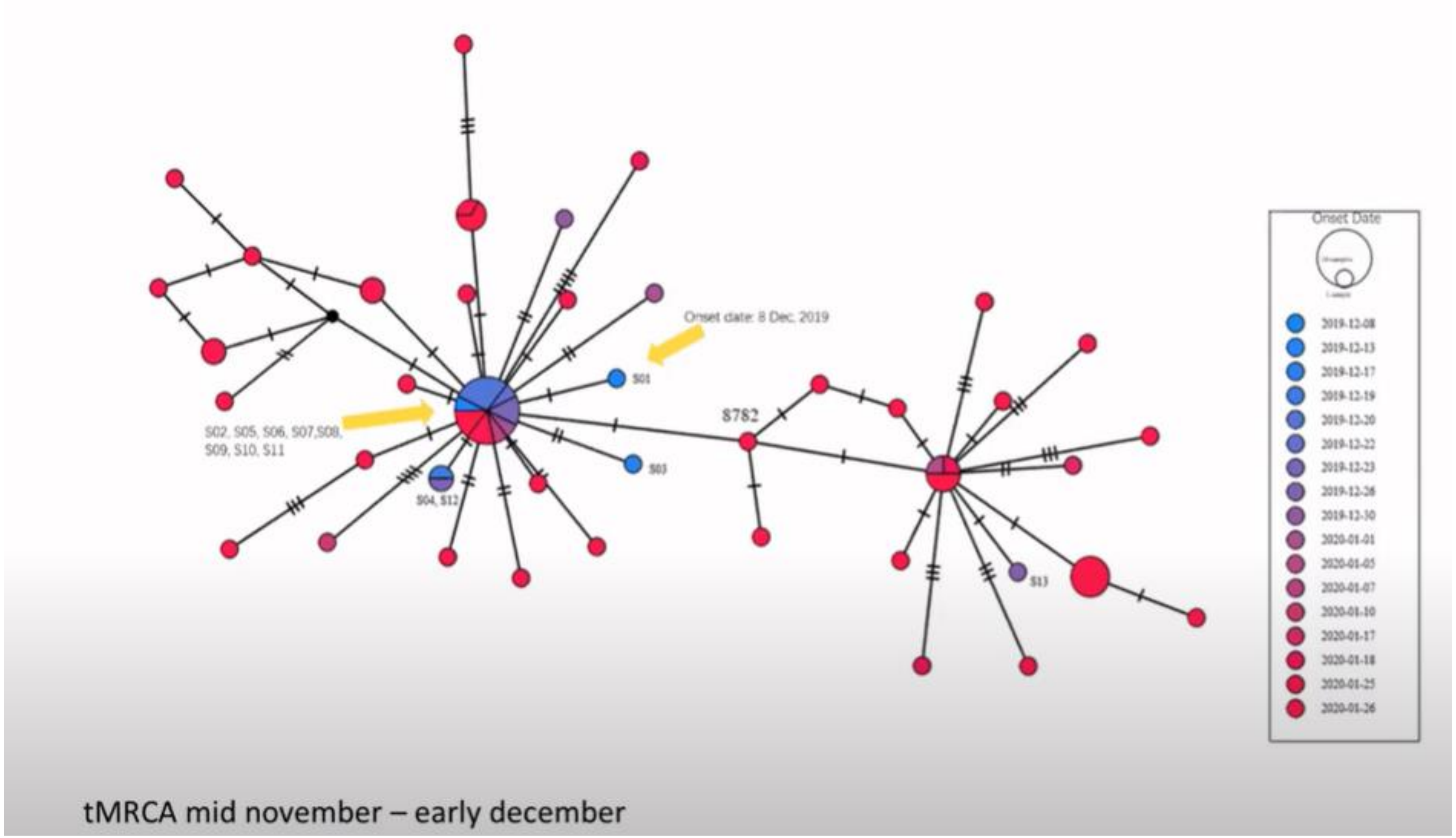
Data from a Marion Koopmans presentation.

A Harvard report looked at Baidu searches for disease symptoms.



Genetic evidence

Genetics can also show where the pandemic started



tMRCA mid november – early december

Early phylogeny from the WHO report. First market cluster, lineage B, on the left. Lineage A on the right. Data from Marion Koopmans.

This has a few mistakes. The December 8th genome was misidentified. He turned out to be Lineage B with no mutations, and he's Dec. 16th. And later work showed that there are likely no intermediate cases between A and B, only sequencing errors.

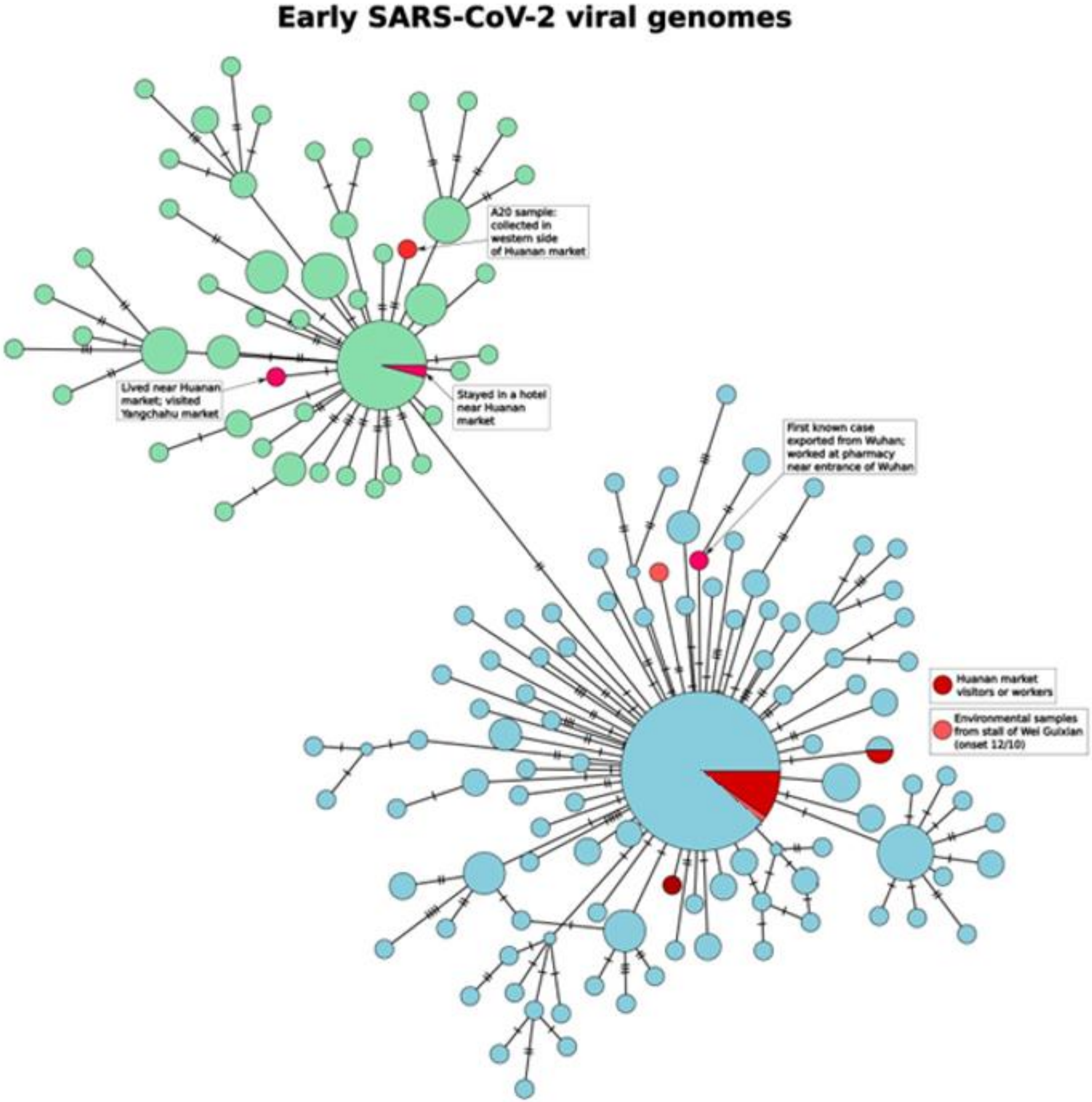
A modern version looks like this.

There are two early lineages in Wuhan.

The sick people at the market are at the root of the main genetic cluster (Lineage B).

The smaller cluster (Lineage A) only has 2 known December cases. Both lived/stayed very close to the market. One is at the root of the genetic cluster, the other is one mutation away.

The market is at the center of the pandemic, both geographically and genetically.



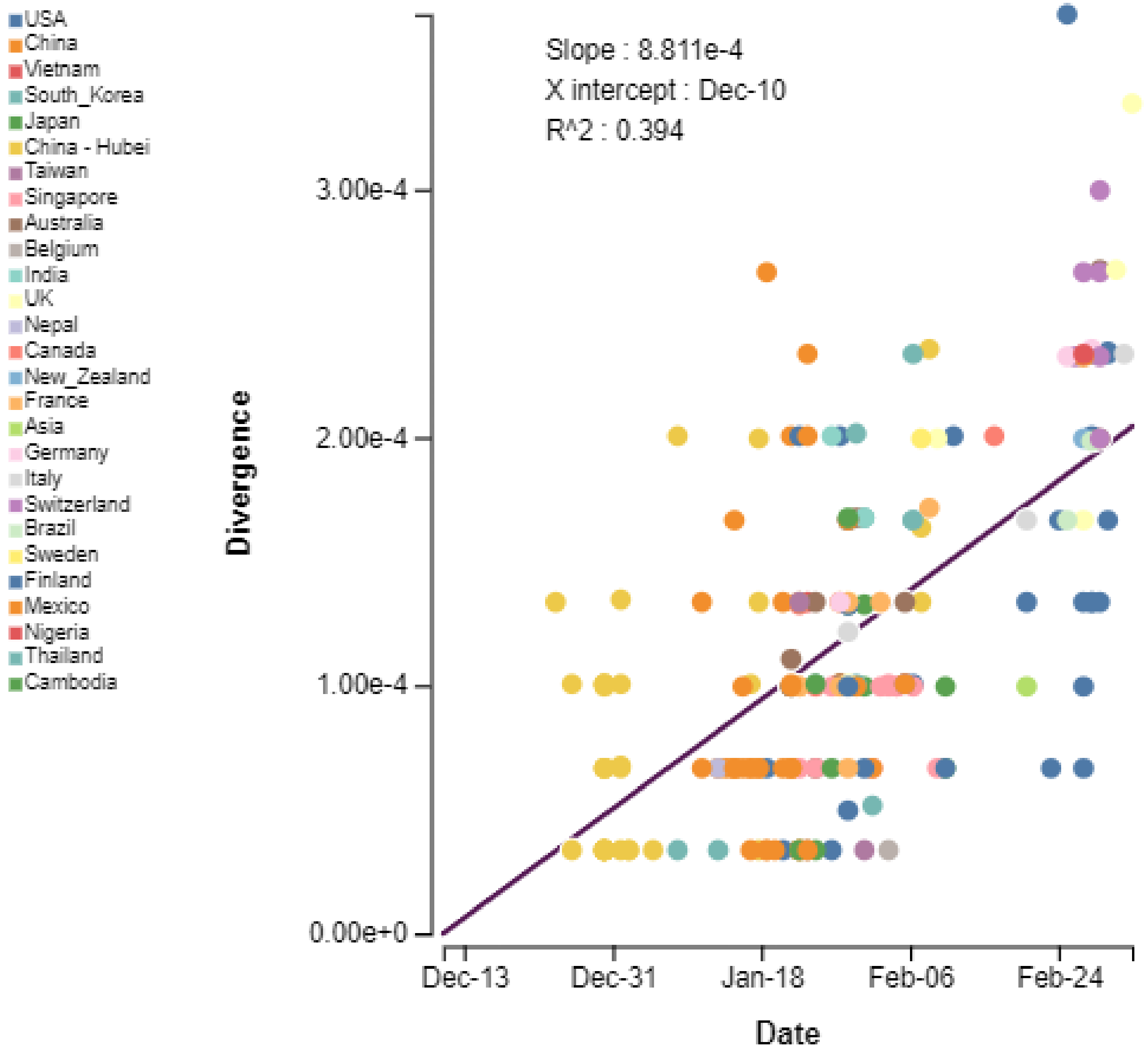
Early SARS-CoV-2 viral genomes

Genetics can also show when the pandemic started

When the virus started, every version was the same. Then it started to mutate.

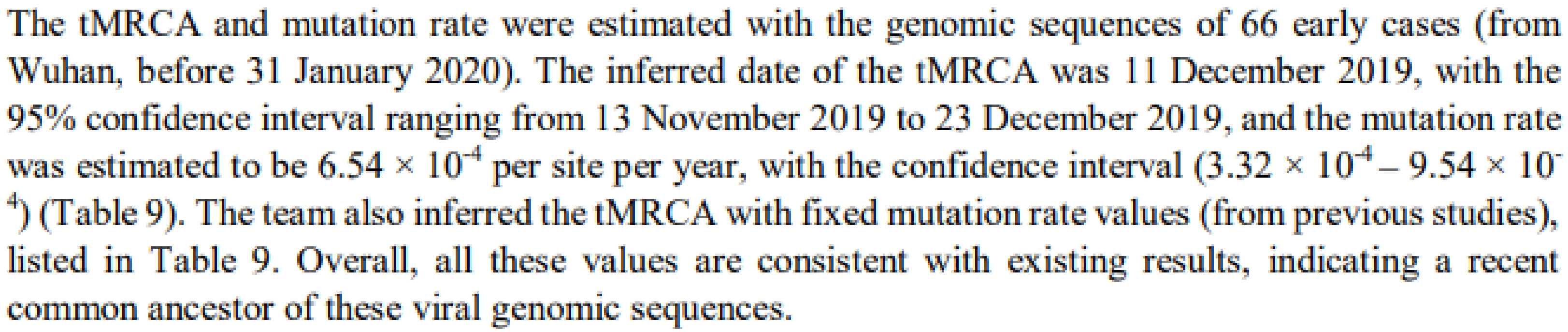
One way to visualize this is to graph out how many mutations each virus has over time.

Fit a line and work backwards to guess where that line hits zero. That's when the virus started.



Analysis by Andrew Rambaut, Mar. 6th, 2020

You can do a more complicated analysis, to come up with a similar answer:



The tMRCA and mutation rate were estimated with the genomic sequences of 66 early cases (from Wuhan, before 31 January 2020). The inferred date of the tMRCA was 11 December 2019, with the 95% confidence interval ranging from 13 November 2019 to 23 December 2019, and the mutation rate was estimated to be 6.54×10^{-4} per site per year, with the confidence interval ($3.32 \times 10^{-4} – 9.54 \times 10^{-4}$) (Table 9). The team also inferred the tMRCA with fixed mutation rate values (from previous studies), listed in Table 9. Overall, all these values are consistent with existing results, indicating a recent common ancestor of these viral genomic sequences.

The answer is only approximate, there's some range of uncertainty:

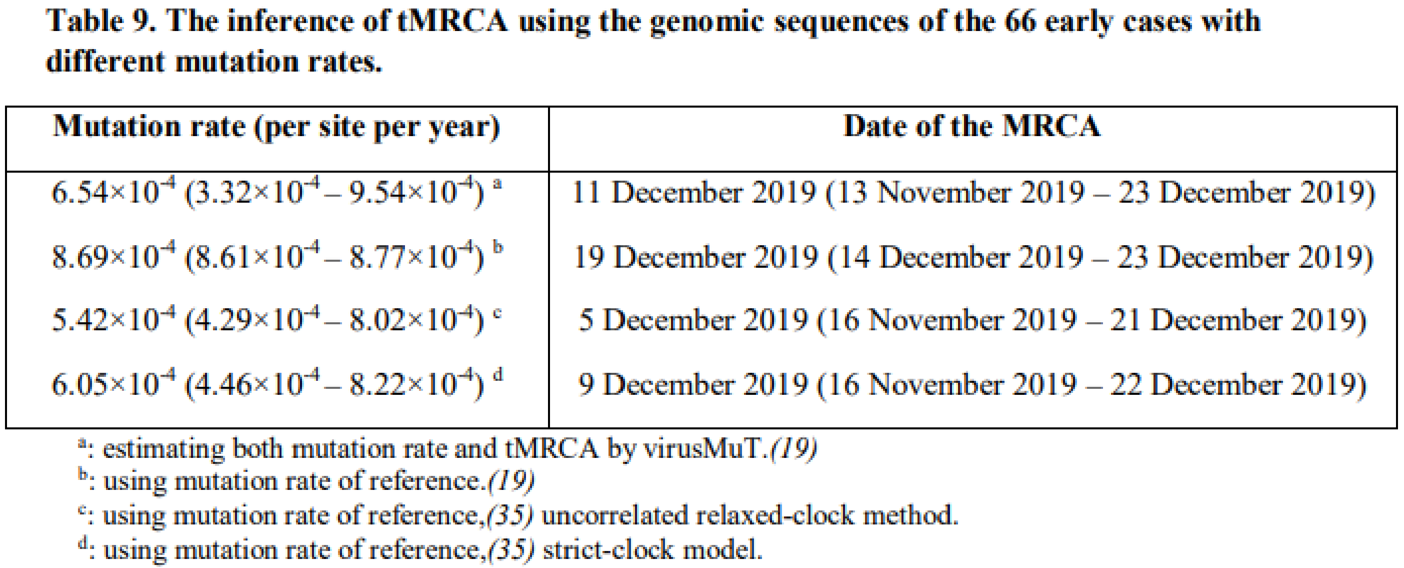


Table 9. The inference of tMRCA using the genomic sequences of the 66 early cases with different mutation rates.

Mutation rate (per site per year)	Date of the MRCA
6.54×10^{-4} ($3.32\times10^{-4} – 9.54\times10^{-4}$) [a]	11 December 2019 (13 November 2019 – 23 December 2019)
8.69×10^{-4} ($8.61\times10^{-4} – 8.77\times10^{-4}$) [b]	19 December 2019 (14 December 2019 – 23 December 2019)
5.42×10^{-4} ($4.29\times10^{-4} – 8.02\times10^{-4}$) [c]	5 December 2019 (16 November 2019 – 21 December 2019)
6.05×10^{-4} ($4.46\times10^{-4} – 8.22\times10^{-4}$) [d]	9 December 2019 (16 November 2019 – 22 December 2019)

[a]: estimating both mutation rate and tMRCA by virusMuT.*(19)*
[b]: using mutation rate of reference.*(19)*
[c]: using mutation rate of reference,*(35)* uncorrelated relaxed-clock method.
[d]: using mutation rate of reference,*(35)* strict-clock model.

Quotes from the
WHO report, page 79

The origin date is similar, whether you use genomes from the market, from Wuhan, or from around the world.

If Wuhan patients were undersampled or hidden by China, there would be an increase in genetic diversity once the virus got outside of China. They couldn't hide that.

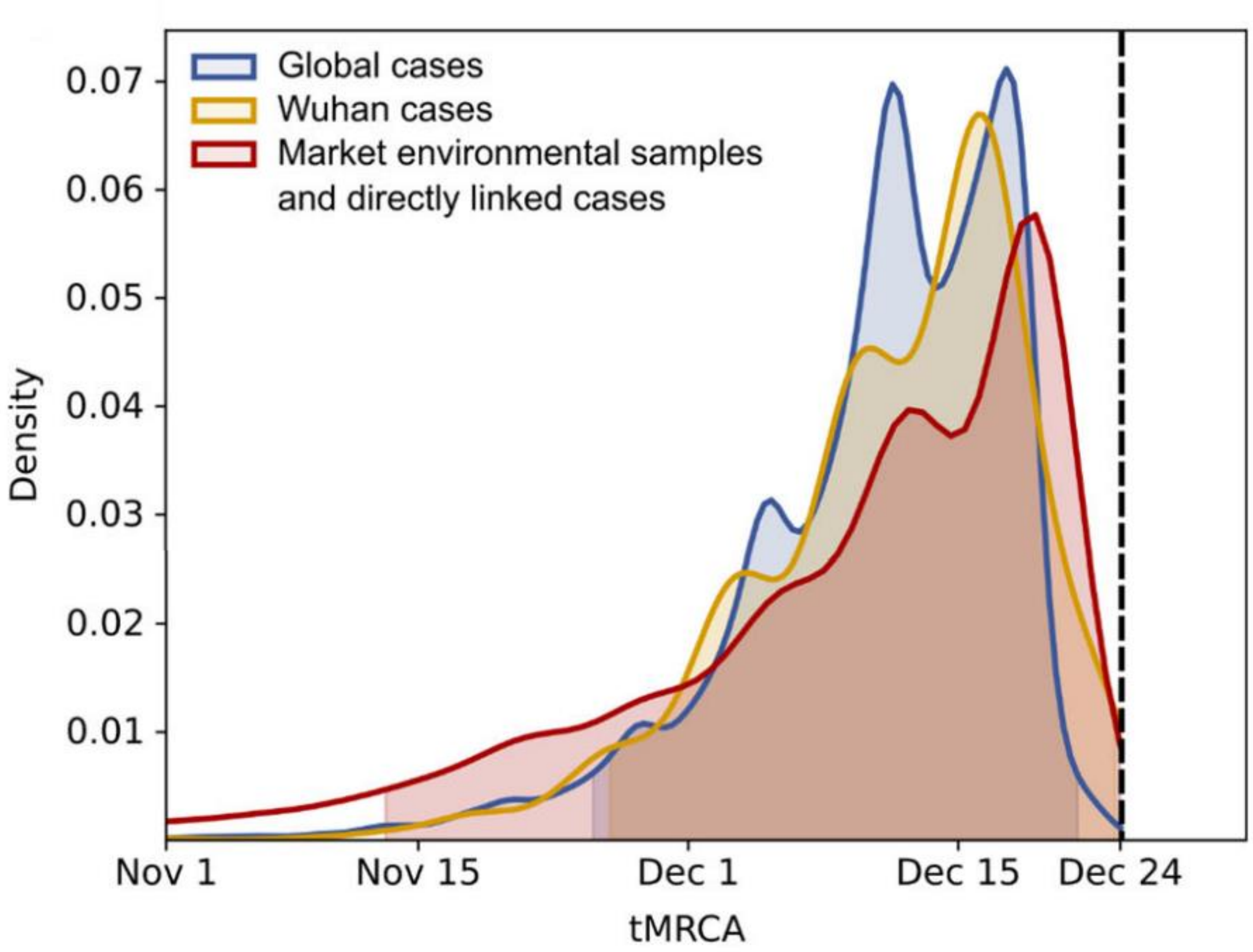


Figure [from Crits Christoph et al, 2023](#)

The earliest case can come earlier than the Most Recent Common Ancestor
But it’s hard for the virus to remain at low numbers for long without spreading widely or going extinct.

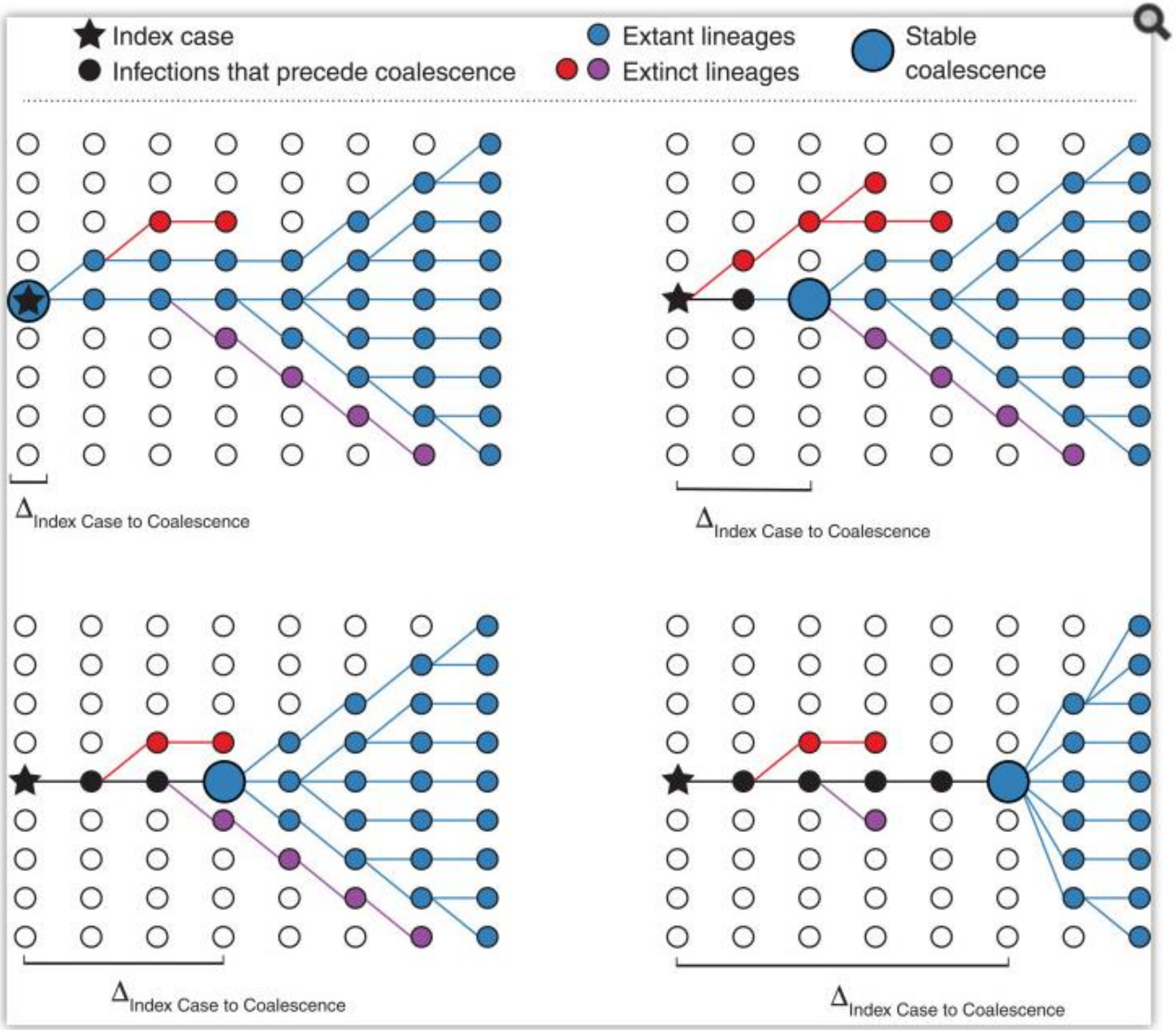
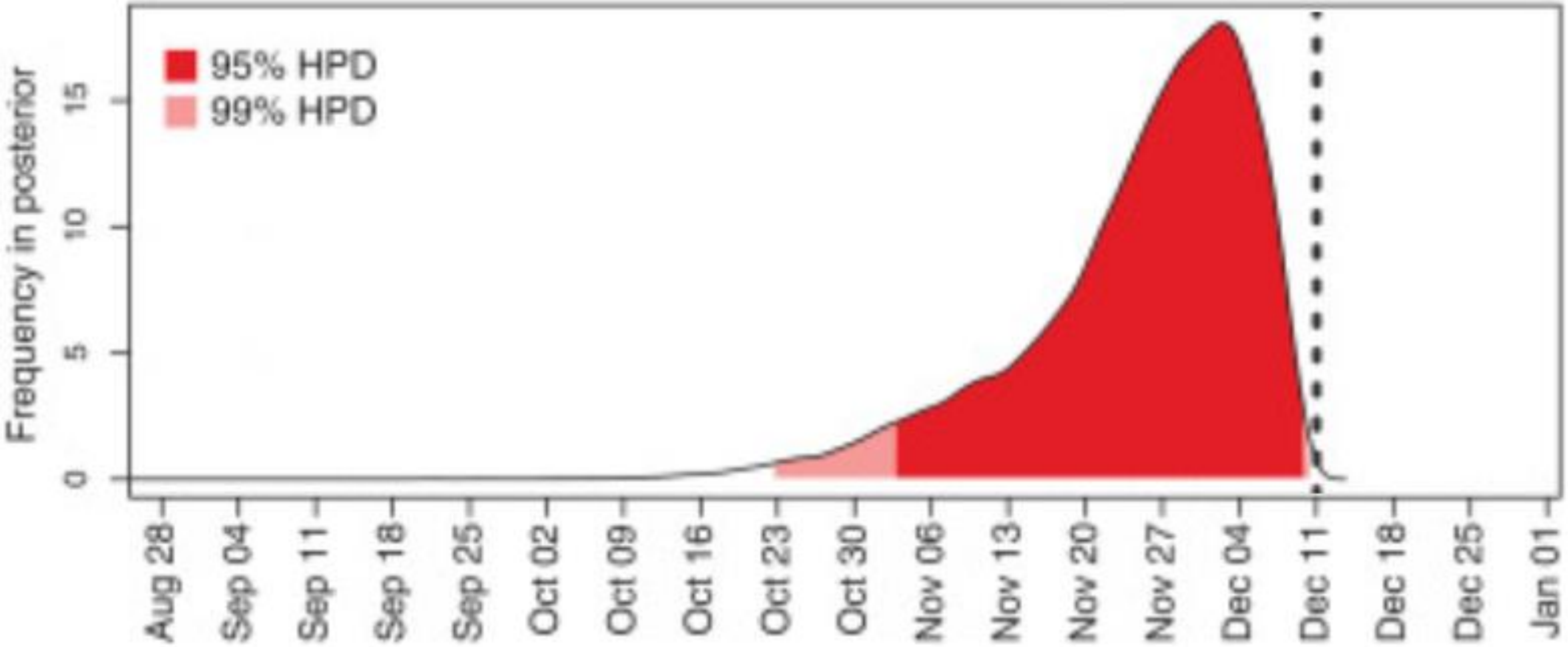


Figure from Pekar et al, 2021

Pekar et al 2021 made a model to predict the earliest case:



Using December 10th as the first ascertained case makes it most likely that the first case is late November or early December.

These models rule out an August or September origin and make October very unlikely.

Pekar et al, 2022 split the data into two lineages, and showed growth in diversity for both:

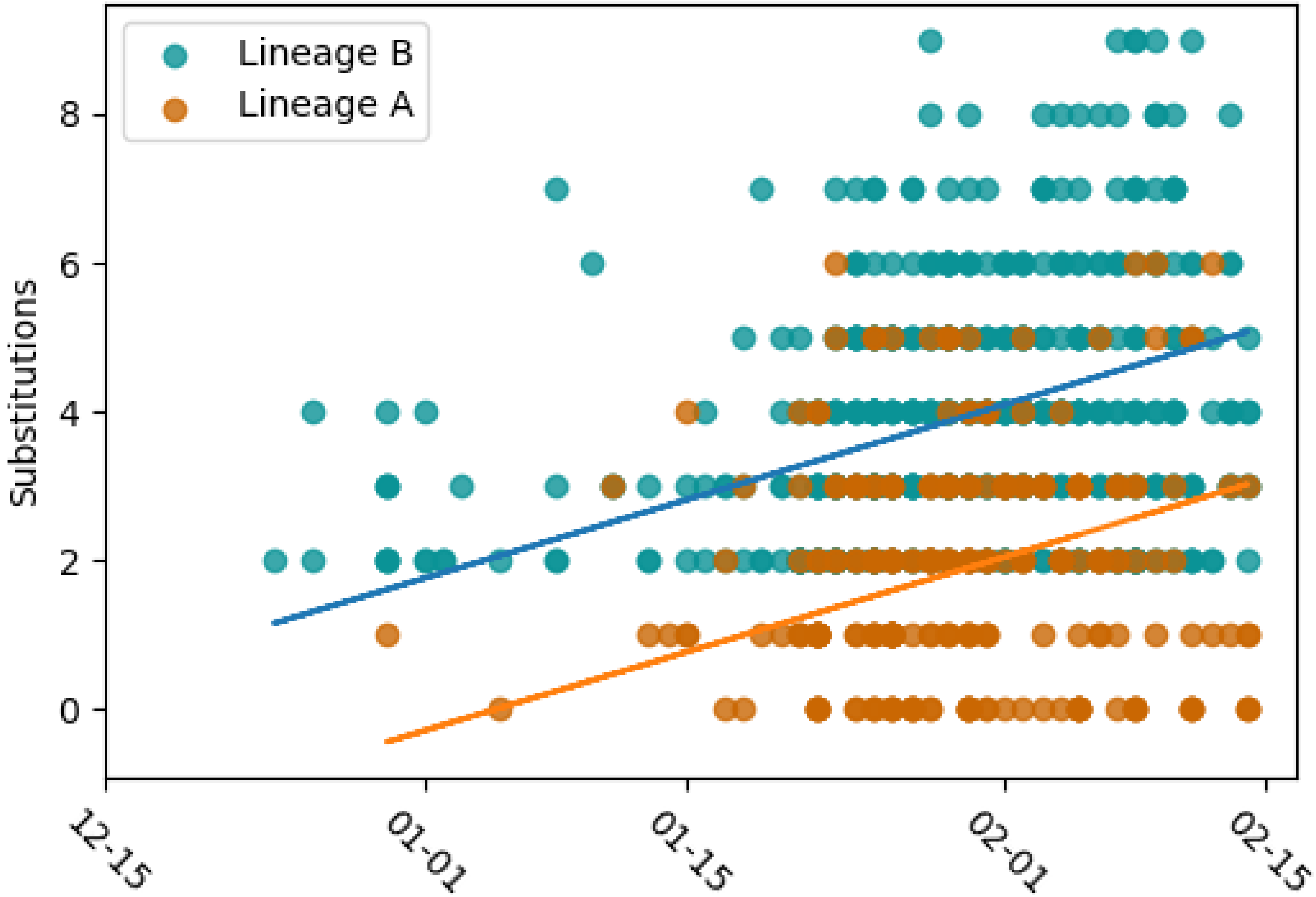
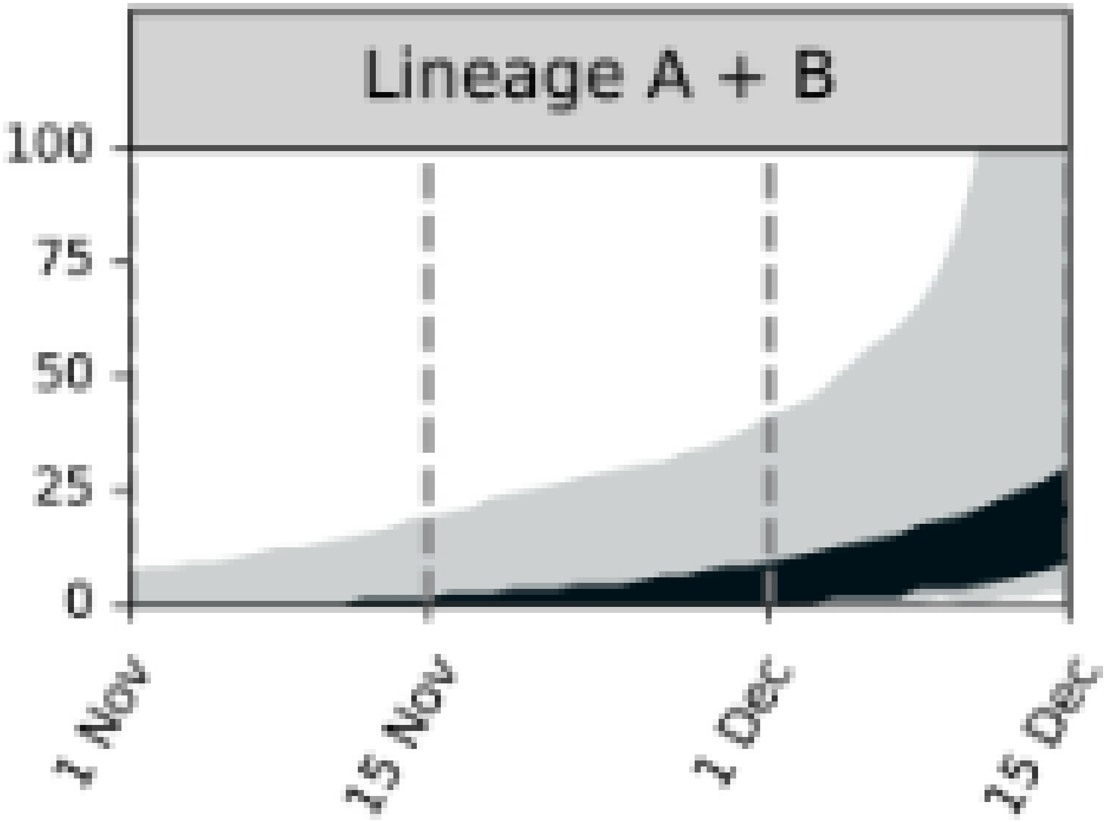


Figure S20. Substitution counts of SARS-CoV-2 genomes through 14 February 2020 from the root of the maximum likelihood tree when rooted on lineage A (Fig. S19). The plotted lines have a slope of 27.51 substitutions/year, are fit to their respective lineages, and are separated by 2.04 substitutions, showcasing the greater divergence of lineage B than lineage A when the tree is rooted on lineage A.

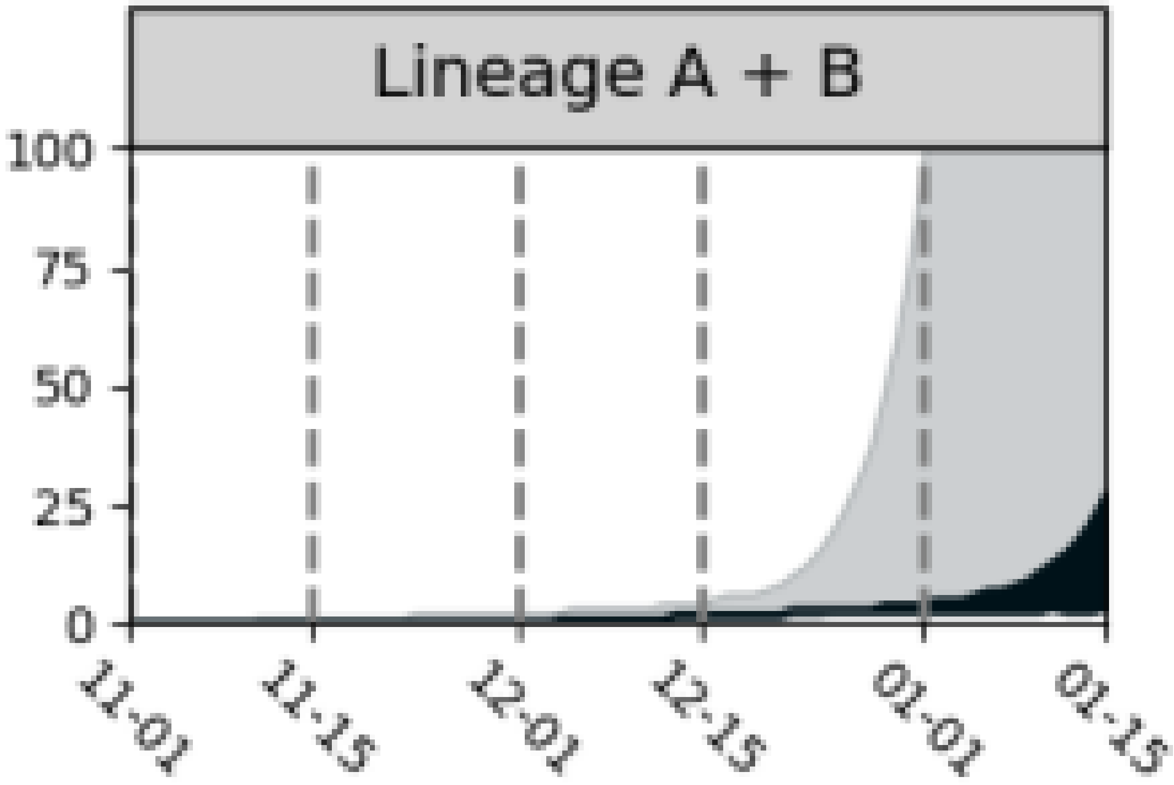
Genetic simulations also tell us roughly how many cases there were, at a given date

> “it is unlikely that there were any COVID-19–related hospitalizations before December because the simulated epidemics show a median of zero (95% HPD, 0 to 2) hospitalizations by 1 December 2019”

Predicted cases:



Predicted hospitalizations:



Figures 4 and S24 from Pekar et al 2022, light gray is 95% confidence interval, black is 50% confidence interval

In summary:

Genetic data confirms the same range of origin dates as case searches.

Lineage B started late November/early December.

Lineage A started later (Pekar says ~5 days)

There's no good evidence of November cases.

We should also not expect many November cases, from the viral diversity.

It's easy to rule out September origin theories.

November lab leak theories are still possible, but it's very unlikely that the virus leaked from the WIV and showed up only at the market.

The market is the center of the pandemic, both genetically and geographically.

Testing within the market

Testing within the market

900+ environmental samples, 73 positive
457 animal samples, all negative.
Live animals weren’t tested, animal sampling started 3 weeks later on a combination of frozen meat and stray animals.

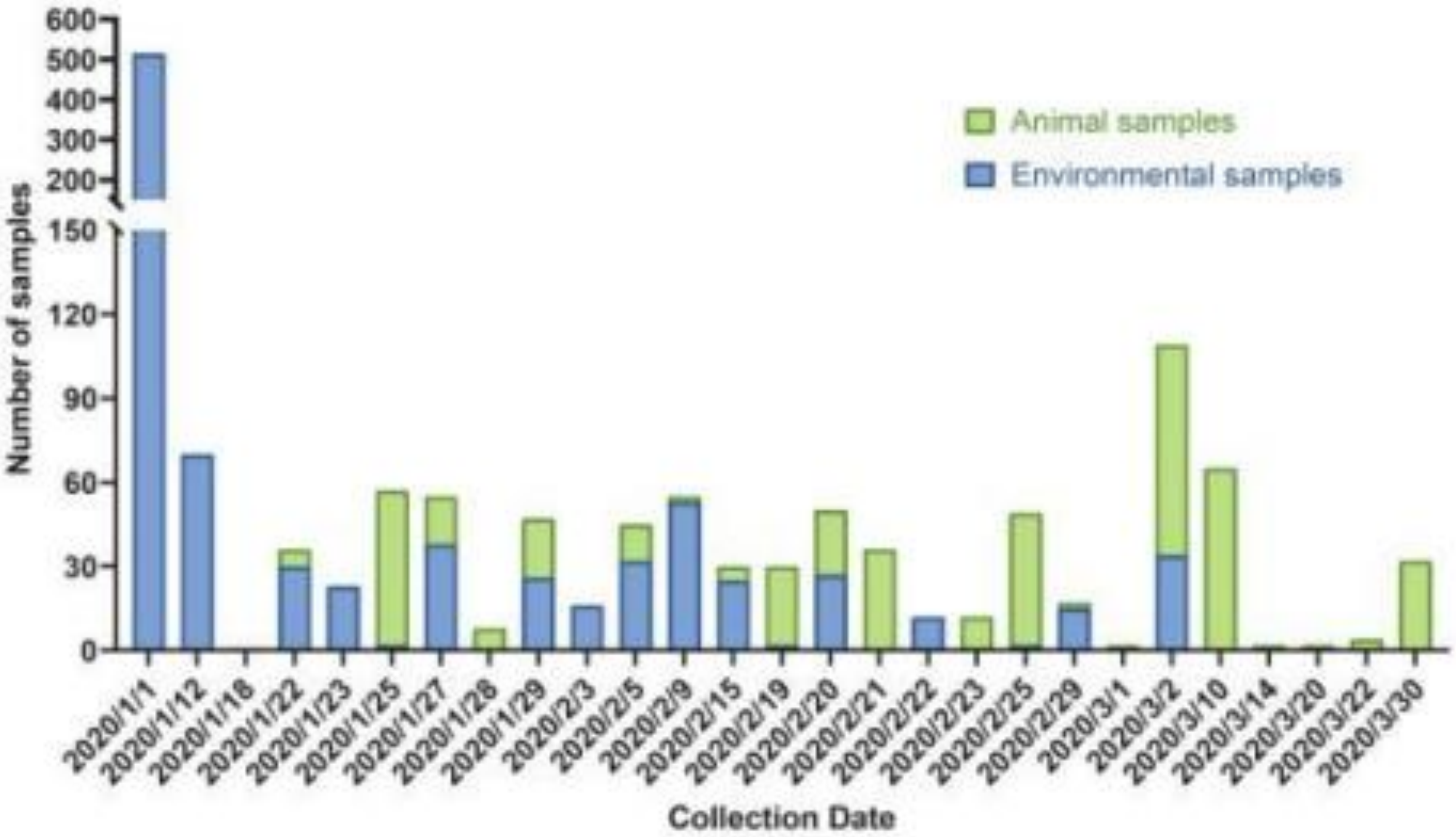


Figure from Gao et al., 2022

“The 457 animal samples included 188 individuals belonging to 18 species (with some stray animals sampled until March 30th). The sources of the samples include unsold goods kept in refrigerators and freezers in the stalls of HSM, and goods kept in warehouses and refrigerators related to the HSM. Samples from stray animals in the market were also collected, i.e. swab samples from 10 stray cats, 27 cat feces, one dog, one weasel, and 10 rats. All the 457 animal samples tested negative for SARS-CoV-2 nucleic acid, suggesting that the animal infections with SARS-CoV-2 might be rare in the market.”

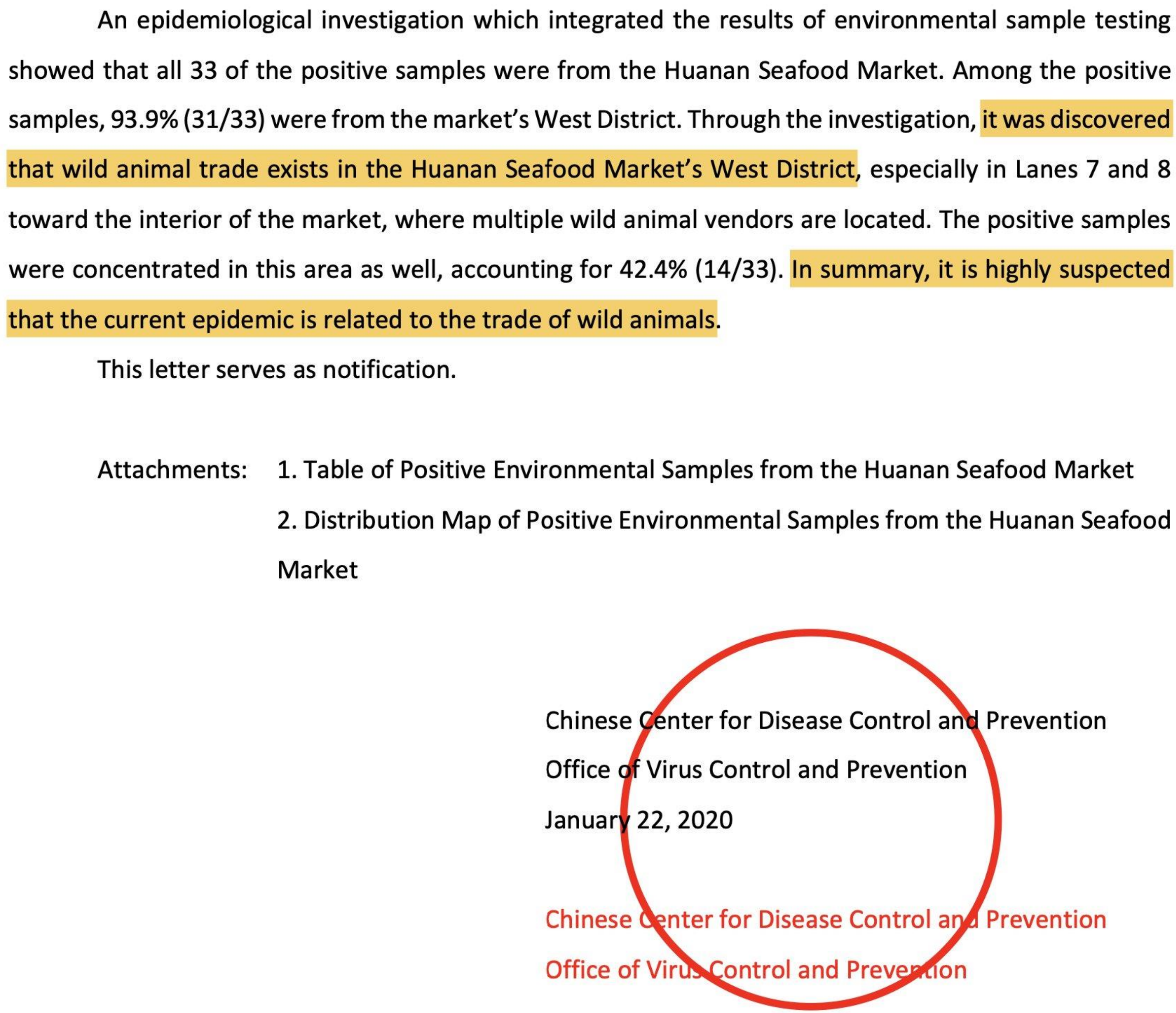
This data wasn't published in full until 2022 and 2023

We got a preview in the 2021 WHO report and in 2020 via a leak in the epoch times.

A news video from January 27th, 2020 described the number of samples and the fact that almost all of the positive samples came from the west side of the market where wildlife was sold.

The numbers and locations have been consistent since January, 2020.

China’s changing position on covid origins:



An epidemiological investigation which integrated the results of environmental sample testing showed that all 33 of the positive samples were from the Huanan Seafood Market. Among the positive samples, 93.9% (31/33) were from the market’s West District. Through the investigation, it was discovered that wild animal trade exists in the Huanan Seafood Market’s West District, especially in Lanes 7 and 8 toward the interior of the market, where multiple wild animal vendors are located. The positive samples were concentrated in this area as well, accounting for 42.4% (14/33). In summary, it is highly suspected that the current epidemic is related to the trade of wild animals.

This letter serves as notification.

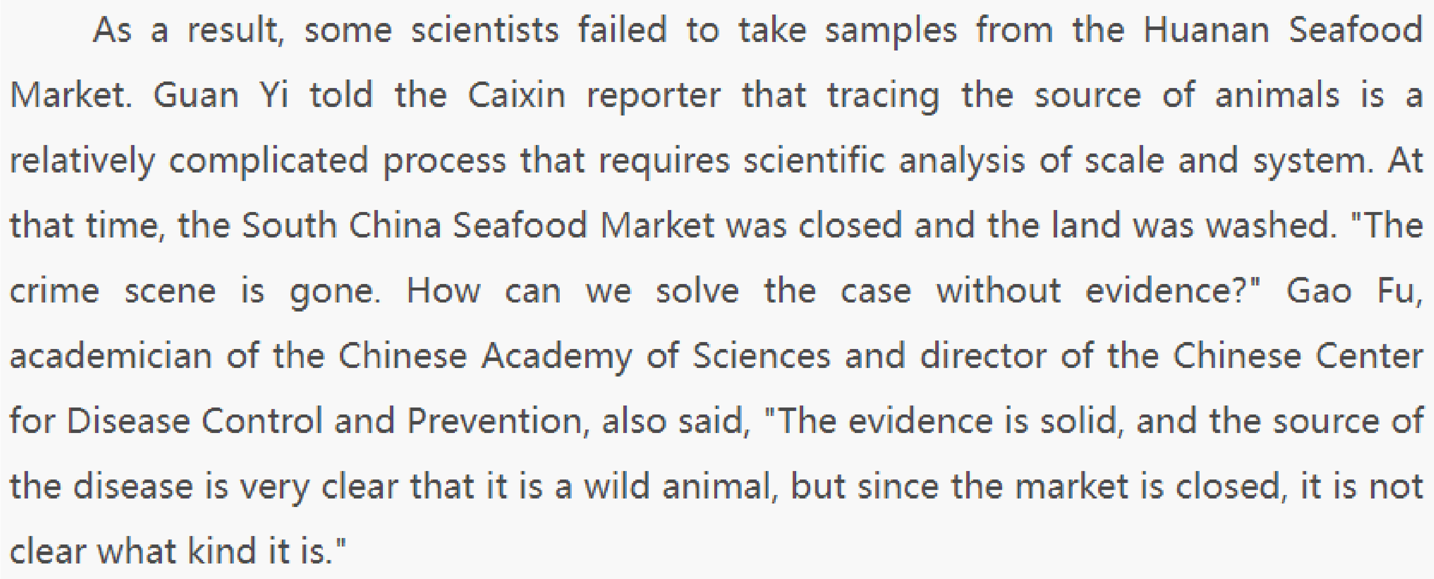
Attachments:
1. Table of Positive Environmental Samples from the Huanan Seafood Market
2. Distribution Map of Positive Environmental Samples from the Huanan Seafood Market

Chinese Center for Disease Control and Prevention
Office of Virus Control and Prevention
January 22, 2020

Chinese Center for Disease Control and Prevention
Office of Virus Control and Prevention

George Gao initially suspected bamboo rats as the host
1/20/2020: Zhong Nanshan also suspected bamboo rats or badgers.

George Gao on 2/1/2020: complains that market was cleaned before samples were taken



As a result, some scientists failed to take samples from the Huanan Seafood Market. Guan Yi told the Caixin reporter that tracing the source of animals is a relatively complicated process that requires scientific analysis of scale and system. At that time, the South China Seafood Market was closed and the land was washed. "The crime scene is gone. How can we solve the case without evidence?" Gao Fu, academician of the Chinese Academy of Sciences and director of the Chinese Center for Disease Control and Prevention, also said, "The evidence is solid, and the source of the disease is very clear that it is a wild animal, but since the market is closed, it is not clear what kind it is."

George Gao on 5/25/2020:

> "Maybe the earliest, we speculated that there may be seafood markets, but now it seems that the seafood market itself is also a victim unit, and the virus already existed before that."

February 2021, WHO report. China denies the sale of these animals:

> *"No illegal trade in wildlife has been found"*
>
> *"No verified reports of live mammals being sold around 2019 were found"*.

There are now 3 sides to this debate:

1. Most western virologists argue for a natural origin of Covid at the market.

2. Lab leak theorists think that Covid was created at the WIV.

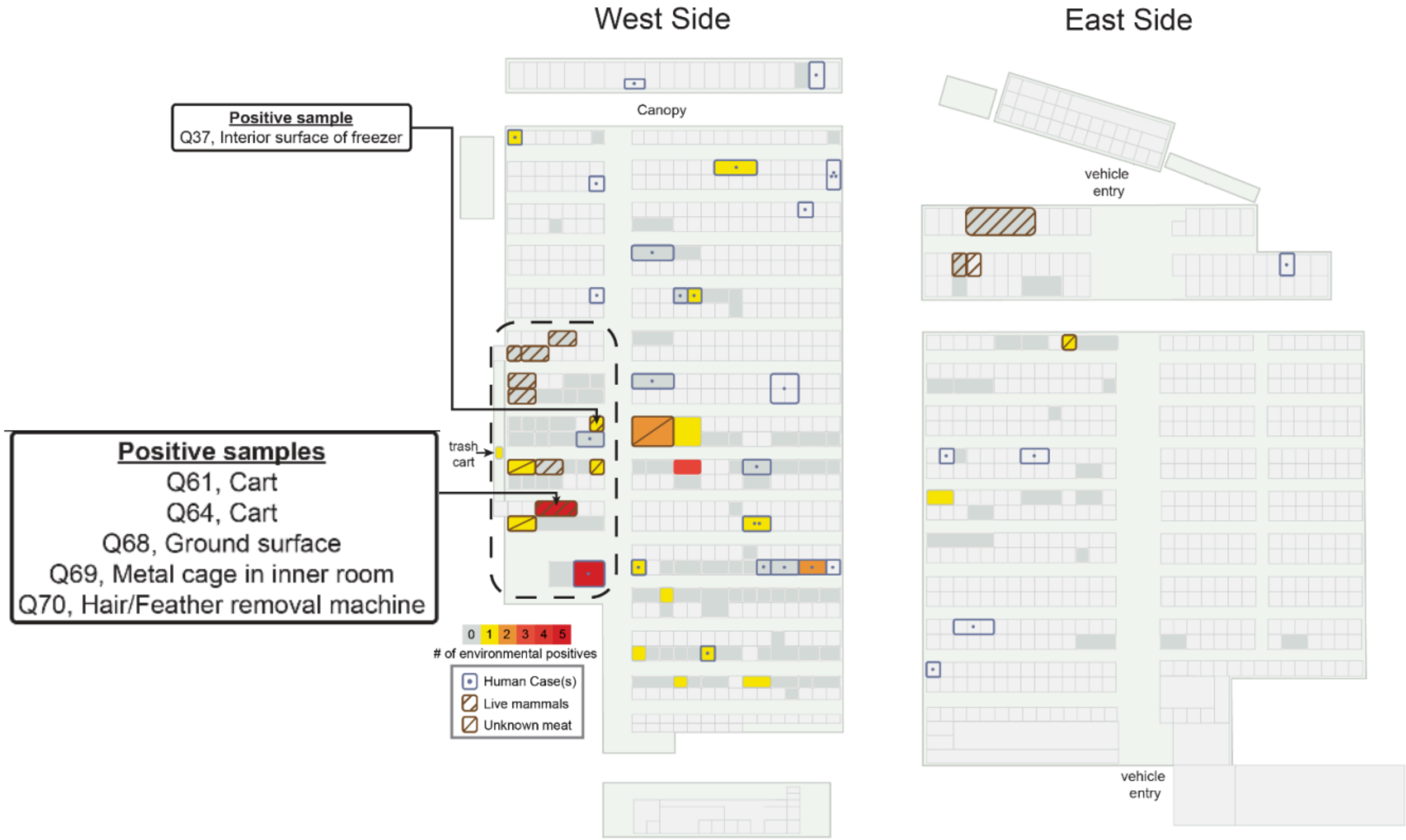
3. The Chinese government claims that Covid started somewhere outside of China.

We'll see a lot of lies told by Chinese authorities, in this discussion. China is not promoting the market theory to distract from a lab accident, they're denying both a market origin and a lab origin. They just don't want to be held accountable for covid.

Ongoing argument in the west between zoonotic origin and the lab leak theory probably benefits China, because it prevents any accountability.

Positive environmental samples were clustered in the southwest corner, where wild animals were sold.

Two shops selling wildlife tested positive: shop 6/29 and 8/25.
One of these shops had 5 positive samples, including one from a cage.

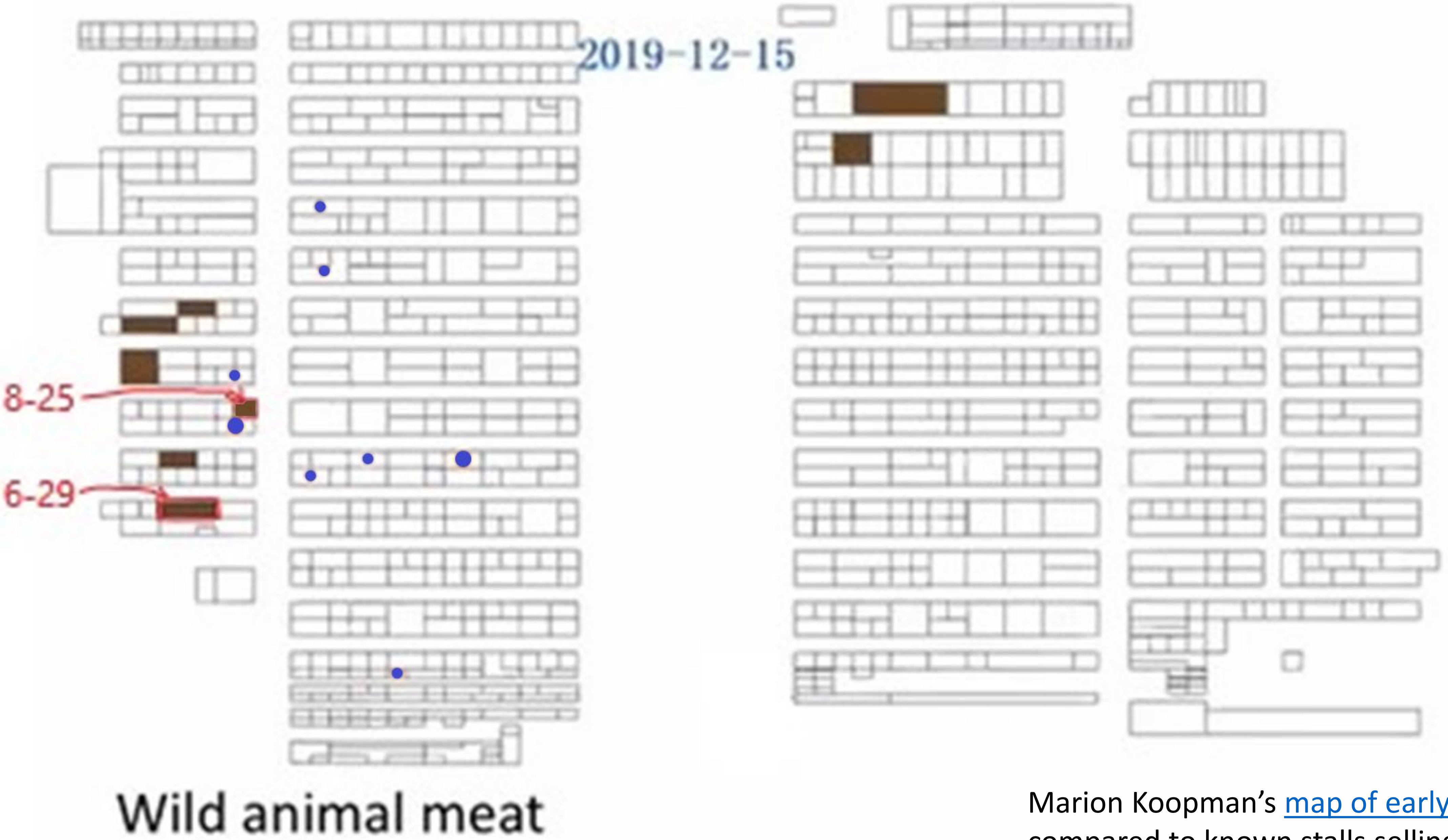


Positive sample
Q37, Interior surface of freezer

Positive samples
Q61, Cart
Q64, Cart
Q68, Ground surface
Q69, Metal cage in inner room
Q70, Hair/Feather removal machine

Environmental samples taken Jan 1st and Jan 12th, Image from Worobey et al, 2022

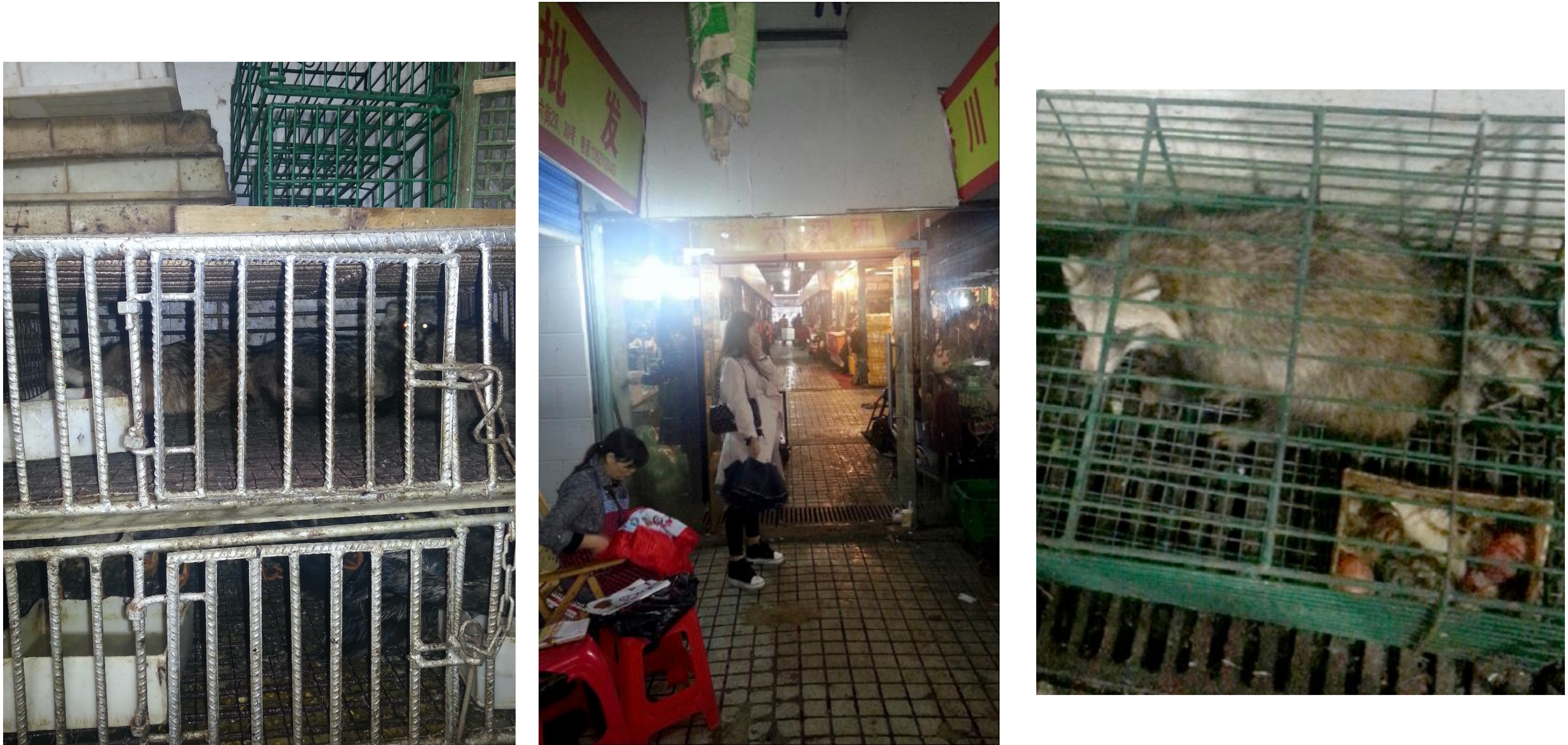
Many of the earliest known covid cases at the market worked close to these 2 suspicious shops:



Marion Koopman’s map of early cases, as compared to known stalls selling wild game.

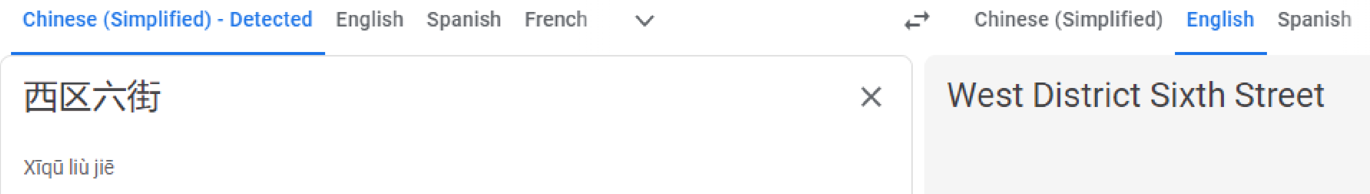
Eddie Holmes visited shop 6-29 in 2014 and photographed raccoon dogs:

Chinese colleagues informed him this was a likely place for a future pandemic to start.



How do we know Eddie’s picture is from the same shop?

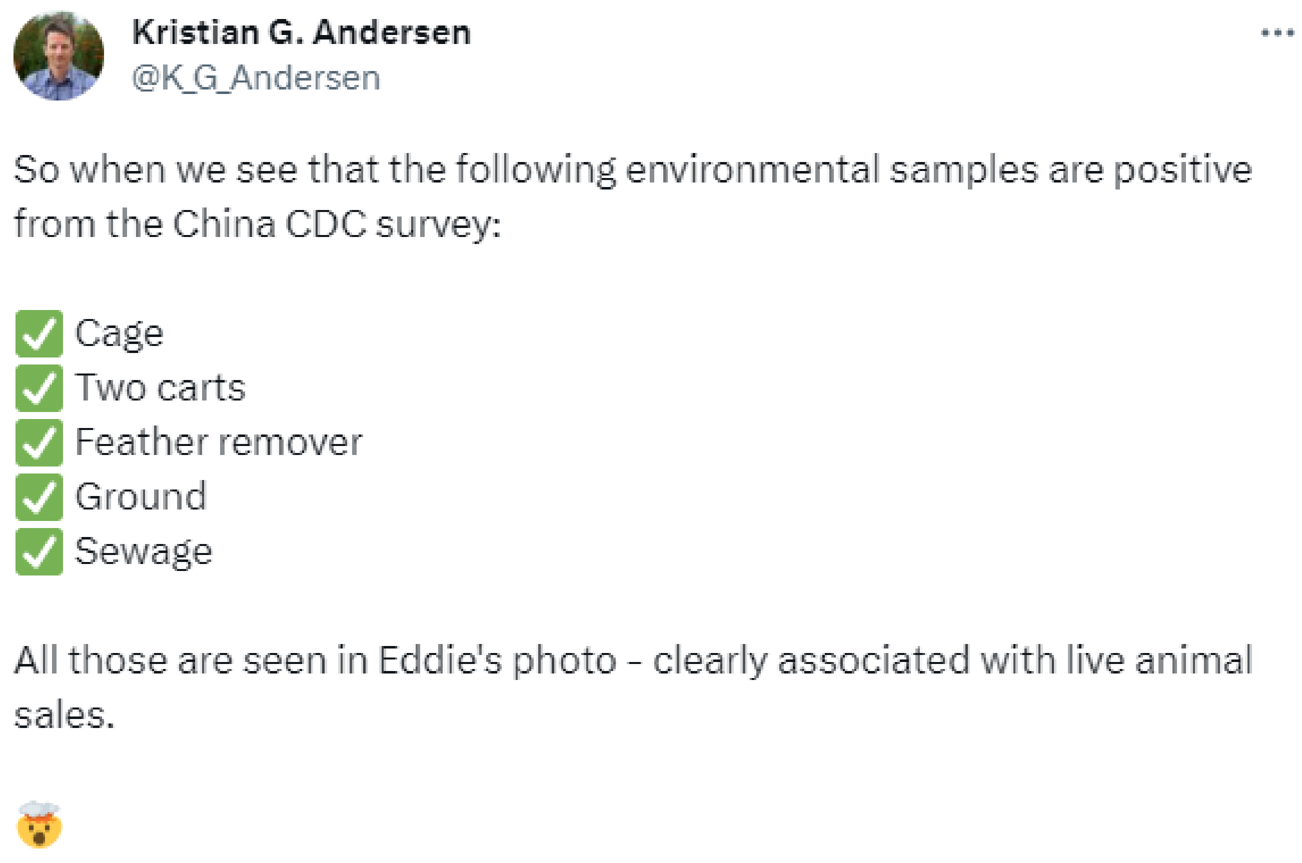
street 6, shop 29, on the western side of the market.
Signs in the photo confirm this.



西区六街

Xīqū liù jiē

West District Sixth Street



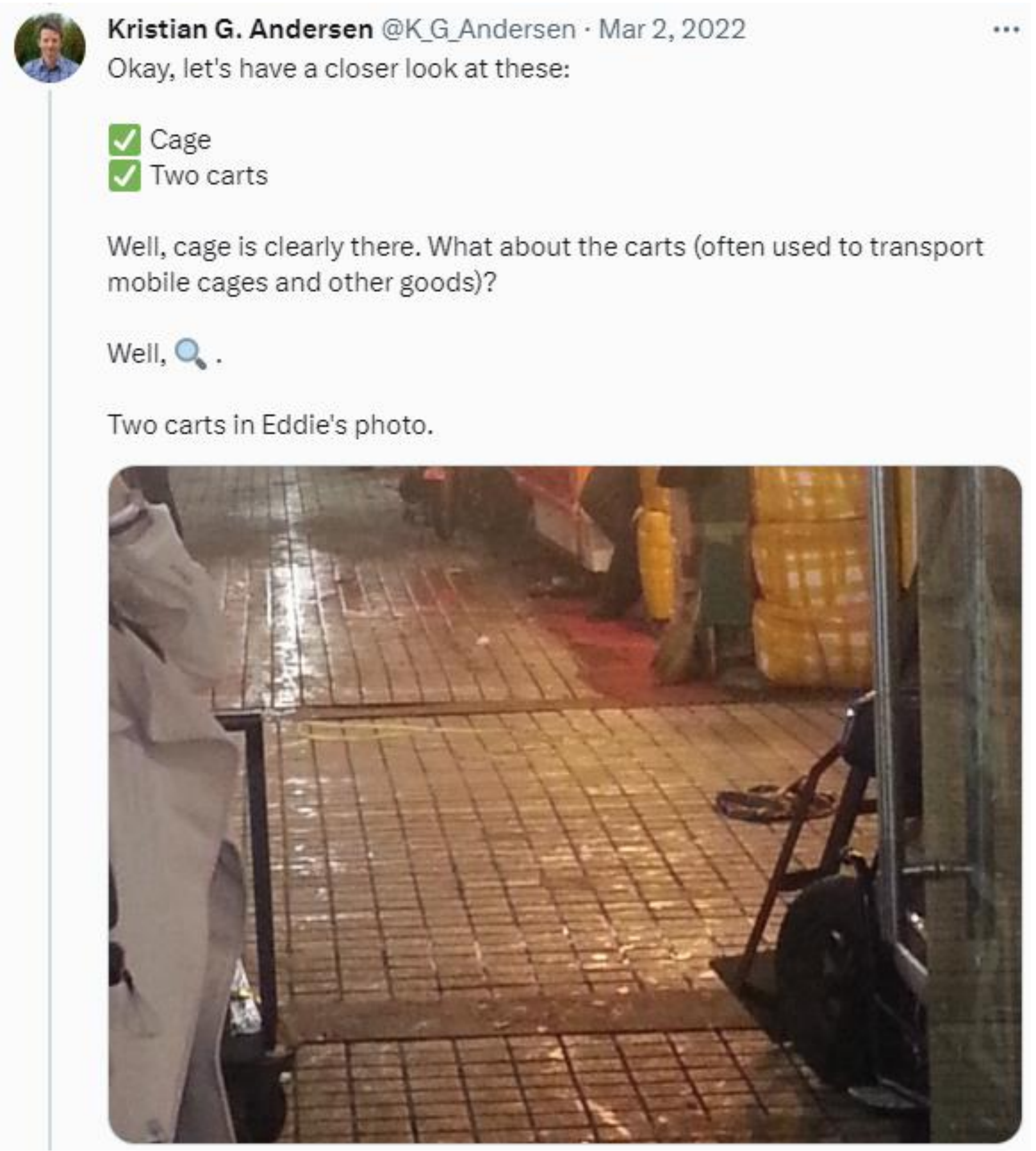
Kristian G. Andersen
@K_G_Andersen

So when we see that the following environmental samples are positive from the China CDC survey:

✅ Cage
✅ Two carts
✅ Feather remover
✅ Ground
✅ Sewage

All those are seen in Eddie's photo - clearly associated with live animal sales.

🤯



Kristian G. Andersen @K_G_Andersen · Mar 2, 2022

Okay, let's have a closer look at these:

✅ Cage
✅ Two carts

Well, cage is clearly there. What about the carts (often used to transport mobile cages and other goods)?

Well, 🔍.

Two carts in Eddie's photo.

Kristian G. Andersen @K_G_Andersen · Mar 2, 2022

What about:

✅ Feather remover

Well, 🔍 .

The raccoon dogs in Eddie's photo sat on top of birds.

Kristian G. Andersen @K_G_Andersen · Mar 2, 2022

What about:

✅ Sewage outside shop

Well, 🔍 .

The raccoon dogs in mobile cages in Eddie's photo sat on top of the sewage system.

There was drainage in front of each of the shops, but that was unrelated to the bathrooms

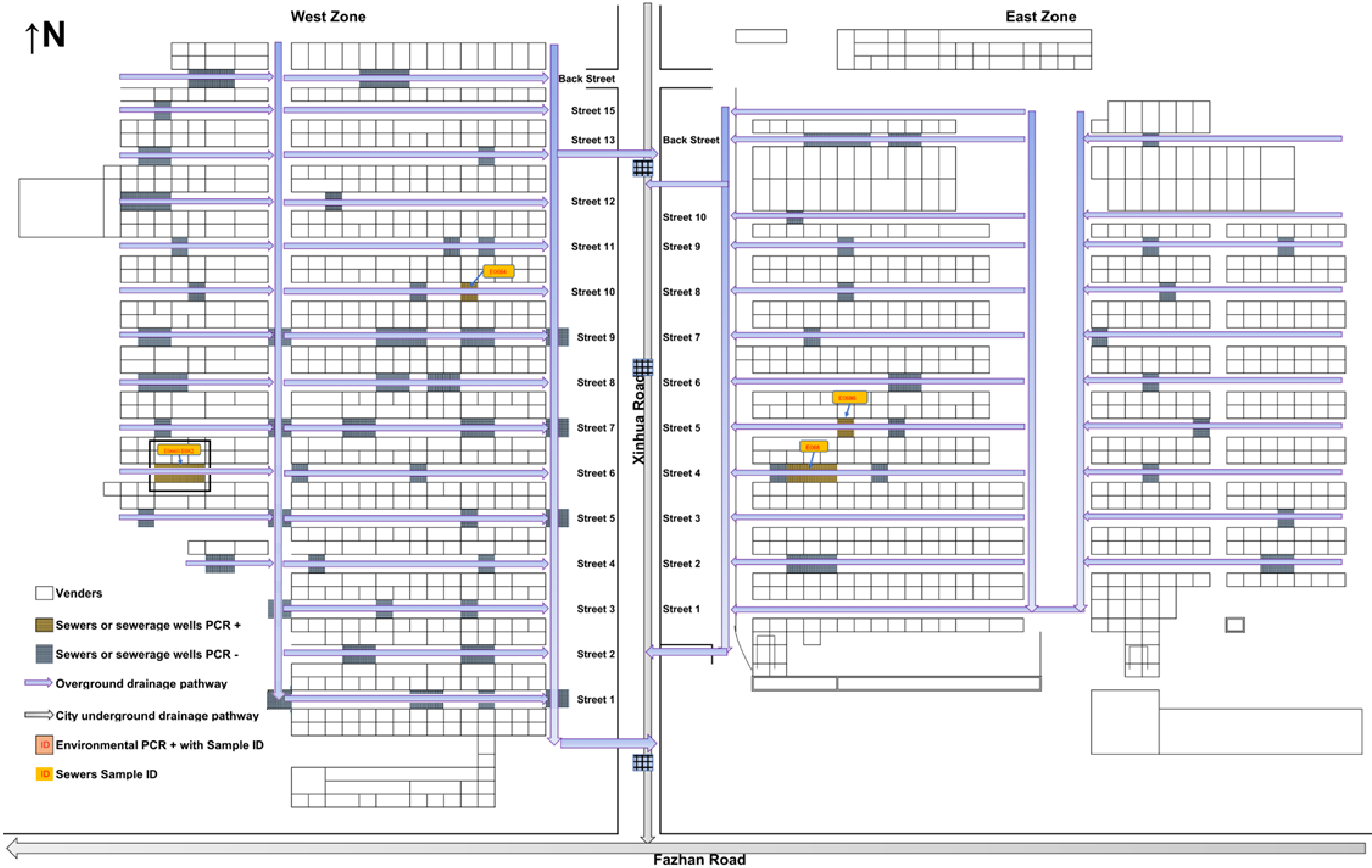
sewage, *not* for the toilets

Drain sampling in the market points to shop 6/29

Jan 27th - 29th

4 out of 60 drains test positive.

One is shop 6-29.

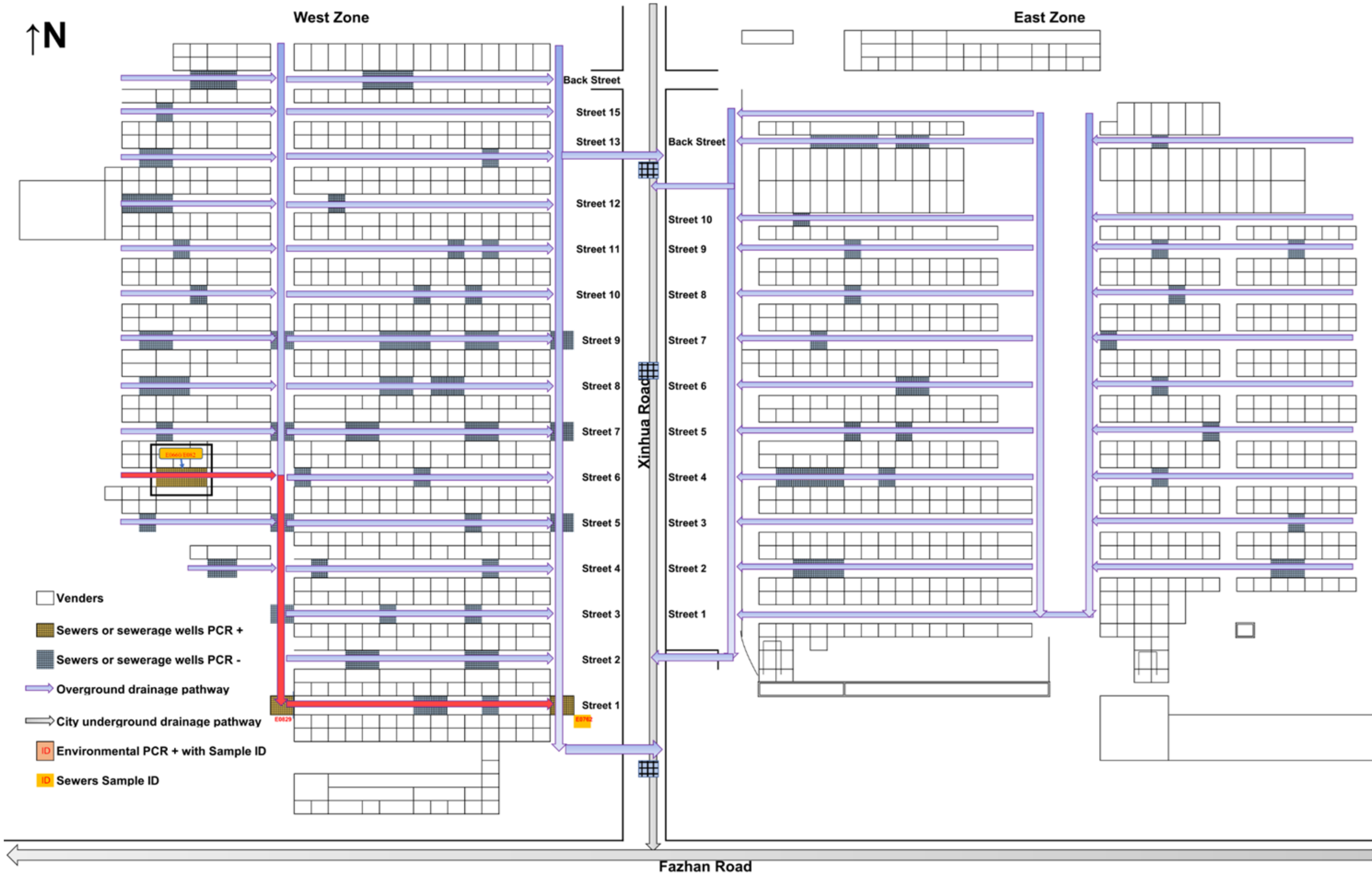


Drain sampling in the market points to shop 6/29

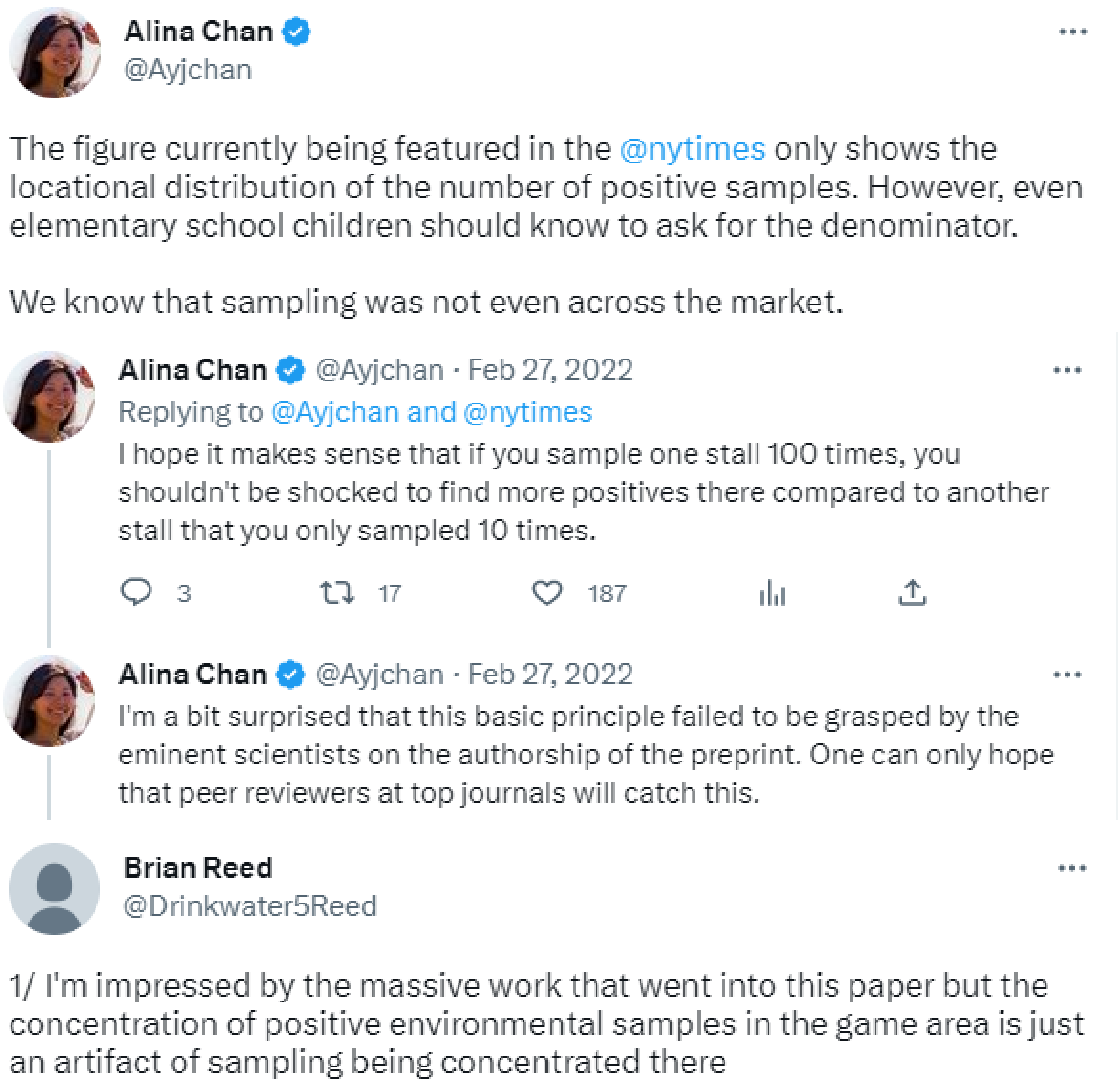
Feb 9th - 15th

3 of 17 drains test positive: only shop 6-29 drain and two places downstream.

(these two downstream drains were not sampled in January)



Lab leak responses: either it's sampling bias or the bathrooms are to blame


Alina Chan
@Ayjchan

The figure currently being featured in the @nytimes only shows the locational distribution of the number of positive samples. However, even elementary school children should know to ask for the denominator.

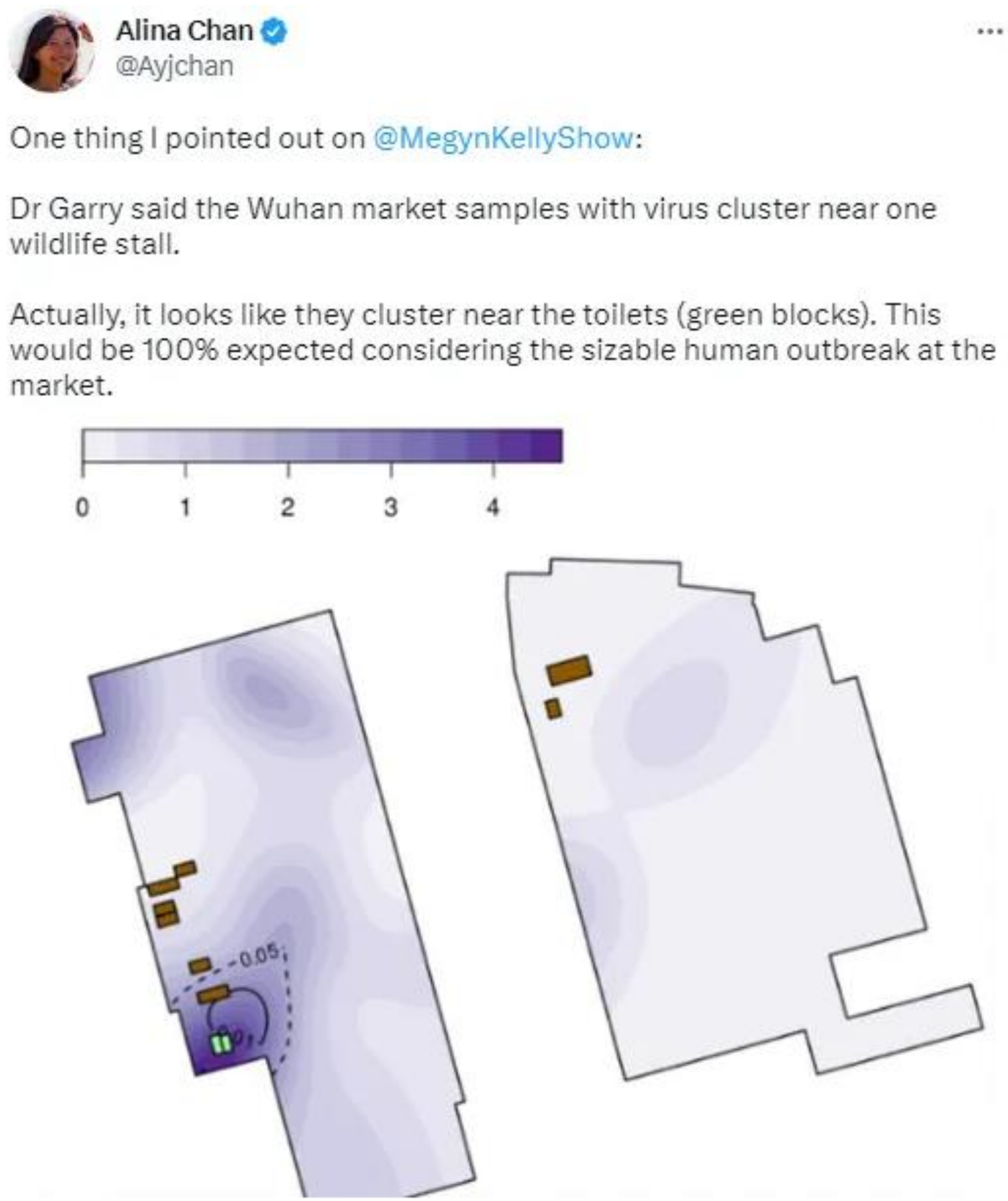
We know that sampling was not even across the market.

Alina Chan @Ayjchan · Feb 27, 2022
Replying to @Ayjchan and @nytimes
I hope it makes sense that if you sample one stall 100 times, you shouldn't be shocked to find more positives there compared to another stall that you only sampled 10 times.

Alina Chan @Ayjchan · Feb 27, 2022
I'm a bit surprised that this basic principle failed to be grasped by the eminent scientists on the authorship of the preprint. One can only hope that peer reviewers at top journals will catch this.

Brian Reed
@Drinkwater5Reed

1/ I'm impressed by the massive work that went into this paper but the concentration of positive environmental samples in the game area is just an artifact of sampling being concentrated there


Alina Chan
@Ayjchan

One thing I pointed out on @MegynKellyShow:

Dr Garry said the Wuhan market samples with virus cluster near one wildlife stall.

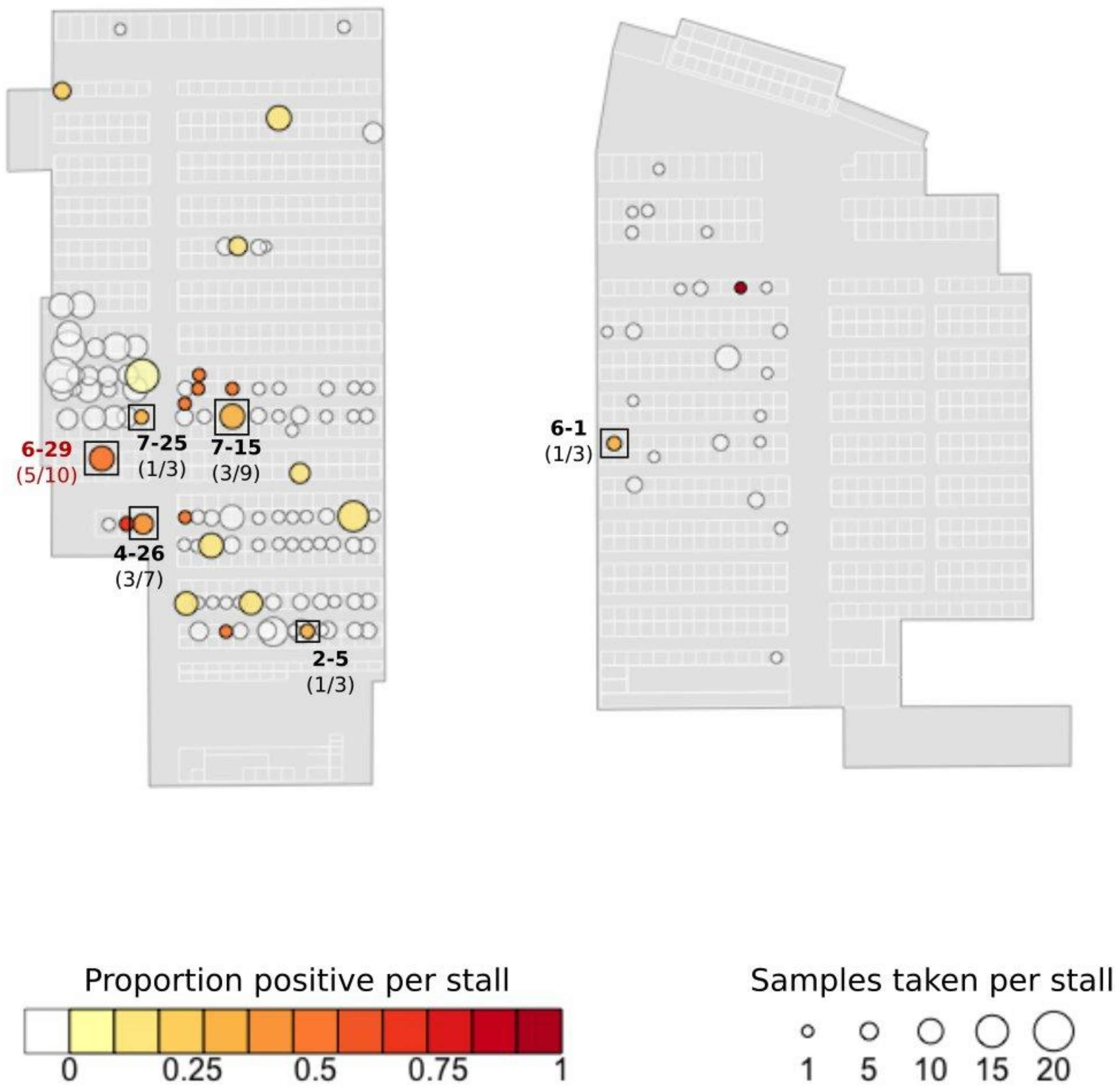
Actually, it looks like they cluster near the toilets (green blocks). This would be 100% expected considering the sizable human outbreak at the market.

First off, those theories contradict each other.

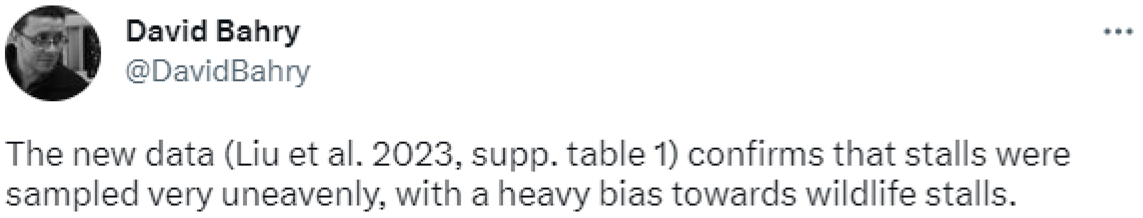
If it’s sampling bias, then the toilets theory also fails.

Second, Sampling bias was ruled out in 2023, when we got data on the total number of samples, and could get a ratio.

The raccoon dog shop still has an abnormally high positive ratio.


SARS-CoV-2 sampling from January 1 to January 12, 2020

Then it becomes a zombie talking point – disproven but not dead.



David Bahry
@DavidBahry

The new data (Liu et al. 2023, supp. table 1) confirms that stalls were sampled very uneavenly, with a heavy bias towards wildlife stalls.

Alina Chan
@Ayjchan

Of 1380 samples collected from the Huanan market by the Chinese CDC investigators, ~220 were from the raccoon dog stall and its associated warehouse space.

That means ~16% of the sampling targeted that wildlife stall.
chinaxiv.org/abs/202303.103...

8:25 AM · Apr 3, 2023 · 21.6K Views

←It's not obvious where she came up with 220.

There were only 10 samples taken when they found the 5 positives.

To get 220, she's including frozen animal samples, which were taken later, mostly from this shop.

Those animal samples were taken precisely because that shop tested positive on the first round.

China focused testing of animals on shop 6-29:

Animals tested per shop:
6-29: 182
10-31: 72
9-37: 20
9-38: 18
9-31: 12
9-X: 12
9-34: 11
8-36: 9
7-30: 5
Other/stray animals: 112

Testing was done on 1/25/2020 to 3/10/2020.

Why did they focus on each of these shops?
6-29: raccoon dog shop with lots of positive samples.
8-25: hedgehog shop with lots of positive samples
10-31: unclear, no positive samples from this shop.
An early theory said snakes were the host species.
The shop owner also had a farm that raised
raccoon dogs, civets, hedgehogs, rabbits, wild boar.

Warehouse samples tested per shop:
8-25: 12 (5 positives)
6-29: 2 (0 positives)

Shop 6-29 animal samples tested:
24 snake
5 bamboo rat samples (from <= 3 animals)
85 rabbit
65 hedgehog samples (from ~14 animals)
3 other

Shop 10-31 animal samples tested:
53 snake
6 stray cat
5 salamander
4 rat
2 hedgehog
2 fish

We have proof that shop sold raccoon dogs in 2014. What about 2019?
March 2021: China denies the sale of wildlife at the market, during the WHO report.
June 2021: Chinese study on tick sampling shows the market sold raccoon dogs and civets, prior to the pandemic.

Photos from the market taken December 3, 2019 (posted on Weibo):

Animals which were sold at the market vs. animals which were tested:

Species (susceptibility*)	Family (susceptibility*)	Order (susceptibility*)	Observed at Huanan market, November 2019
Raccoon dog (*Nyctereutes procyonoides*) (Y)	Canidae (Y)	Carnivora (Y)	Y
Amur hedgehog (*Erinaceus amurensis*)	Erinaceidae	Eulipotyphla	Y
Hog badger (*Arctonyx albogularis*) (Y)	Mustelidae (Y)	Carnivora (Y)	Y
Asian badger (*Meles leucurus*)	Mustelidae (Y)	Carnivora (Y)	Y
Chinese hare (*Lepus sinensis*)	Leporidae (Y)	Lagomorpha (Y)	Y
Chinese bamboo rat (*Rhizomys sinensis*) (Y)	Spalacidae (Y)	Rodentia (Y)	Y
Malayan porcupine (*Hystrix brachyura*)	Hystricidae	Rodentia (Y)	Y
Chinese muntjac (*Muntiacus reevesi*)	Cervidae (Y)	Artiodactyla (Y)	Y
Marmot (*Marmota himalayana*)	Sciuridae	Rodentia (Y)	Y
Red fox (*Vulpes vulpes*) (Y)	Canidae (Y)	Carnivora (Y)	Y

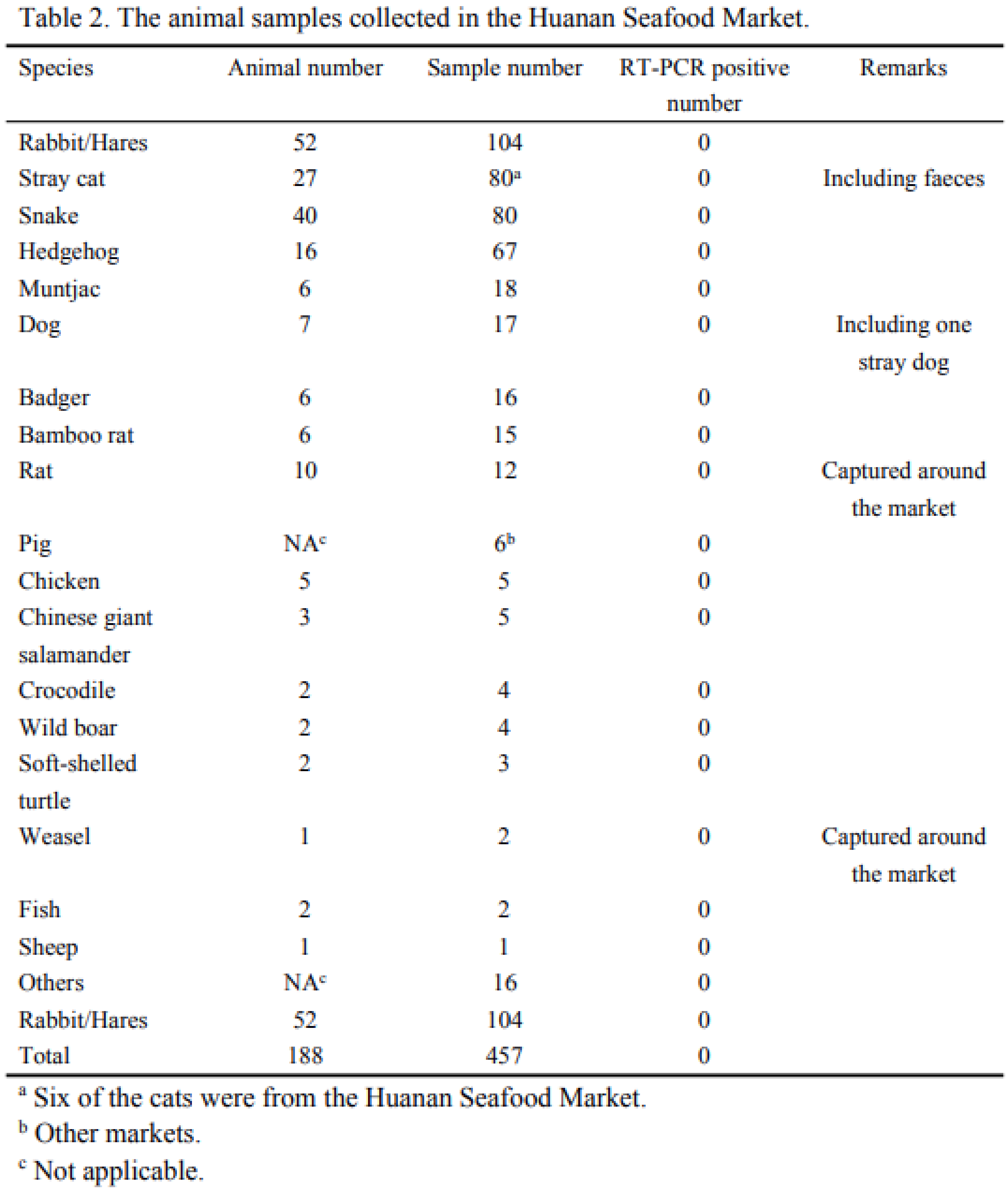


Table 2. The animal samples collected in the Huanan Seafood Market.

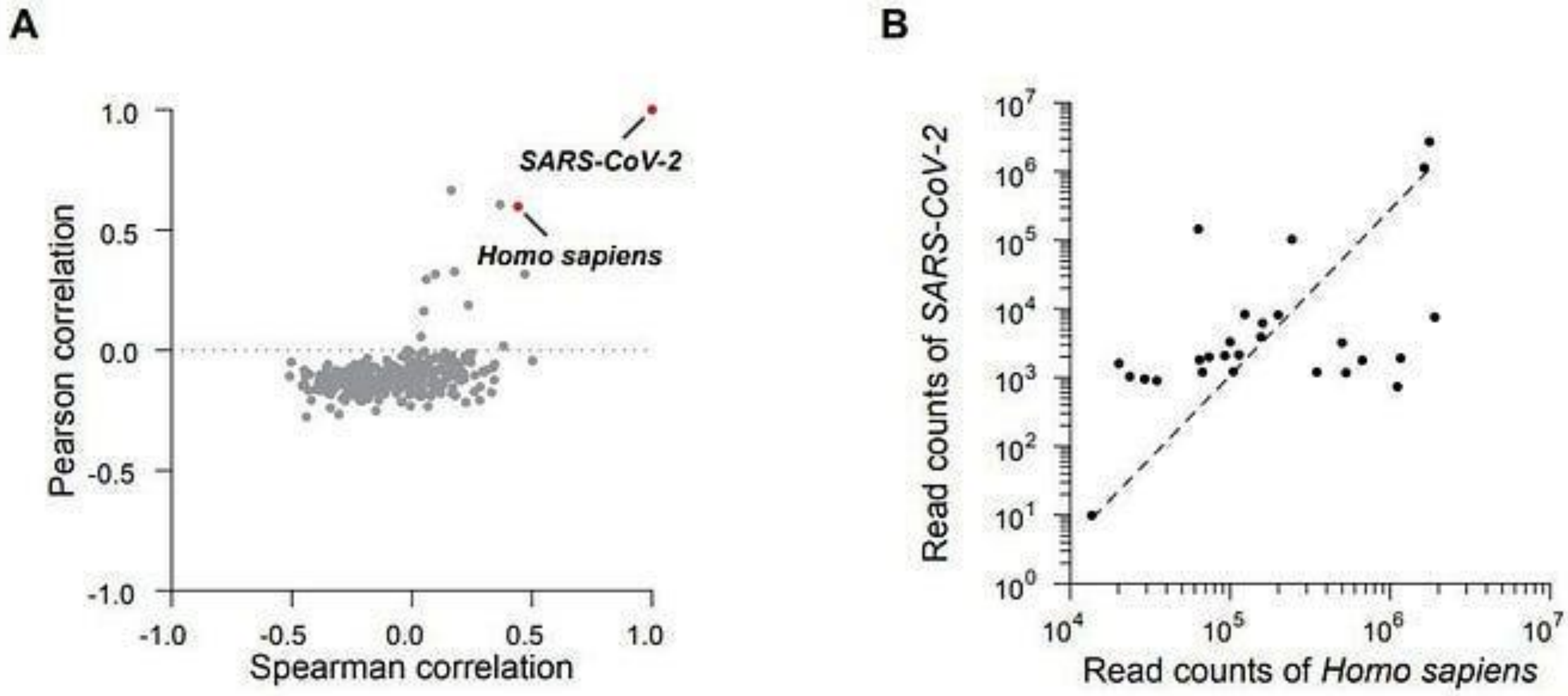
Species	Animal number	Sample number	RT-PCR positive number	Remarks
Rabbit/Hares	52	104	0	
Stray cat	27	80[a]	0	Including faeces
Snake	40	80	0	
Hedgehog	16	67	0	
Muntjac	6	18	0	
Dog	7	17	0	Including one stray dog
Badger	6	16	0	
Bamboo rat	6	15	0	
Rat	10	12	0	Captured around the market
Pig	NA[c]	6[b]	0	
Chicken	5	5	0	
Chinese giant salamander	3	5	0	
Crocodile	2	4	0	
Wild boar	2	4	0	
Soft-shelled turtle	2	3	0	
Weasel	1	2	0	Captured around the market
Fish	2	2	0	
Sheep	1	1	0	
Others	NA[c]	16	0	
Rabbit/Hares	52	104	0	
Total	188	457	0	

[a] Six of the cats were from the Huanan Seafood Market.
[b] Other markets.
[c] Not applicable.

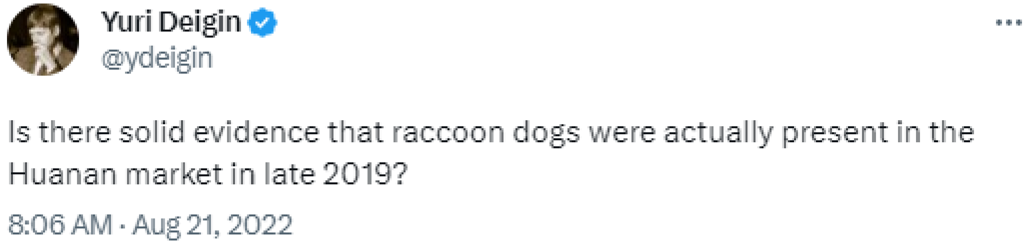
Gao 2022 preprint revealed that sampling at the market found animal DNA, but refused to say which animals.

The paper argued that Covid started somewhere outside China.

Western scientists predicted that the animal DNA would show Covid susceptible species, like raccoon dogs, if China would release the data.



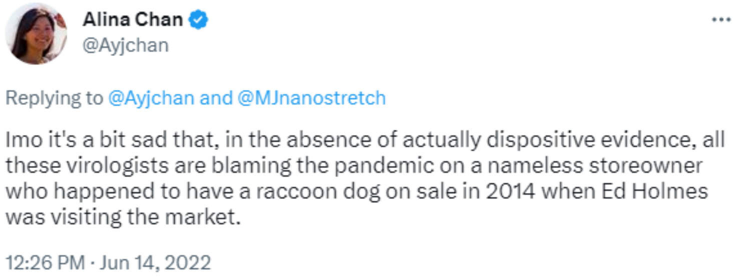
2021-2022: Lab leak supporters doubted the presence of raccoon dogs:



Yuri Deigin @ydeigin

Is there solid evidence that raccoon dogs were actually present in the Huanan market in late 2019?

8:06 AM · Aug 21, 2022



Alina Chan @Ayjchan

Replying to @Ayjchan and @MJnanostretch

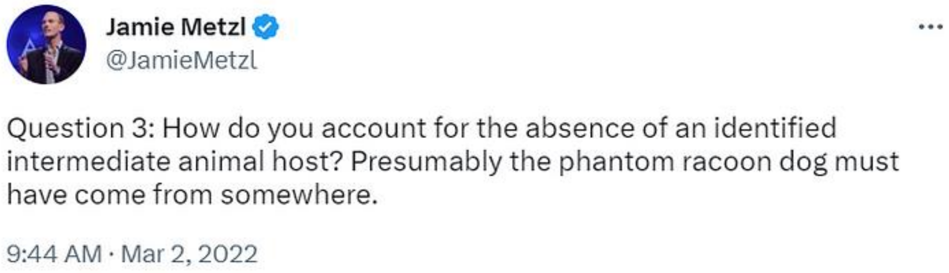
Imo it's a bit sad that, in the absence of actually dispositive evidence, all these virologists are blaming the pandemic on a nameless storeowner who happened to have a raccoon dog on sale in 2014 when Ed Holmes was visiting the market.

12:26 PM · Jun 14, 2022

Alina Chan @Ayjchan

Looks like they gave up and settled for "many of the early cases were at the market!" and "I took a photo of a raccoon dog at that market several years ago!"

3:33 PM · Apr 11, 2022



Jamie Metzl @JamieMetzl

Question 3: How do you account for the absence of an identified intermediate animal host? Presumably the phantom racoon dog must have come from somewhere.

9:44 AM · Mar 2, 2022

Alina Chan @Ayjchan

Are we all going to be back in this situation in 2031 trying to track the natural origin of a novel viral outbreak occurring on the doorsteps of a lab studying that same type of virus?

Where are my raccoon dogs?

5:01 AM · Oct 6, 2021

Alina Chan @Ayjchan

There's a lot of people talking about raccoon dogs and frozen ferret badgers, but they got nothing - absolute zero evidence for a natural origin of SARS2 in Wuhan.

11:12 AM · Sep 29, 2021

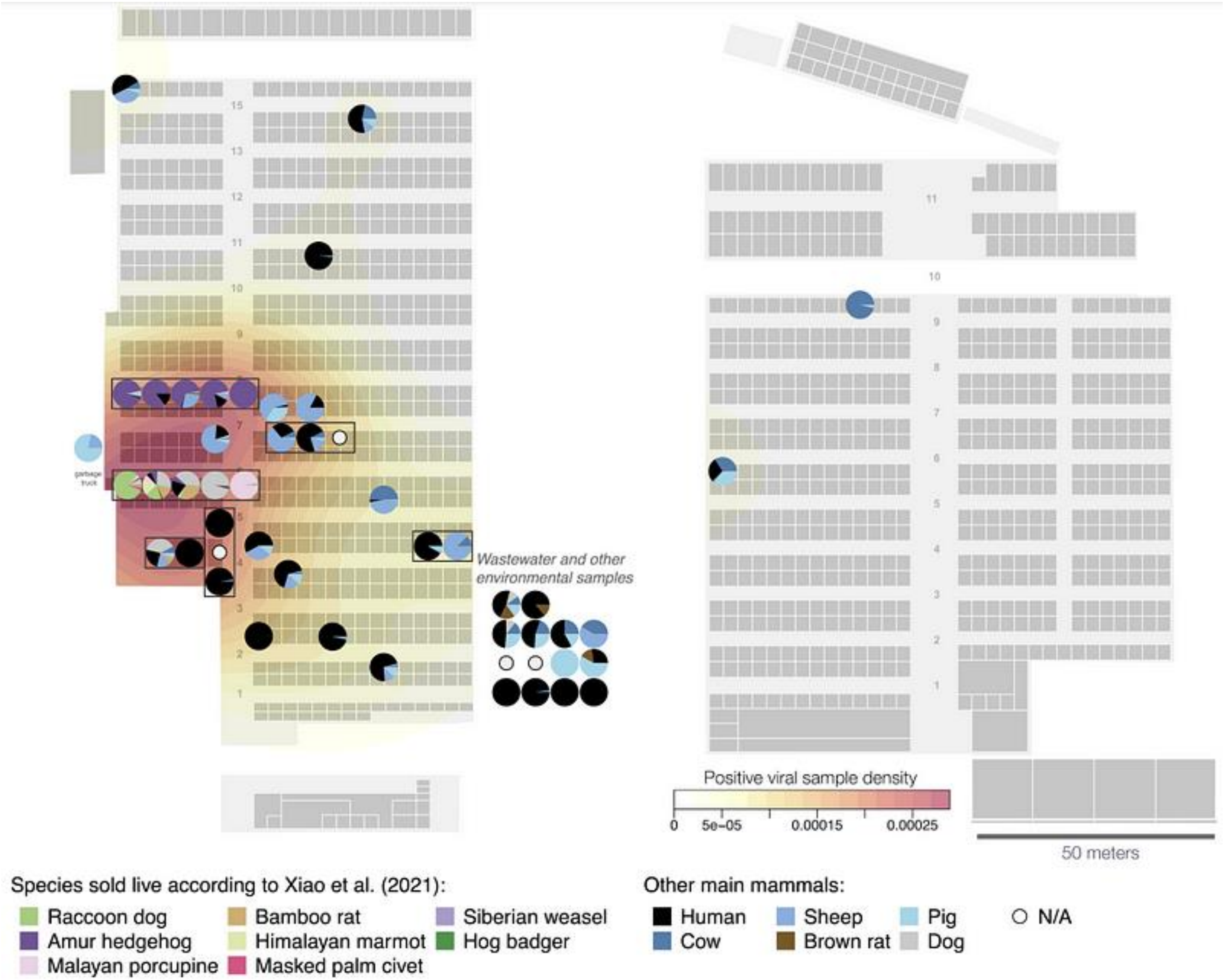
43 Retweets **2** Quotes **337** Likes **2** Bookmarks

Alina Chan @Ayjchan · Sep 29, 2021

Replying to @Ayjchan

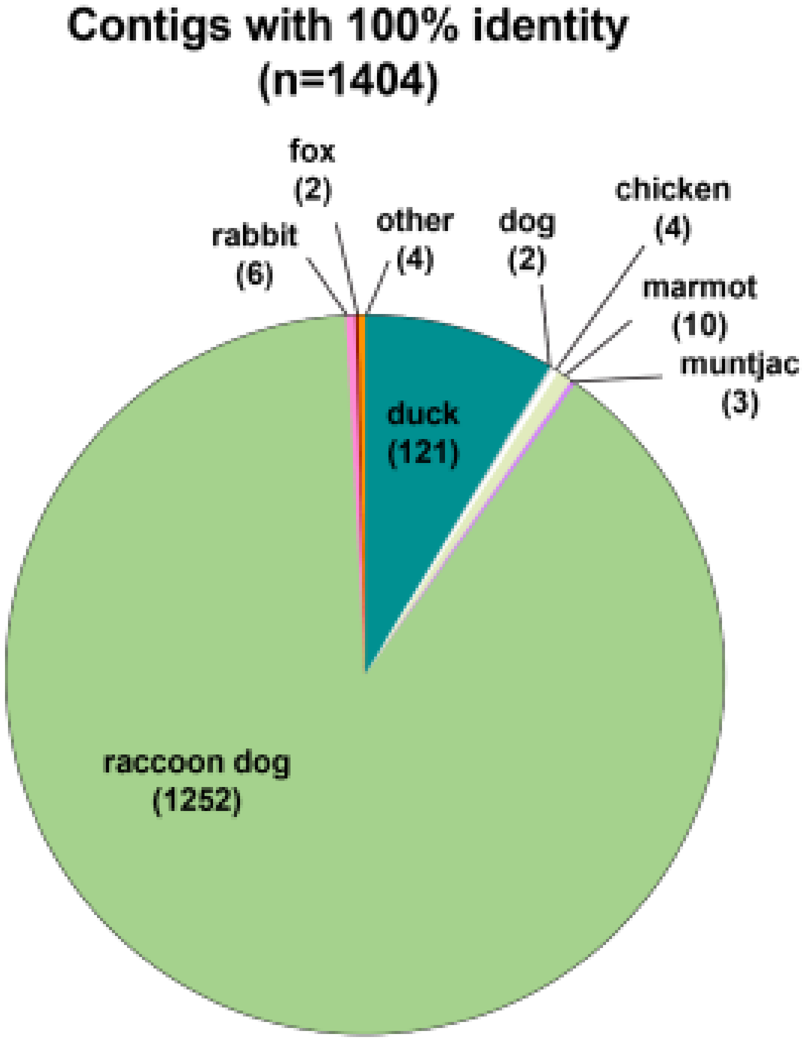
Where is the mythical accumulating evidence for a natural origin of SARS2?

2023: Western scientists got their hands on environmental DNA samples from the market



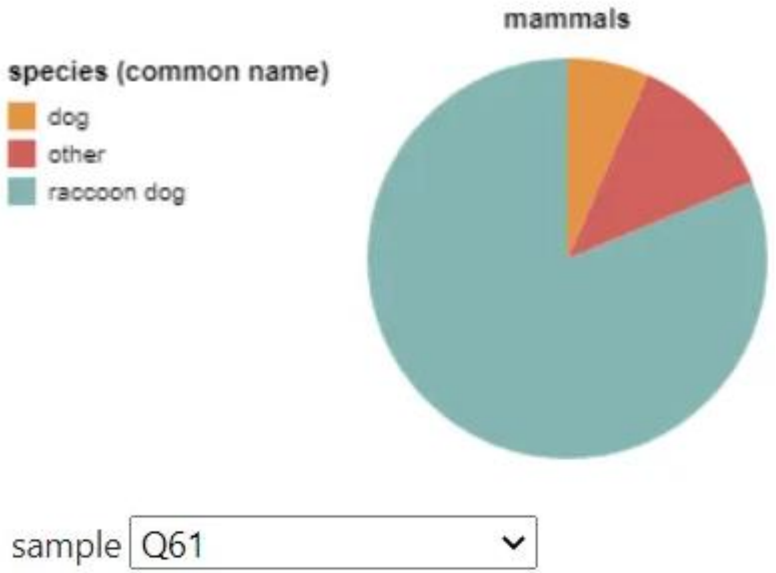
This should disprove the “toilets theory” – many of these samples taken from wild animal shops had animal DNA, not human DNA.

Raccoon dogs were found in exactly the shop they predicted.
One covid positive sample had raccoon dog DNA, but no human DNA:

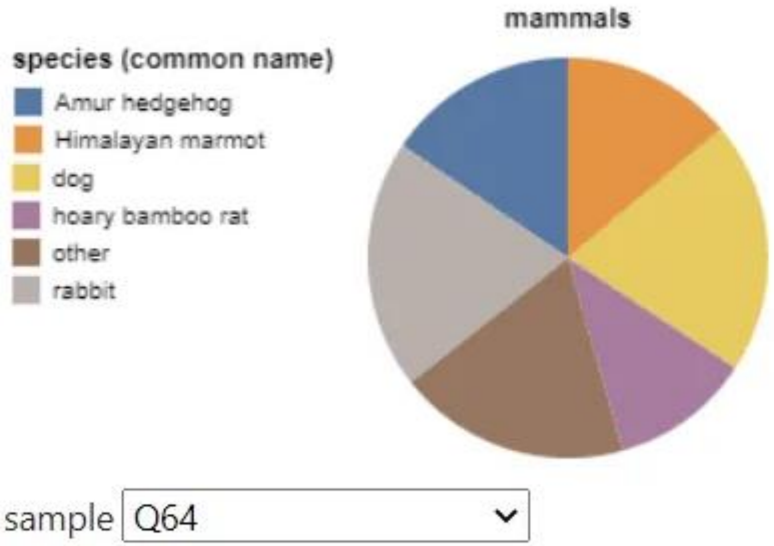


Birds in Eddie Holmes' photo might have been ducks:

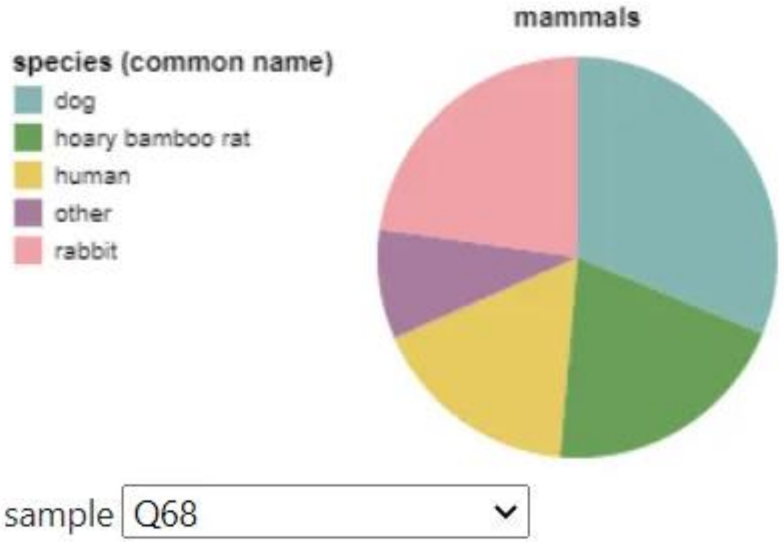
Other positive samples from the 6-29 shop:



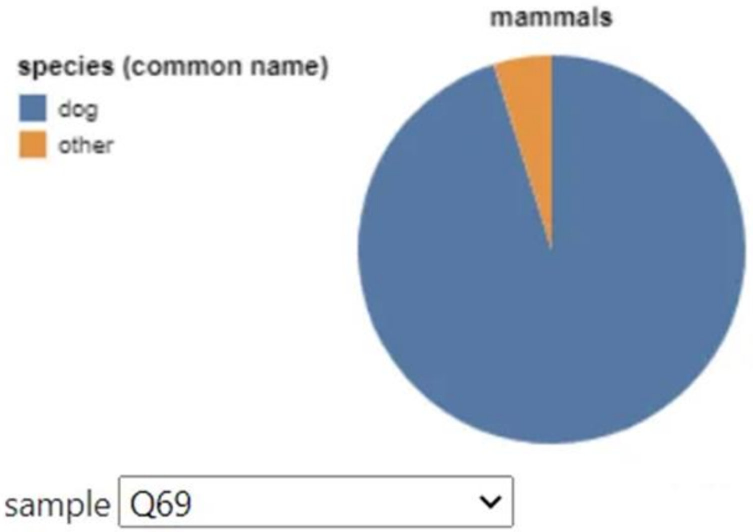
sample Q61



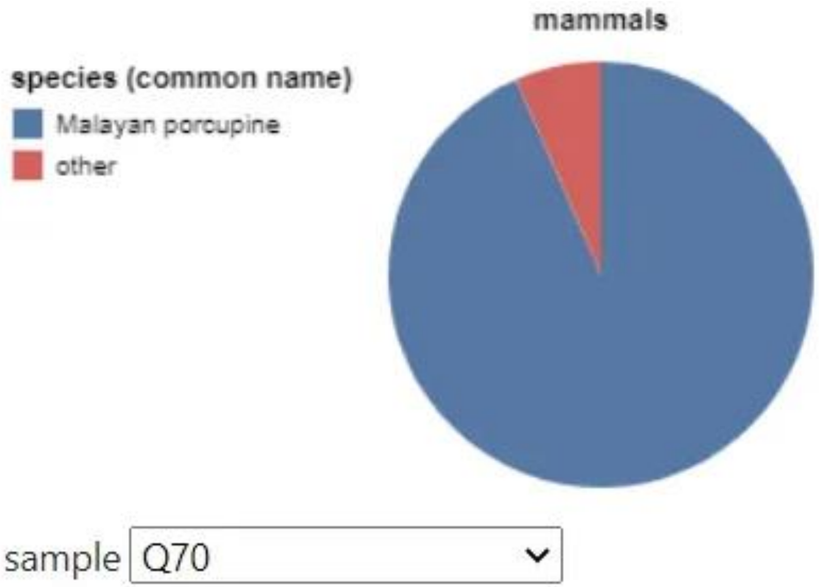
sample Q64



sample Q68



sample Q69



sample Q70

It's hard to know which is the host animal because they sold so many different animals in this shop.

Images from Jesse Bloom's interactive tool.

These animals don't match the WHO report

West 6-29,31,33 (1134)	Giant salamander	Guangzhou city, Guangdong
	Snake	Xiangyang city, Hubei
	Rabbit	Zhoukou city, Henan
	Pheasant	Yangxin county, Huangshi city, Hubei
	Hedgehog	Unknown private breeder

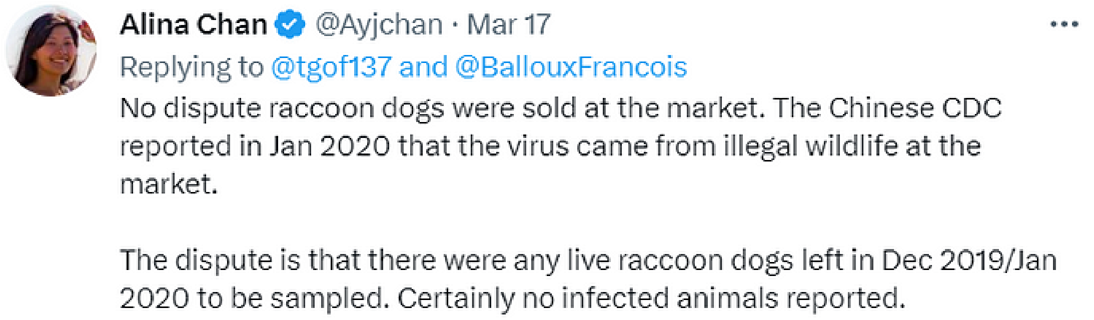
WHO report, Annexes page 190

2023: Lab leak theory adjusts to deny that the new evidence is important:

Jamie Metzl
@JamieMetzl

As I stated in my congressional testimony, I welcome all additional evidence and am open to evolving my views re #COVID19 origins. But I see nothing in the Atlantic article which would inspire such a shift. We've known for a while that raccoon dogs were sold in the Wuhan market.

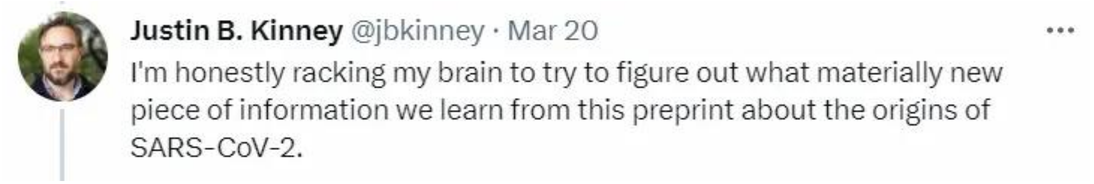
5:15 AM · Mar 17, 2023 from Queens, NY · 16.5K Views



Alina Chan @Ayjchan · Mar 17
Replying to @tgof137 and @BallouxFrancois

No dispute raccoon dogs were sold at the market. The Chinese CDC reported in Jan 2020 that the virus came from illegal wildlife at the market.

The dispute is that there were any live raccoon dogs left in Dec 2019/Jan 2020 to be sampled. Certainly no infected animals reported.



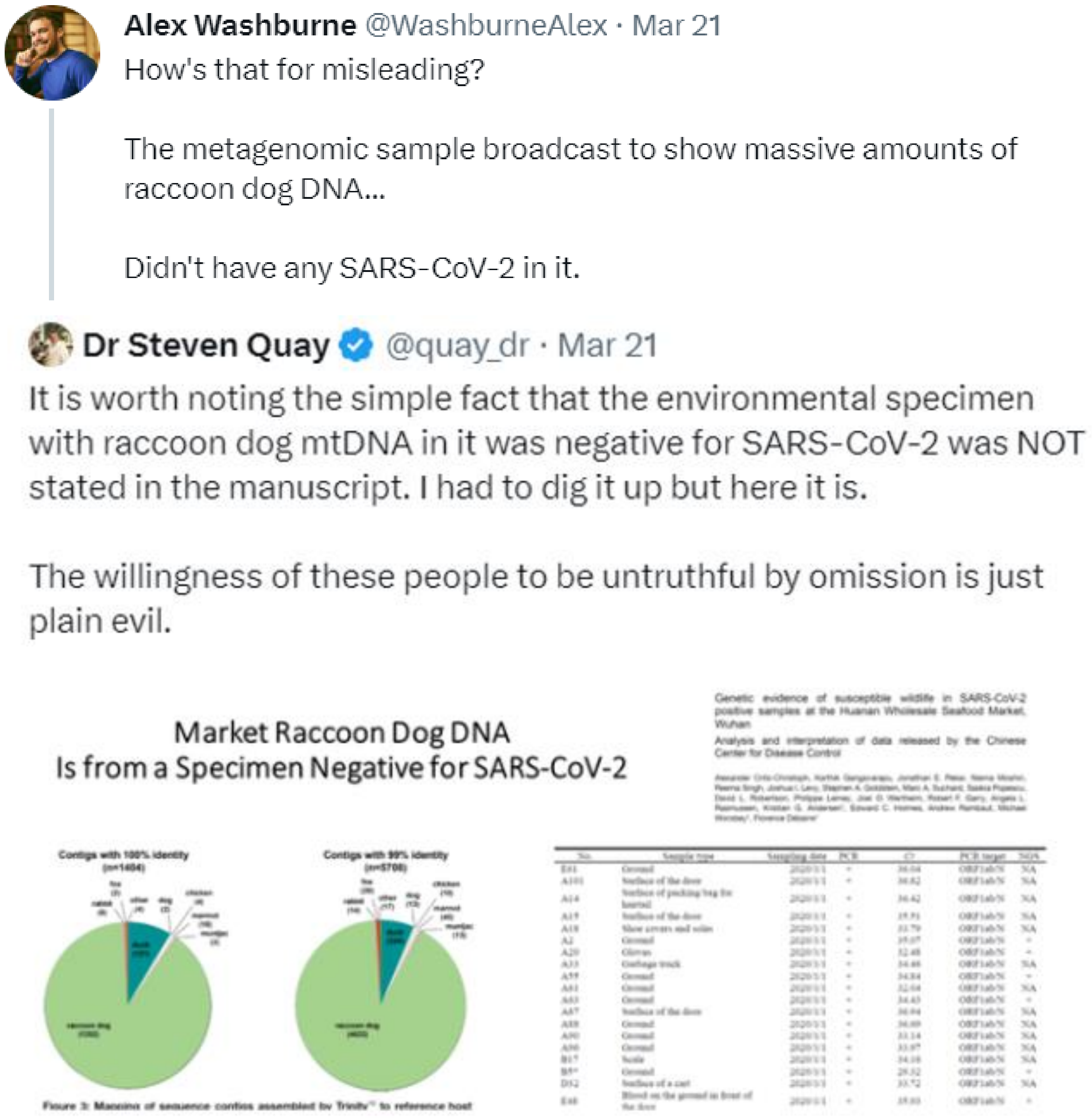
Justin B. Kinney @jbkinney · Mar 20
I'm honestly racking my brain to try to figure out what materially new piece of information we learn from this preprint about the origins of SARS-CoV-2.

Billy Bostickson 🏴 👁 & 👁 🆓
@BillyBostickson

Did I see a raccoon dog?

Keoni Everington @keverington · Mar 19
Wait, the Wuhan Institute of Virology has a zoo of animals it experiments on and otherwise abuses? Why weren't these animals tested for Covid right away???
Show this thread

Lab leak theorists also claimed that the raccoon dog sample was covid negative



Alex Washburne @WashburneAlex · Mar 21

How's that for misleading?

The metagenomic sample broadcast to show massive amounts of raccoon dog DNA...

Didn't have any SARS-CoV-2 in it.

Dr Steven Quay @quay_dr · Mar 21

It is worth noting the simple fact that the environmental specimen with raccoon dog mtDNA in it was negative for SARS-CoV-2 was NOT stated in the manuscript. I had to dig it up but here it is.

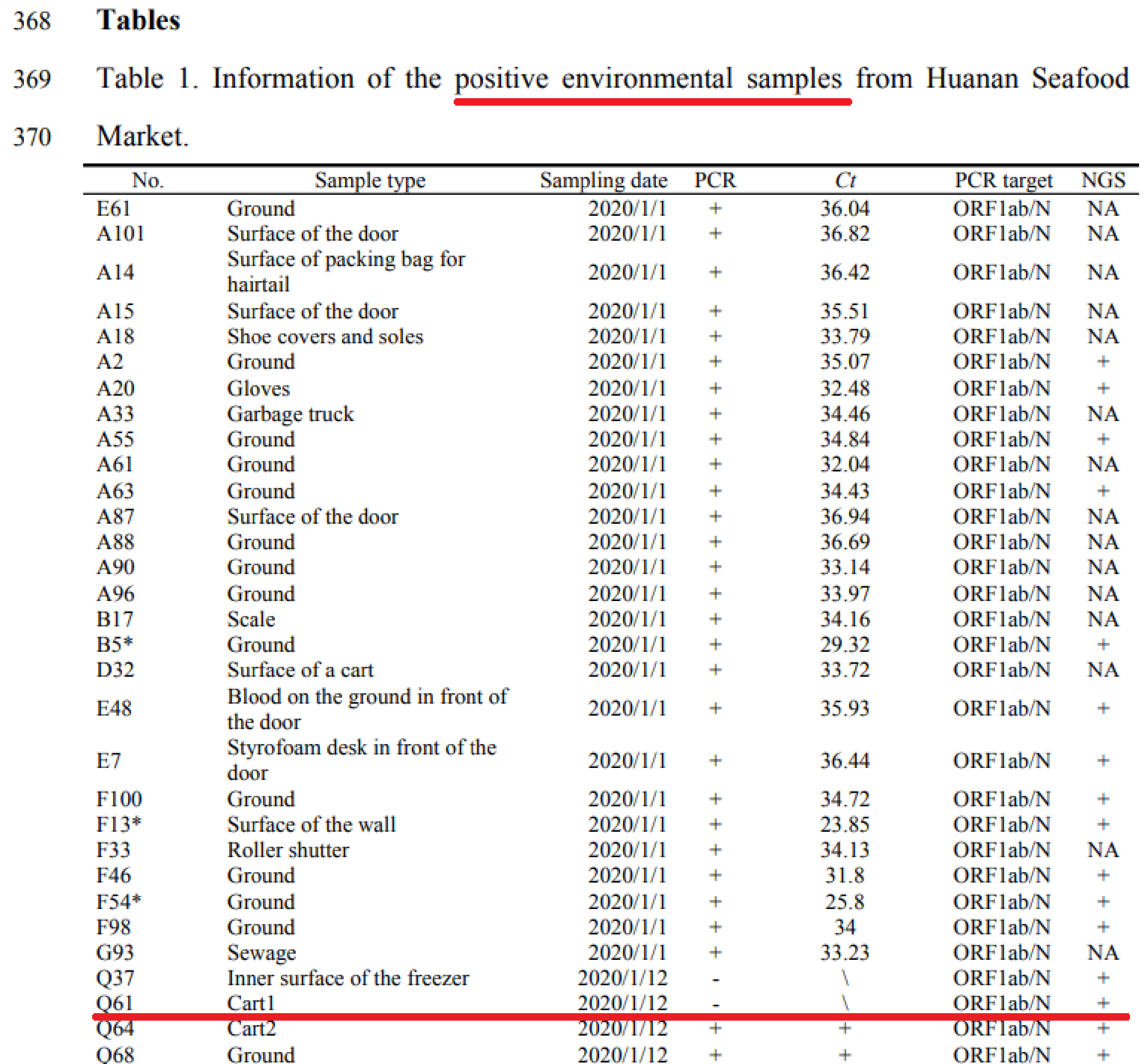
The willingness of these people to be untruthful by omission is just plain evil.

Market Raccoon Dog DNA
Is from a Specimen Negative for SARS-CoV-2

Genetic evidence of susceptible wildlife in SARS-CoV-2 positive samples at the Huanan Wholesale Seafood Market, Wuhan

Analysis and interpretation of data released by the Chinese Center for Disease Control

The truth is it was Covid positive via NGS but PCR negative:
(image from Gao et al, 2022)



Tables

Table 1. Information of the positive environmental samples from Huanan Seafood Market.

No.	Sample type	Sampling date	PCR	*Ct*	PCR target	NGS
E61	Ground	2020/1/1	+	36.04	ORF1ab/N	NA
A101	Surface of the door	2020/1/1	+	36.82	ORF1ab/N	NA
A14	Surface of packing bag for hairtail	2020/1/1	+	36.42	ORF1ab/N	NA
A15	Surface of the door	2020/1/1	+	35.51	ORF1ab/N	NA
A18	Shoe covers and soles	2020/1/1	+	33.79	ORF1ab/N	NA
A2	Ground	2020/1/1	+	35.07	ORF1ab/N	+
A20	Gloves	2020/1/1	+	32.48	ORF1ab/N	+
A33	Garbage truck	2020/1/1	+	34.46	ORF1ab/N	NA
A55	Ground	2020/1/1	+	34.84	ORF1ab/N	+
A61	Ground	2020/1/1	+	32.04	ORF1ab/N	NA
A63	Ground	2020/1/1	+	34.43	ORF1ab/N	+
A87	Surface of the door	2020/1/1	+	36.94	ORF1ab/N	NA
A88	Ground	2020/1/1	+	36.69	ORF1ab/N	NA
A90	Ground	2020/1/1	+	33.14	ORF1ab/N	NA
A96	Ground	2020/1/1	+	33.97	ORF1ab/N	NA
B17	Scale	2020/1/1	+	34.16	ORF1ab/N	NA
B5*	Ground	2020/1/1	+	29.32	ORF1ab/N	+
D32	Surface of a cart	2020/1/1	+	33.72	ORF1ab/N	NA
E48	Blood on the ground in front of the door	2020/1/1	+	35.93	ORF1ab/N	+
E7	Styrofoam desk in front of the door	2020/1/1	+	36.44	ORF1ab/N	+
F100	Ground	2020/1/1	+	34.72	ORF1ab/N	+
F13*	Surface of the wall	2020/1/1	+	23.85	ORF1ab/N	+
F33	Roller shutter	2020/1/1	+	34.13	ORF1ab/N	NA
F46	Ground	2020/1/1	+	31.8	ORF1ab/N	+
F54*	Ground	2020/1/1	+	25.8	ORF1ab/N	+
F98	Ground	2020/1/1	+	34	ORF1ab/N	+
G93	Sewage	2020/1/1	+	33.23	ORF1ab/N	NA
Q37	Inner surface of the freezer	2020/1/12	-	\	ORF1ab/N	+
Q61	Cart1	2020/1/12	-	\	ORF1ab/N	+
Q64	Cart2	2020/1/12	+	+	ORF1ab/N	+
Q68	Ground	2020/1/12	+	+	ORF1ab/N	+

Lab leak theorists also claimed that the human DNA had been removed from the samples:

Alina Chan @Ayjchan · 22h

Another serious case of the Proximal Origin authors not carefully reading the methods section of the Chinese CDC's paper whose data they used in their #OriginOfCovid analysis.

Samples were processed in a way such that human genetic material was removed.

Flo Débarre @flodebarre · 22h

Replying to @Ayjchan

Hi Alina, Have a look at Figure 1 and check what the black color stands for.

1 1 16 2,029

Alina Chan @Ayjchan · 22h

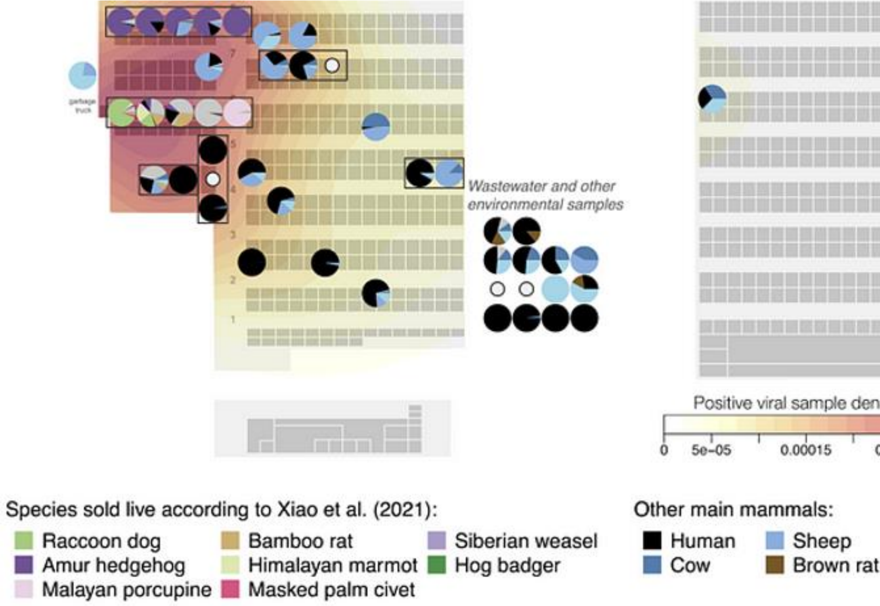
Replying to @flodebarre

(De)enrichment kits are never 100% effective. You'd still see some human material.

What is important here is that you cannot interpret the ratio of human:non-human material.

3 3 35 1,733

(black was used to represent human DNA. It was abundant in many of the samples despite Alina's claim that it had somehow been removed)



These samples also had other animal viruses in them:

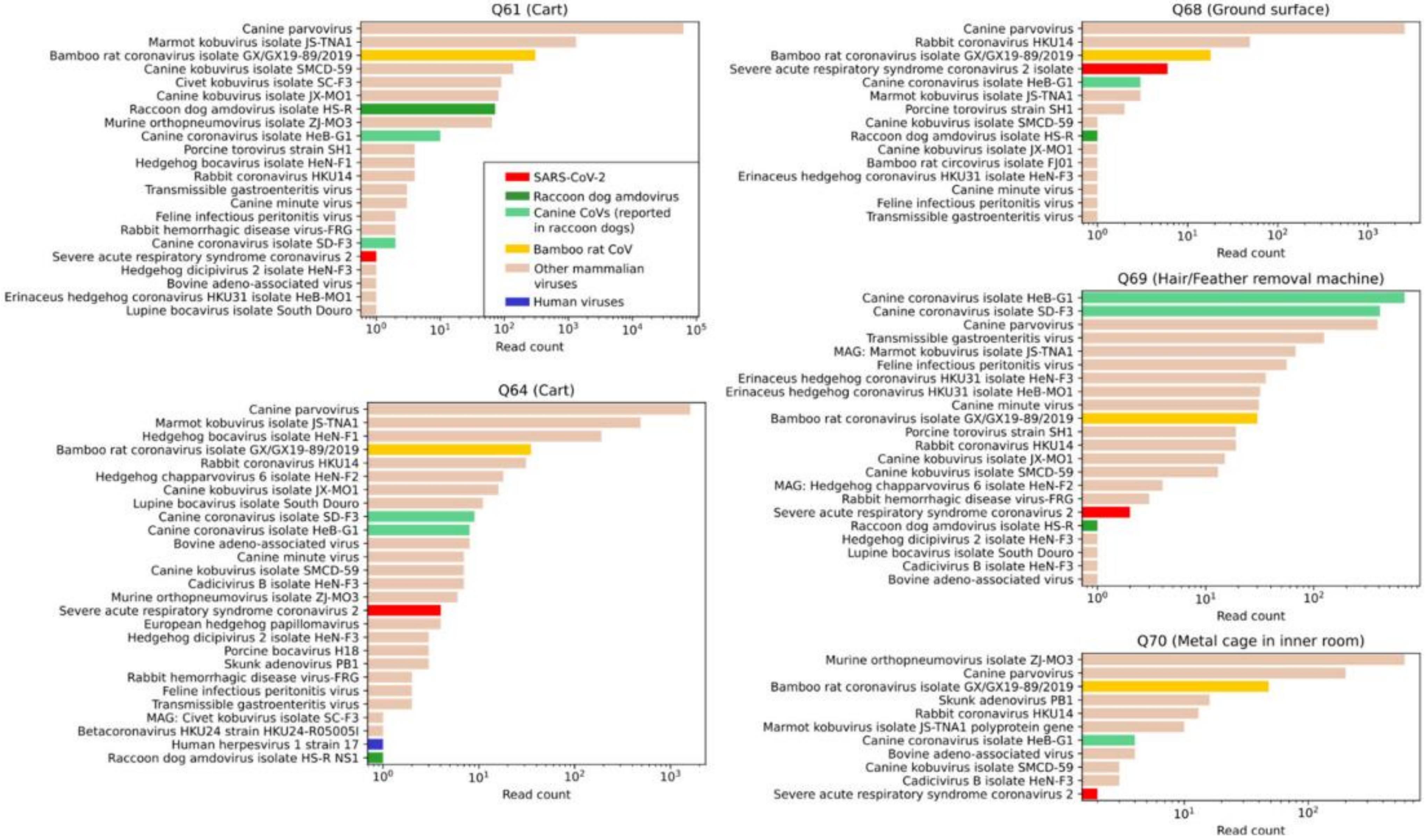


Figure from Crits Christoph et al, 2023

Some of these viruses trace back to southern China, suggesting that the wildlife trade connects these regions.

One is a bamboo rat coronavirus, from southern China, which contains a furin cleavage site.

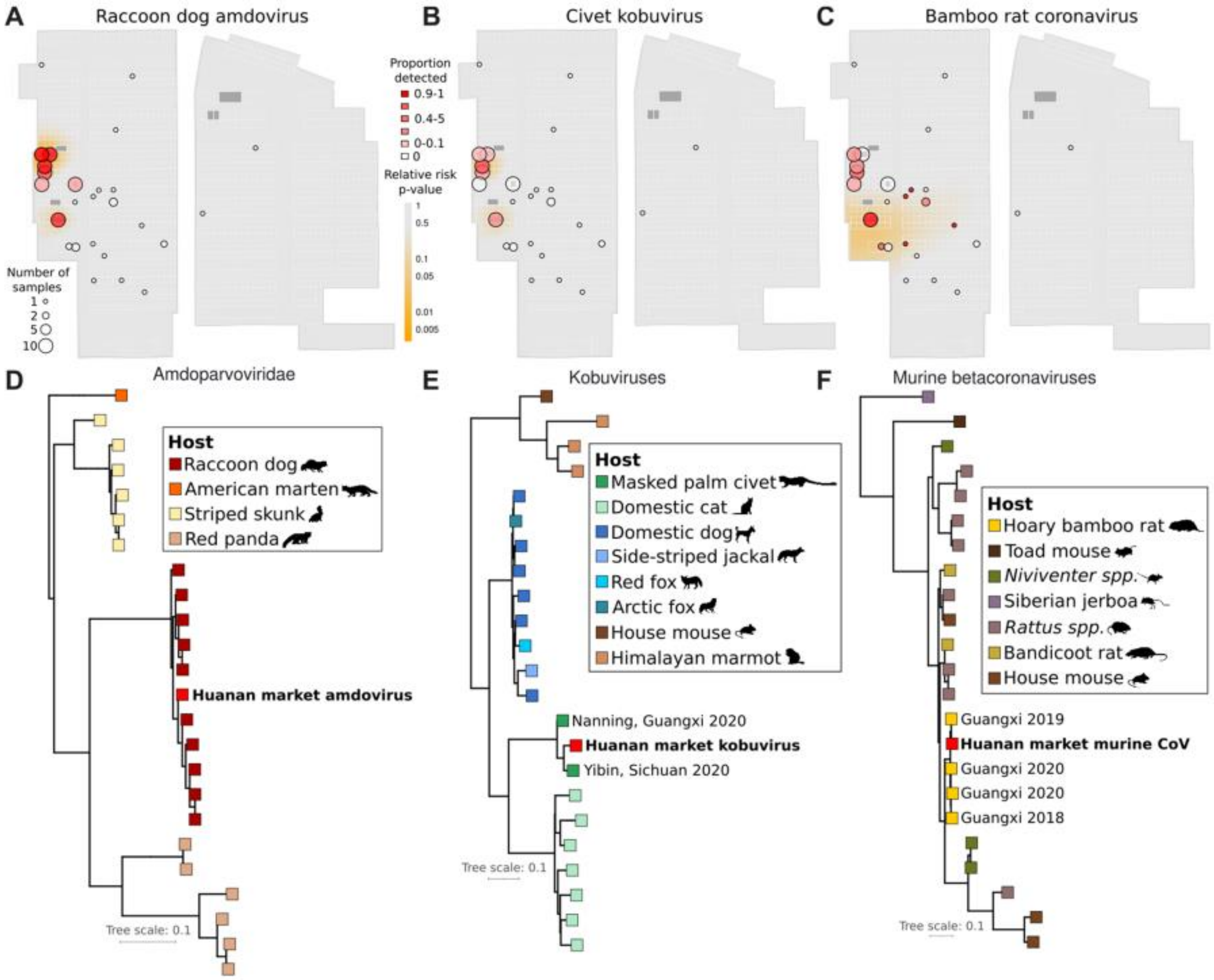


Figure from Crits Christoph et al, 2023

Who owned the shops selling wildlife?

3 sellers at the Wuhan market were fined in May, 2019 for selling illegal live hedgehogs (shops 6-29, 8-25, and 9-37)

The fines were given on 5/29/2019 for Mr Jin, Mr Song, and Mr Zheng

Shop 6-29, with the raccoon dogs, was owned by Mr Jin. (Jin Xiushan, 金秀山)
The shop name might be translated as Jianghan Poultry Management Department.

Shop 8-25, owned by Mr Song Fabao, also had positive samples and positive warehouse samples.
Shop name is E'Dong Red Star Game Shop.

The fine notices were taken down off the web after Michael Standaert asked about them.

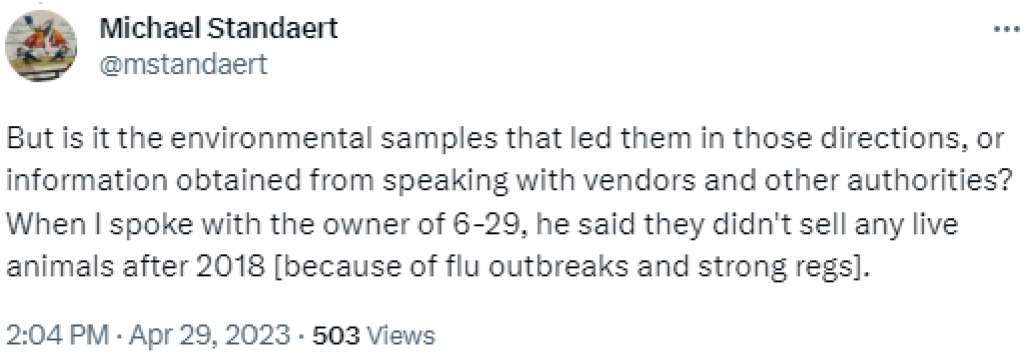
When the shops were found selling hedgehogs, they were fined 220 yuan (30 dollars) and the animals were confiscated.

If China doesn’t change those incentives, we’re going to have another pandemic like this in 20 years.

China has already eased restrictions on wildlife farming. They’re farming civets and raccoon dogs again.

If Mr Jin or Mr Song started the pandemic, do they even know it?

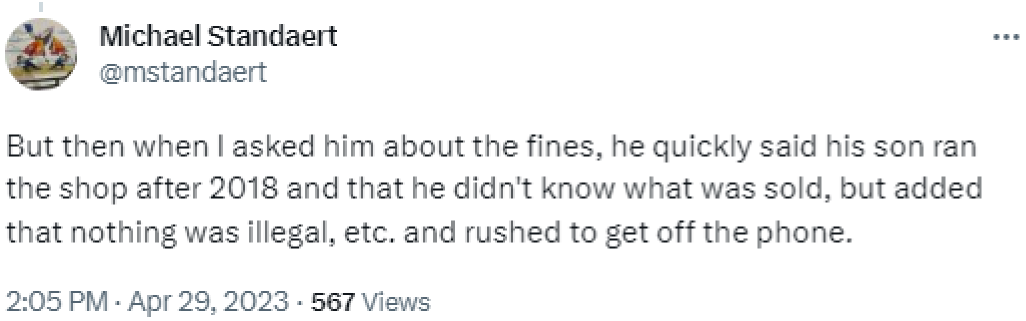
Maybe. Mr Jin was evasive when asked.



Michael Standaert
@mstandaert

But is it the environmental samples that led them in those directions, or information obtained from speaking with vendors and other authorities? When I spoke with the owner of 6-29, he said they didn't sell any live animals after 2018 [because of flu outbreaks and strong regs].

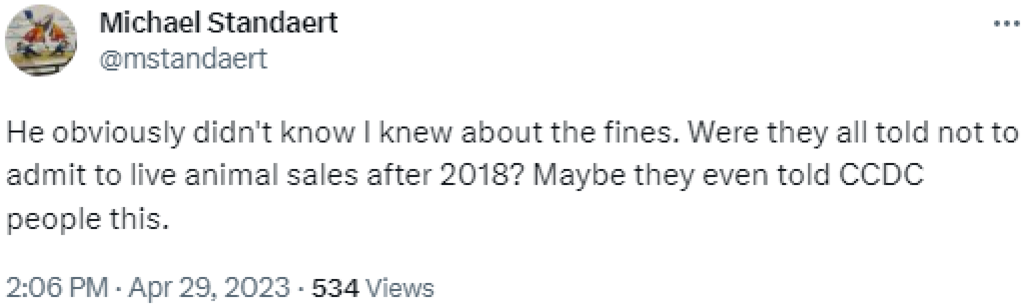
2:04 PM · Apr 29, 2023 · **503** Views



Michael Standaert
@mstandaert

But then when I asked him about the fines, he quickly said his son ran the shop after 2018 and that he didn't know what was sold, but added that nothing was illegal, etc. and rushed to get off the phone.

2:05 PM · Apr 29, 2023 · **567** Views

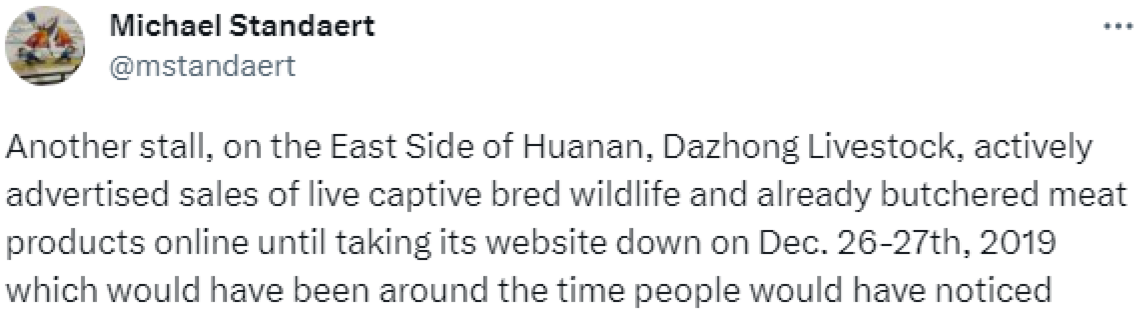


Michael Standaert
@mstandaert

He obviously didn't know I knew about the fines. Were they all told not to admit to live animal sales after 2018? Maybe they even told CCDC people this.

2:06 PM · Apr 29, 2023 · **534** Views

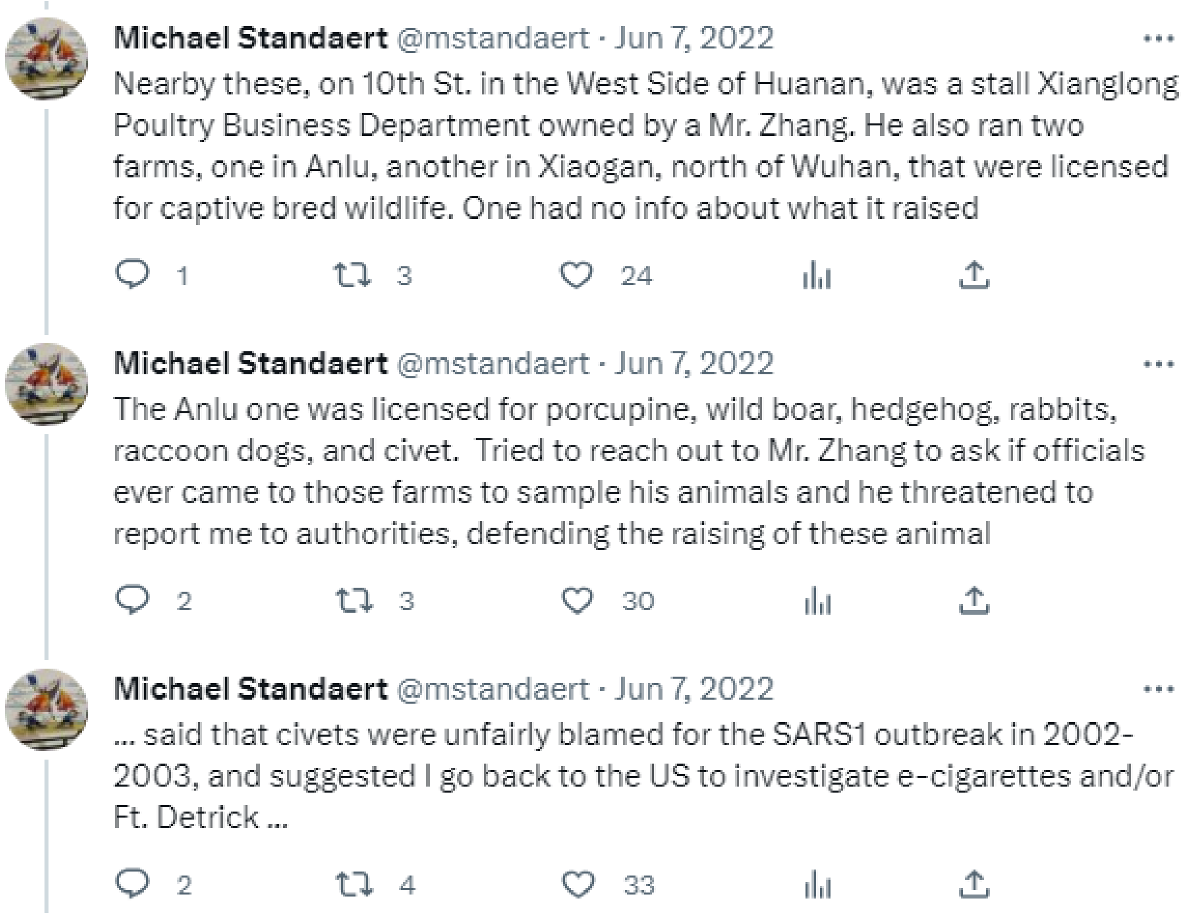
Other vendors started hiding their activities:



Michael Standaert
@mstandaert

Another stall, on the East Side of Huanan, Dazhong Livestock, actively advertised sales of live captive bred wildlife and already butchered meat products online until taking its website down on Dec. 26-27th, 2019 which would have been around the time people would have noticed

But, maybe not.
Another seller in the market doesn't even believe SARS was caused by civets, and he thinks the pandemic started at Fort Detrick, a lab in the United States.



Michael Standaert @mstandaert · Jun 7, 2022

Nearby these, on 10th St. in the West Side of Huanan, was a stall Xianglong Poultry Business Department owned by a Mr. Zhang. He also ran two farms, one in Anlu, another in Xiaogan, north of Wuhan, that were licensed for captive bred wildlife. One had no info about what it raised

Michael Standaert @mstandaert · Jun 7, 2022

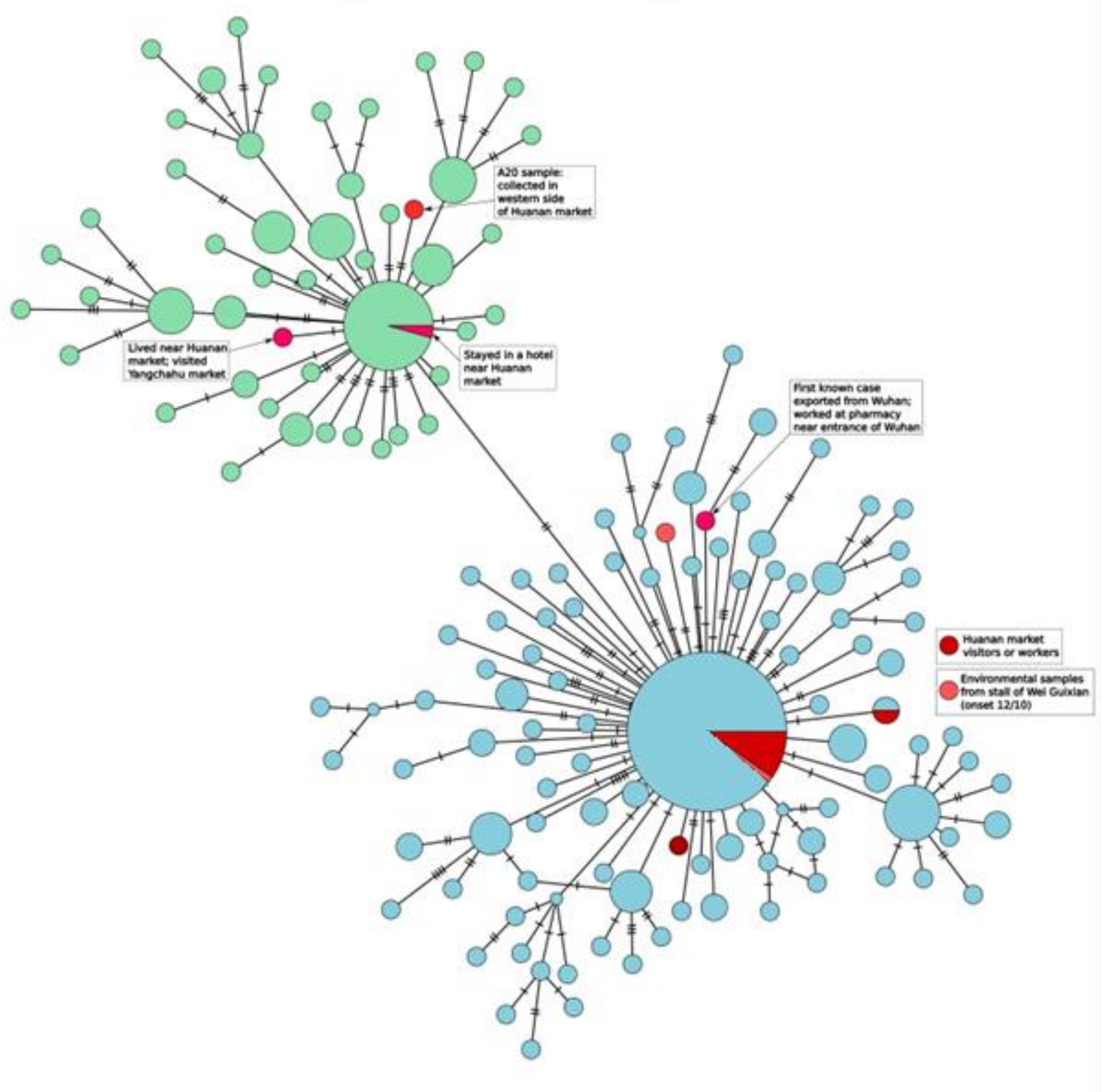
The Anlu one was licensed for porcupine, wild boar, hedgehog, rabbits, raccoon dogs, and civet. Tried to reach out to Mr. Zhang to ask if officials ever came to those farms to sample his animals and he threatened to report me to authorities, defending the raising of these animal

Michael Standaert @mstandaert · Jun 7, 2022

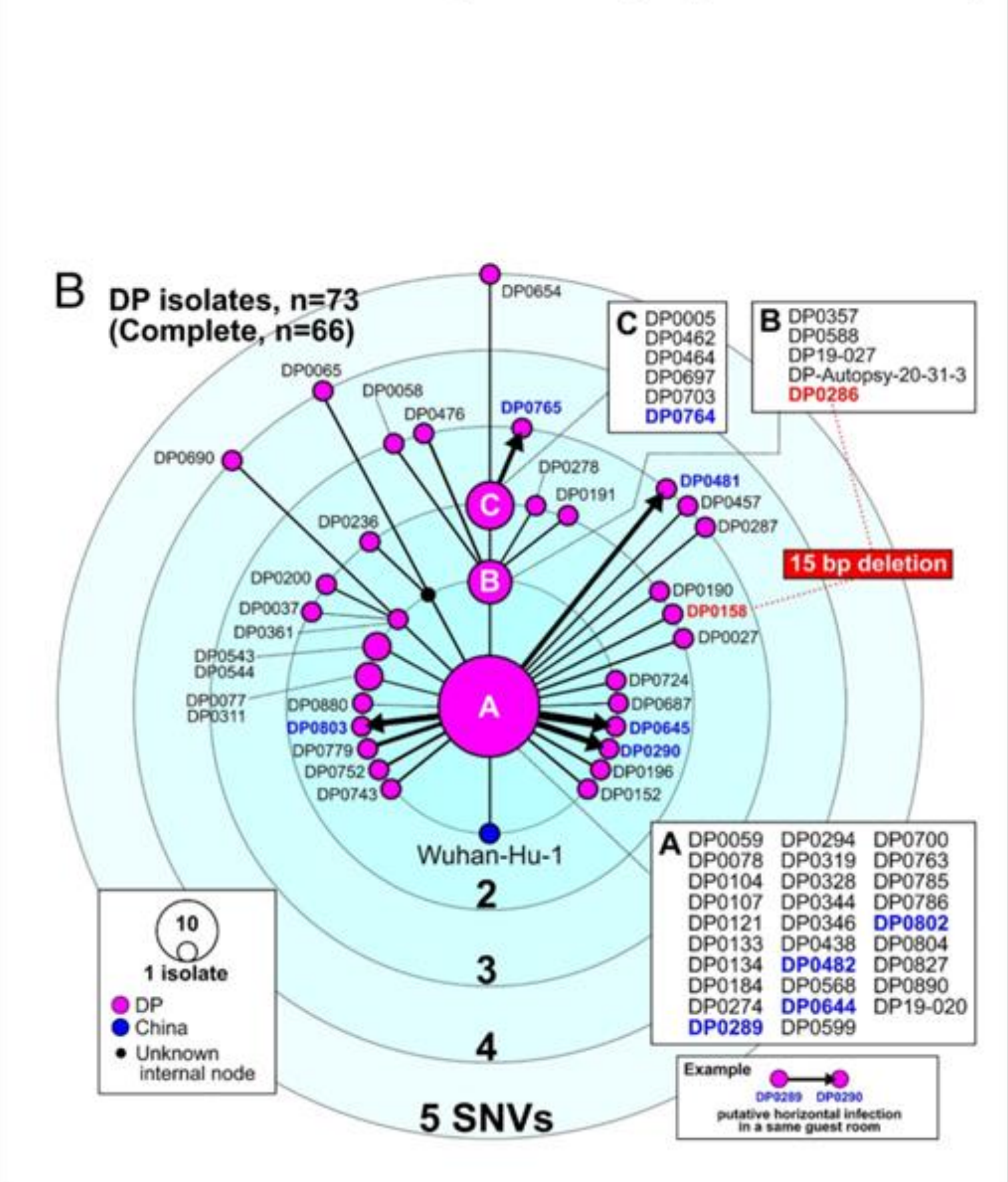
... said that civets were unfairly blamed for the SARS1 outbreak in 2002-2003, and suggested I go back to the US to investigate e-cigarettes and/or Ft. Detrick ...

We're not a very rational species…

Two spillovers at the market



Early SARS-CoV-2 viral genomes



Diamond Princess viral genomes (single introduction)

There are several ways to find the root of the genetic tree.

A 2021 review paper discussed all the discrepancies:

> A Bayesian analysis showed a 96% chance that Lineage B is the root.
>
> Lineage A is 2 mutations closer to the closest known bat viruses, so other people say that A came earlier.
>
> Some people prefer to say that A started at the lab and then B spread at the market.
>
> In 2021, Jesse Bloom predicted A was not associated with the market. Michael Worobey predicted A was associated, because the first two A cases were very near the market.

If lineage A came first, it should have evolved more than lineage B

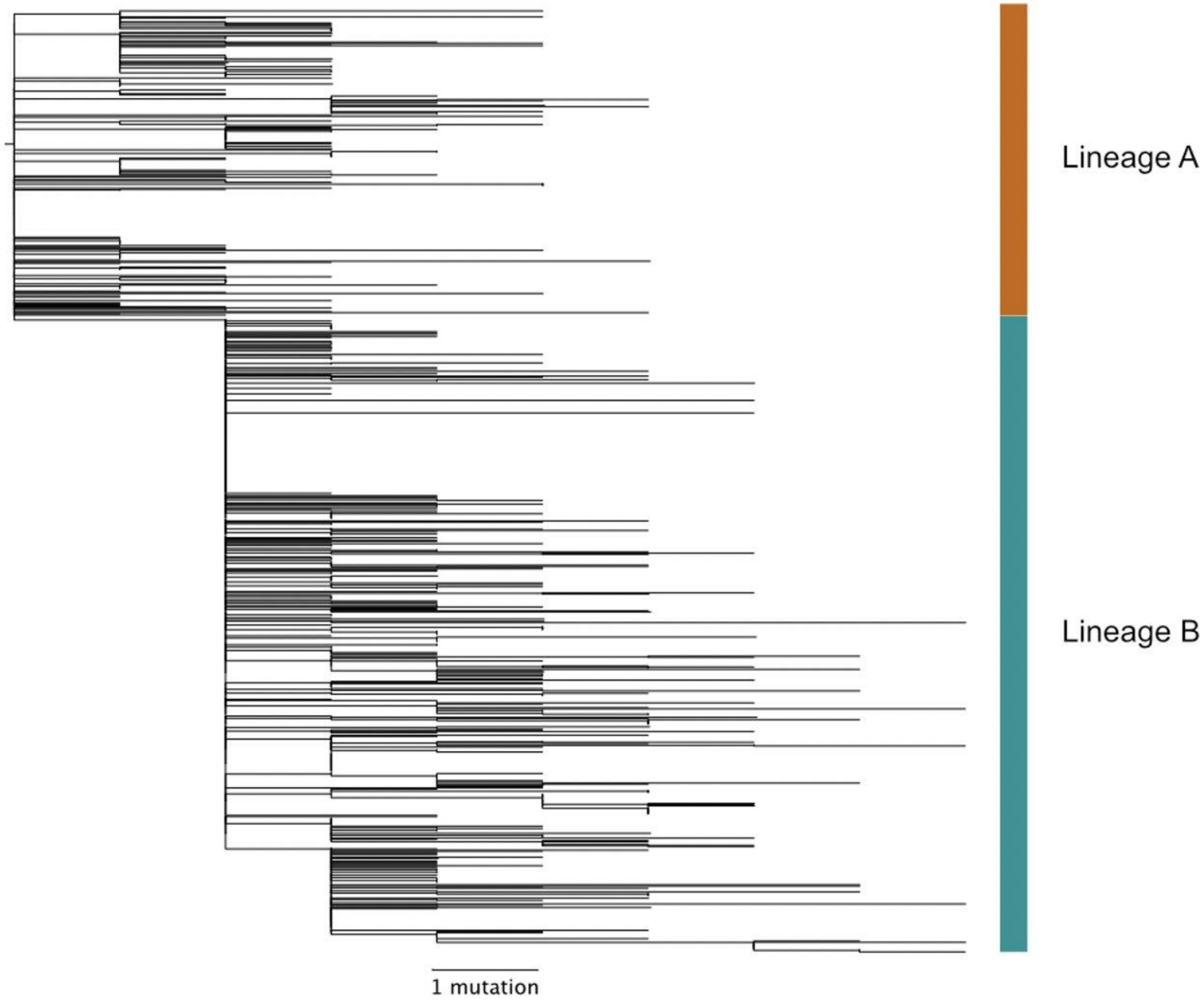
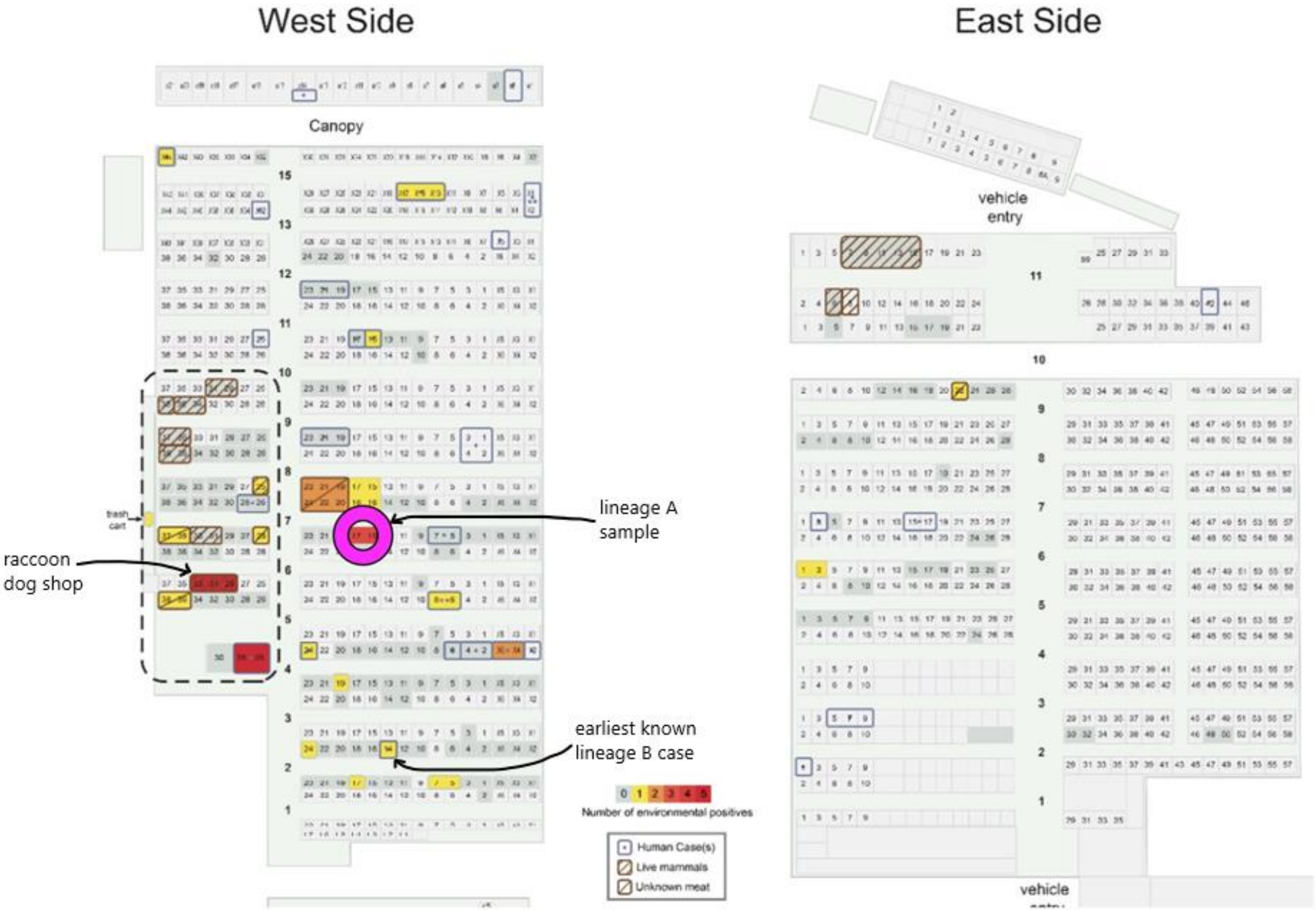


Figure S19. SARS-CoV-2 maximum likelihood tree rooted on lineage A (n=787 taxa, through 14 February 2020).

2022: China releases market samples

Lineage A was found in 1 out of 4 samples sequenced at the market:



Possible resolutions to this puzzle:

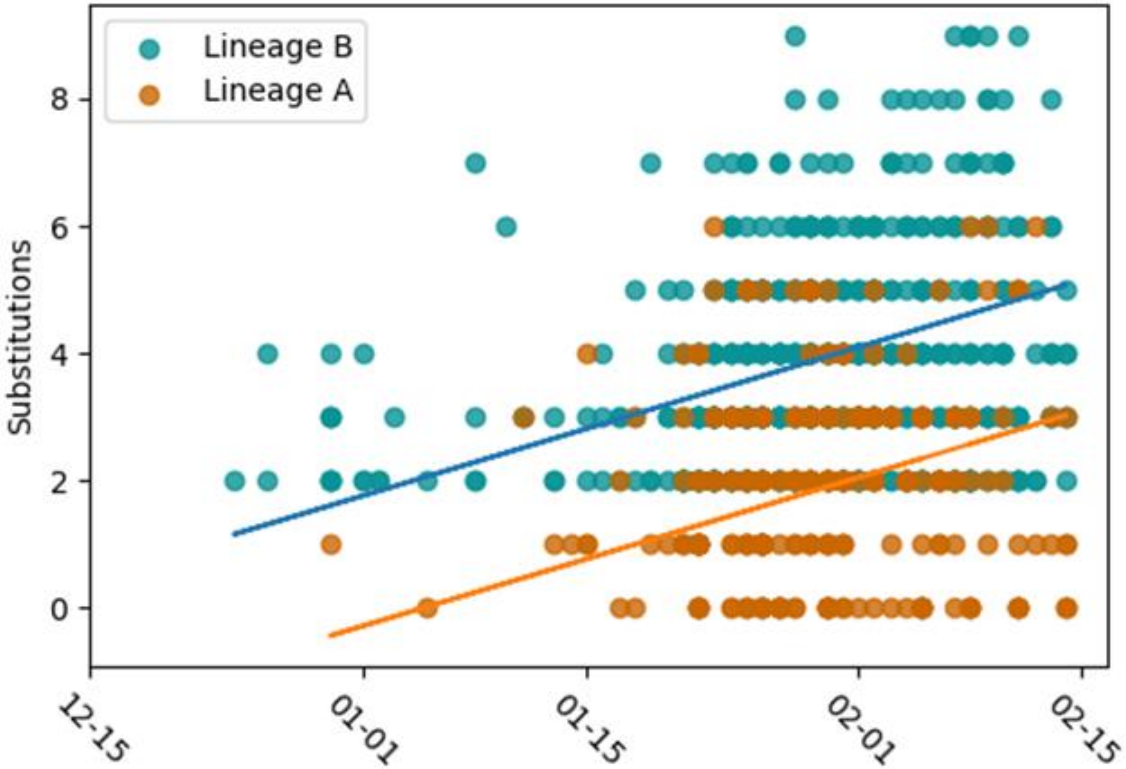
We don’t actually know what the ancestor of Covid is. If Lineage B is 1,000 mutations away from the closest bat virus, A is 998 mutations away.

But we’re just comparing to distantly related viruses. The actual ancestor might look like B.

Some people still argue there must be unsampled A cases, maybe A was elsewhere in Wuhan, or elsewhere in China, then it turned into B at the market.

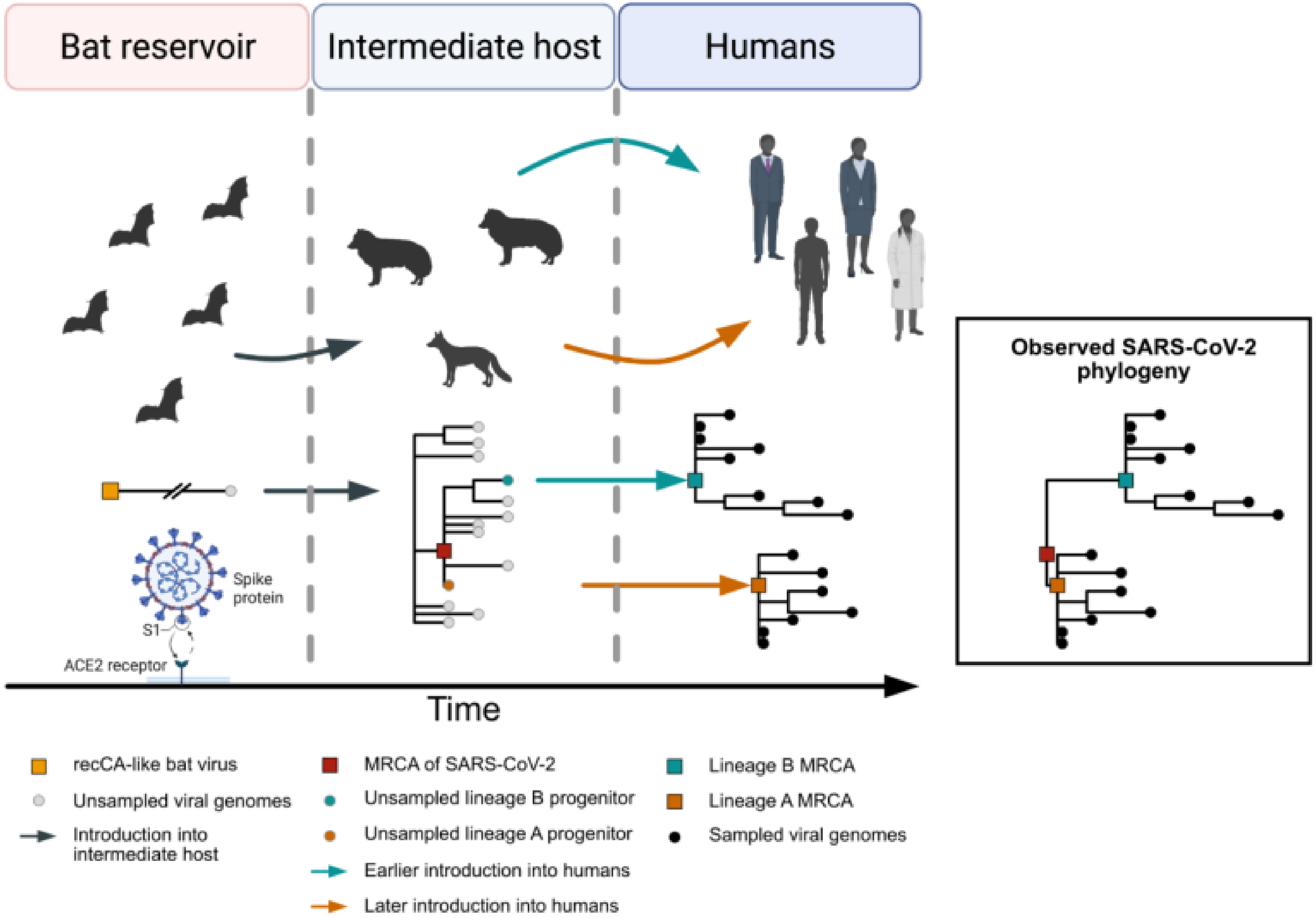
These theories posit a hidden reservoir of A cases.

It could only be a small reservoir, otherwise we would have detected some of those cases or seen more diversity.



How 2 spillovers resolves the lineage A/B puzzle:

The hidden lineage A reservoir was in the intermediate host animals, not in people.



Bat reservoir

Intermediate host

Humans

Spike protein

S1

ACE2 receptor

Time

Observed SARS-CoV-2 phylogeny

🟧 recCA-like bat virus

○ Unsampled viral genomes

→ Introduction into intermediate host

🟥 MRCA of SARS-CoV-2

● Unsampled lineage B progenitor

🟠 Unsampled lineage A progenitor

→ Earlier introduction into humans

→ Later introduction into humans

🟦 Lineage B MRCA

🟧 Lineage A MRCA

● Sampled viral genomes

With 1 lineage, the odds are 1 in 10,000 that the market would be the first cluster of cases, if this was a lab leak.

With 2 lineages, the odds are 1 in 100 million that the virus would come from the lab to the market twice.

Mutations can also make it look like 2 spillovers just by chance. Pekar's paper says there's a 3% chance it would look like 2 lineages by chance. (bayes factor 4.2)

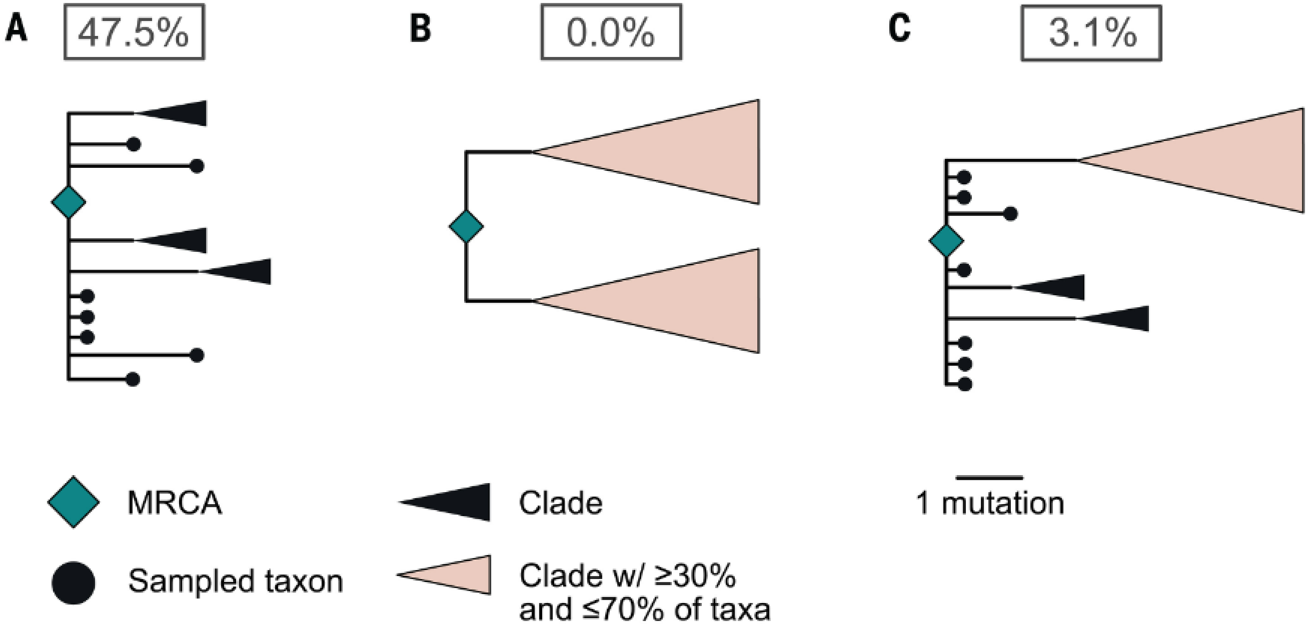


Fig. 2. **Probability of phylogenetic structures arising from a single introduction of SARS-CoV-2 in epidemic simulations.**

(**A**) A large polytomy of at least 100 descendent lineages, which is consistent with the base of both lineages A and B. (**B**) Topology matching a C/C ancestral haplotype: two clades, each one mutation from the ancestor, both with polytomies of at least 100 descendent lineages. (**C**) Topology matching either a lineage A or lineage B ancestral haplotype: a basal polytomy with at least 100 descendent lineages, including a large clade separated by two mutations, also possessing a polytomy of at least 100 descendent lineages. Basal taxa have short branch lengths for clarity. The probability of each phylogenetic structure after a single introduction is reported in the respective boxes.

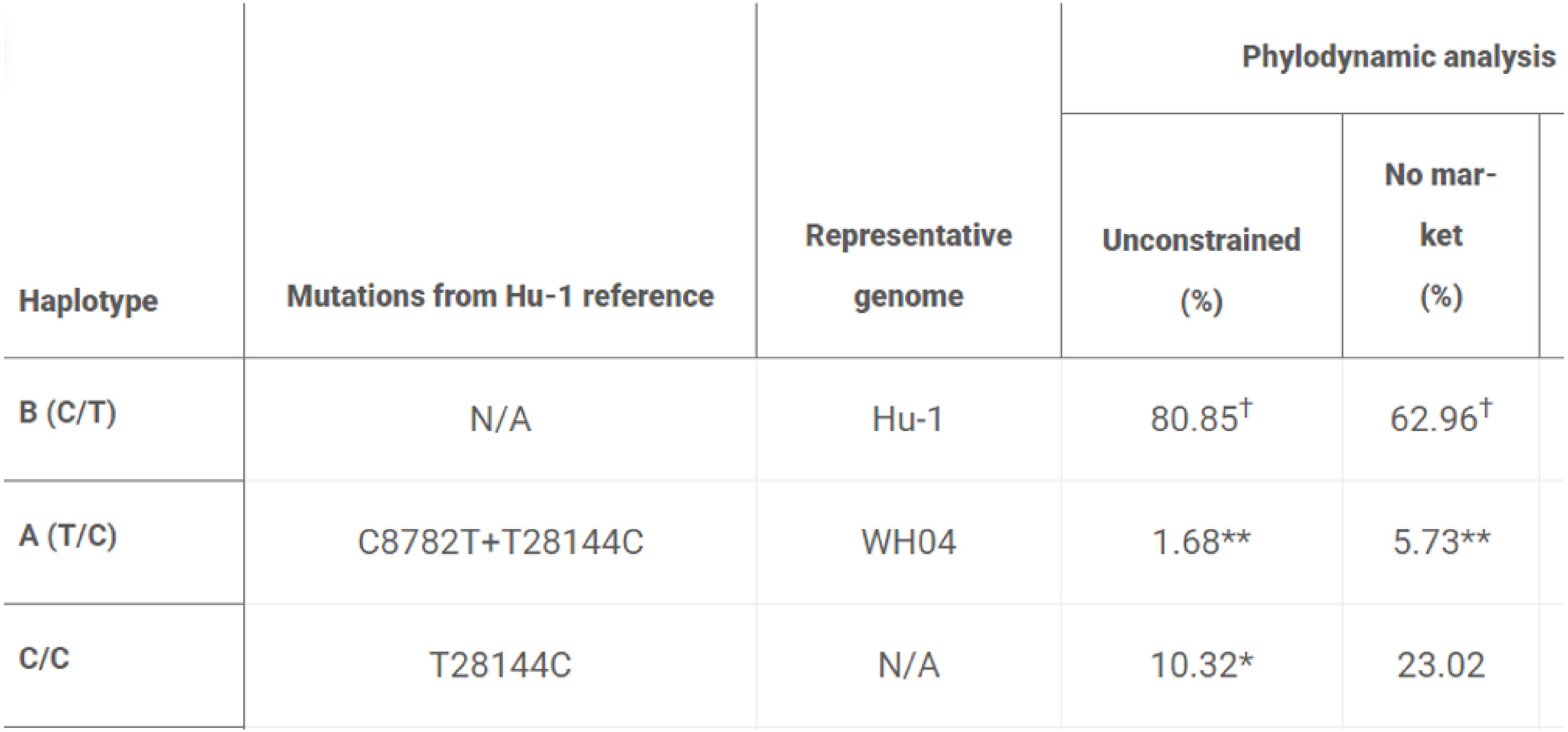
Figure from Pekar et al, 2022

Probabilities:

The odds of a lab leak are even lower than 3%.

If you think lineage A came from the lab, you need to explain why B looks older.

That’s bayes factor 48. Even if you ignore all the market genomes, it’s bayes factor of 11.

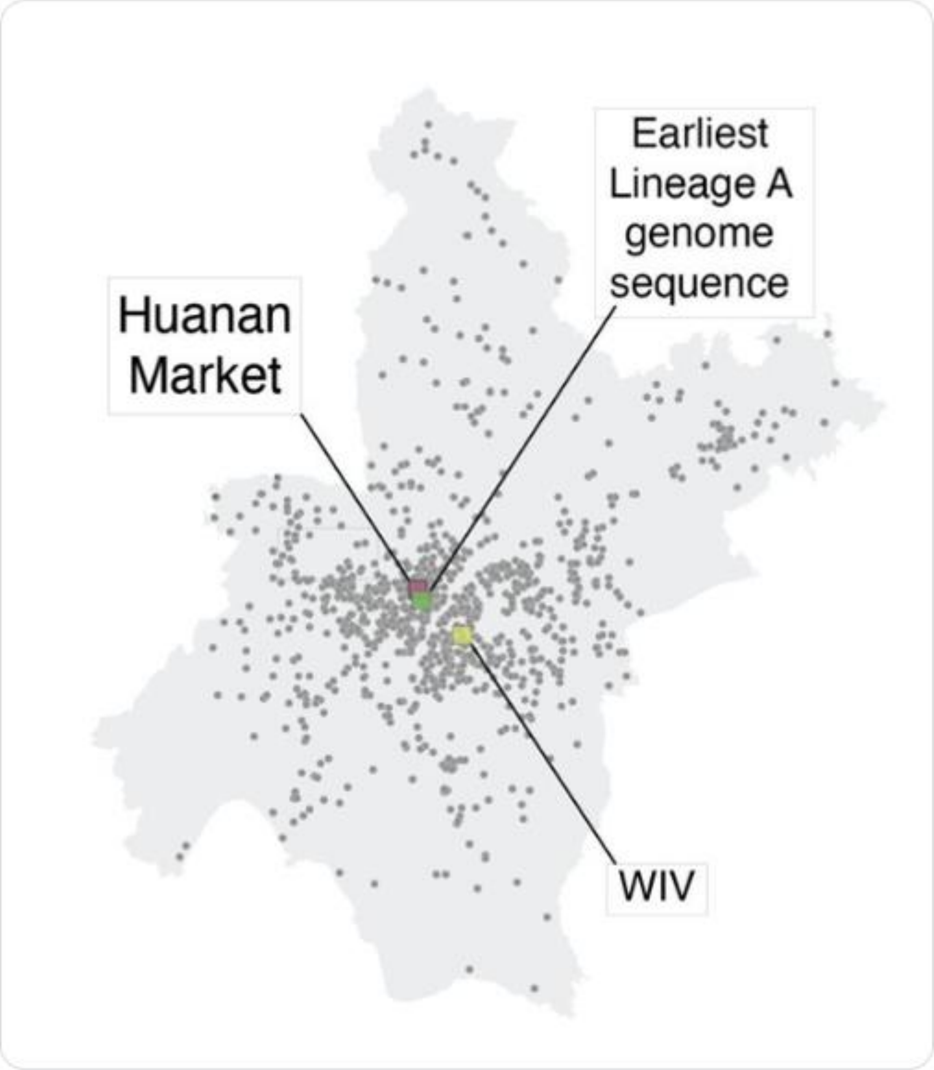


Haplotype	Mutations from Hu-1 reference	Representative genome	Phylodynamic analysis	
			Unconstrained (%)	No market (%)
B (C/T)	N/A	Hu-1	80.85[†]	62.96[†]
A (T/C)	C8782T+T28144C	WH04	1.68**	5.73**
C/C	T28144C	N/A	10.32*	23.02

Probabilities:

The first 2 lineage A cases were found closer to the market than expected by chance, if you think covid was actually all over town. (p = .001)

Maybe that’s a bayes factor of 50? Or 100?



Probabilities:

A lab leak spreads at the market: 1 in 10,000
It looks like 2 lineages: 1 in 4.2
It looks like B started before A: 1 in 11? Or 1 in 48?
2 earliest A cases found near market: 1 in 50?

The most positive samples are found
at a shop selling wild animals: 1 in 68
(10 out of 680 shops at the market)
That shop was previously fined
for illegal wildlife sales: 3 in 10

SARS and Covid started
in the same month: 1 in 12? Or 1 in 6?

Combined odds 1 in 63 billion chance

Any Bayesian analysis of covid's origins needs to account for all these coincidences,
not just the coincidence that the market is in the same city as a lab.
The odds of a lab leak are still lower than this -- we also need to include the odds that the lab had a precursor virus, that they modified it this way, that it leaked, that they successfully covered it up (we'll talk more about those things in the next debate).

Can the market origin be disproven?

I’d want to see clear proof of earlier cases, unlinked to the market.

That wouldn’t disprove a natural origin, since Covid could have started elsewhere in China.
The train station origin may still be more likely than the lab. But it could disprove the market origin.

Another line of argument might show genetic proof that the virus shows engineering, or something about it is so unlikely that it must have been created in a lab.

Evidence from the lab could also prove a lab origin, as could earlier cases linked to the lab.

Lots of other people have looked for earlier cases without finding any proof.

For examples, see searches by Jesse bloom or Francisco de Asis.

They found all the same articles I did.

Not only is there no good proof, people cite debunked arguments, like linking to the early paper with a December 1st case or pointing out the December 8th case even though both sides of the debate admit that's not the earliest case.

Is it possible the earliest cases were at the lab?

There are some claims from “anonymous US government sources”.

The sources are actually people from Trump’s state department.

The information is highly questionable.

THE WALL STREET JOURNAL.

◆ WSJ NEWS EXCLUSIVE | WORLD

Intelligence on Sick Staff at Wuhan Lab Fuels Debate on Covid-19 Origin

Report says researchers went to hospital in November 2019, shortly before confirmed outbreak; adds to calls for probe of whether virus escaped lab

A World Health Organization-led team investigating the origins of the Covid-19 pandemic visited the Wuhan Institute of Virology on Feb. 3.

PHOTO: HECTOR RETAMAL/AGENCE FRANCE-PRESSE/GETTY IMAGES

By Michael R. Gordon , Warren P. Strobel and Drew Hinshaw

May 23, 2021 2:57 pm ET

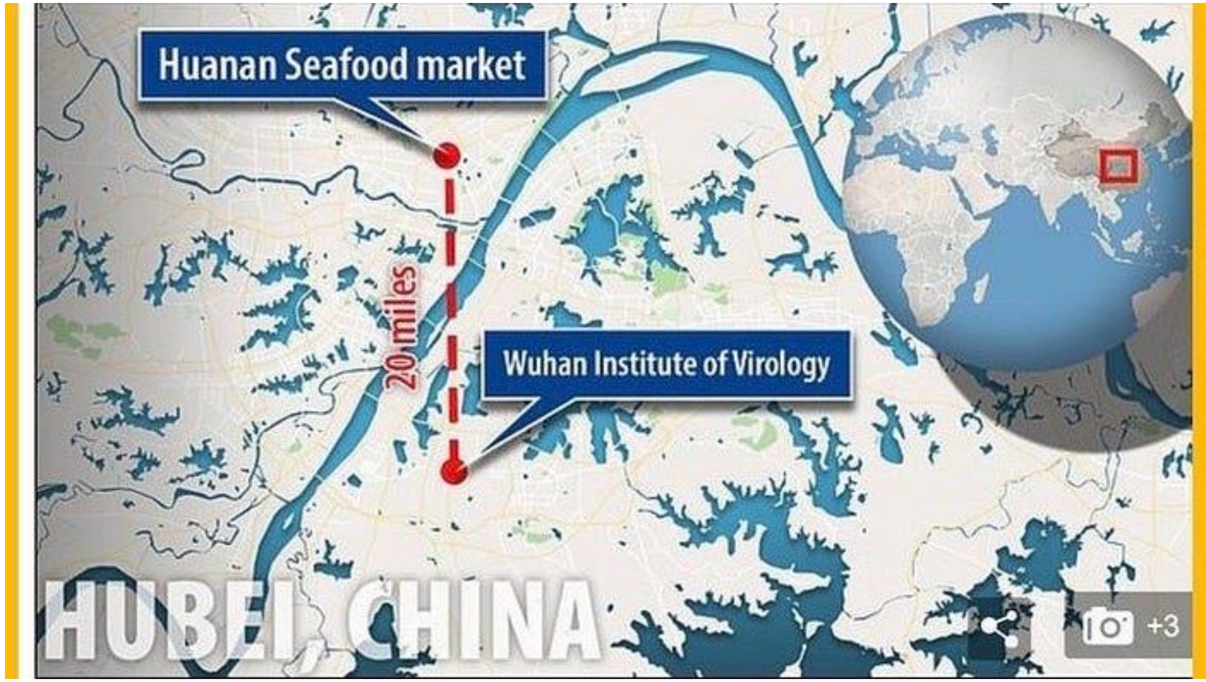
A brief history of the lab leak theory.

Brief history of lab leak theories:

January 9, 2020: Article on Radio Free Asia, a US-government-funded media outlet

January 19th, 2020: video in Chinese by Wang DingGang, a critic of the Chinese government

January 25th, 2020: Article on Gnews, a site run by Steve Bannon and the man funding him, Chinese billionaire Guo Wengui (also known as Miles Guo).



January 31st, 2020 preprint: Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV

Guo and Bannon teamed up with Hong Kong scientist Li Meng Yan, who claimed to be a Chinese whistleblower exposing the lab.

In September, 2020, she wrote a paper saying covid is a bioweapon. There's a critical review here.

Li Meng Yan is pictured here with Steve Bannon, Rudy Giuliani, and Wang DingGang, an associate of Guo:

In a 2020 interview with Li Meng Yan on Tucker Carlson, she describes the virus being intentionally released.

Bannon, Guo, DingGang, and Giuliani went on to be involved with a disinformation campaign about the 2020 presidential election.
(the election was most likely not stolen -- see Rootclaim's analysis or my analysis).

Steve Bannon has since been sentenced to jail time for contempt of Congress.

Guo Wengui was charged with defrauding people out of 1 billion dollars, in 2023.

When the authorities went to search Guo's apartment, his apartment building was mysteriously lit on fire.

$32m penthouse mysteriously catches fire during arrest of Chinese billionaire ally of Steve Bannon

Exiled Chinese billionaire Guo Wengui was taken into custody early Wednesday when federal agents swooped on his Central Park penthouse in the Sherry-Netherland Hotel on Manhattan's Upper East Side

Rachel Sharp, Alex Woodward • Thursday 16 March 2023 12:54

2021: lab leak goes mainstream

Nicholas Wade wrote an influential article for the Bulletin of Atomic scientists,
a non-profit that mostly worries about nuclear safety (“90 seconds to midnight”)

Jon Stewart supported lab leak in a Steven Colbert interview.

Lots of work from the DRASTIC collective.

Jesse Bloom and other scientists write a letter demanding a better Covid origins investigation.

“Viral” book by Matt Ridley and Alina Chan.

The Wall Street Journal reported that 3 workers were sick at the Wuhan institute of virology,
based on anonymous US government sources.

2021 article Wall Street Journal article by Michael Gordon

THE WALL STREET JOURNAL.

◆ WSJ NEWS EXCLUSIVE | WORLD

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PHOTO: HECTOR RETAMAL/AGENCE FRANCE-PRESSE/GETTY IMAGES

By Michael R. Gordon , Warren P. Strobel and Drew Hinshaw

May 23, 2021 2:57 pm ET

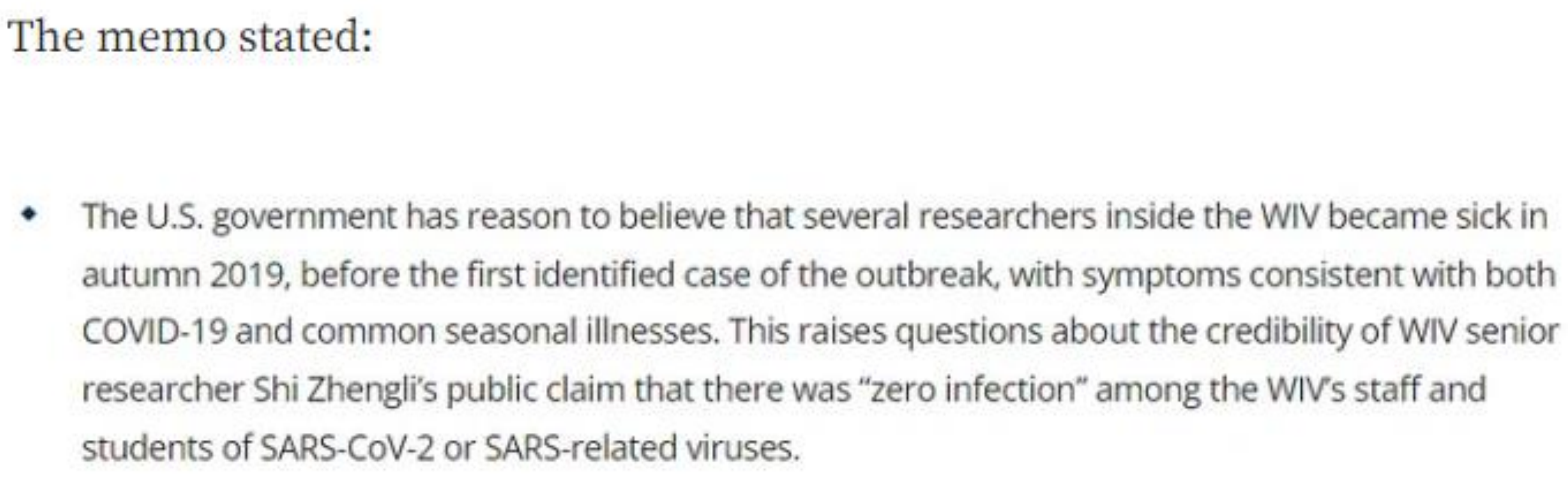
“One person said that [the intelligence] was provided by an international partner and was potentially significant but still in need of further investigation and additional corroboration.”

“Another person described the intelligence as stronger. “The information that we had coming from the various sources was of exquisite quality. It was very precise. What it didn’t tell you was exactly why they got sick,” he said, referring to the researchers.”

Did those 3 people at the WIV actually get sick?

We’ve never seen that intelligence.

It was first [mentioned by the US state department]() on January 15th, 2020, five days before the end of the Trump administration



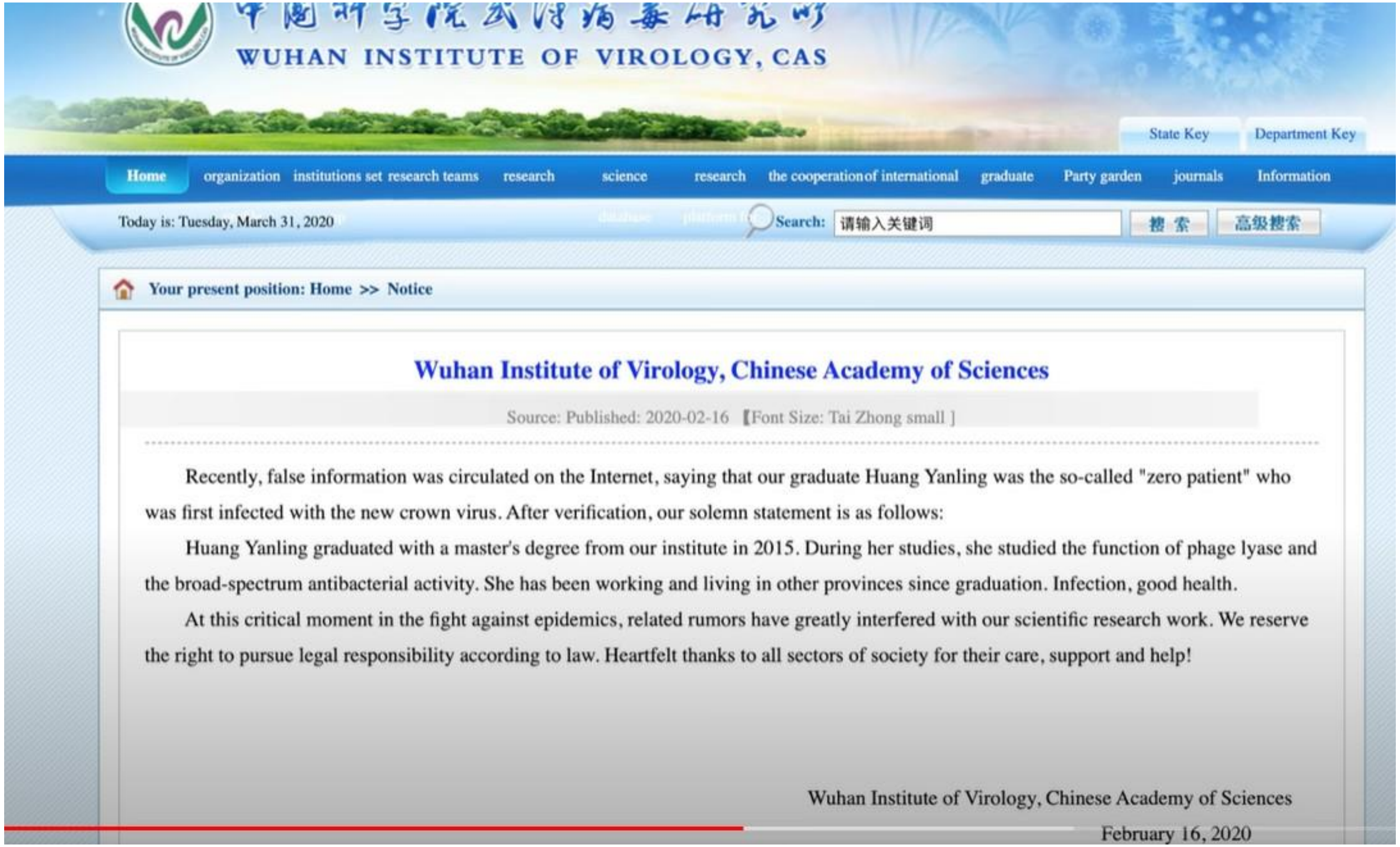
The memo stated:

- The U.S. government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illnesses. This raises questions about the credibility of WIV senior researcher Shi Zhengli’s public claim that there was “zero infection” among the WIV’s staff and students of SARS-CoV-2 or SARS-related viruses.

In February 2020, Chinese internet rumors said a woman named Huang Yanling was patient zero, at the lab, and she died from Covid.

She graduated from the WIV in 2015, it looks like [she was working in Guangzhou in 2019](#).

The Wuhan lab denied the rumors that she died:



Today is: Tuesday, March 31, 2020

Your present position: Home >> Notice

Wuhan Institute of Virology, Chinese Academy of Sciences

Source: Published: 2020-02-16 【Font Size: Tai Zhong small]

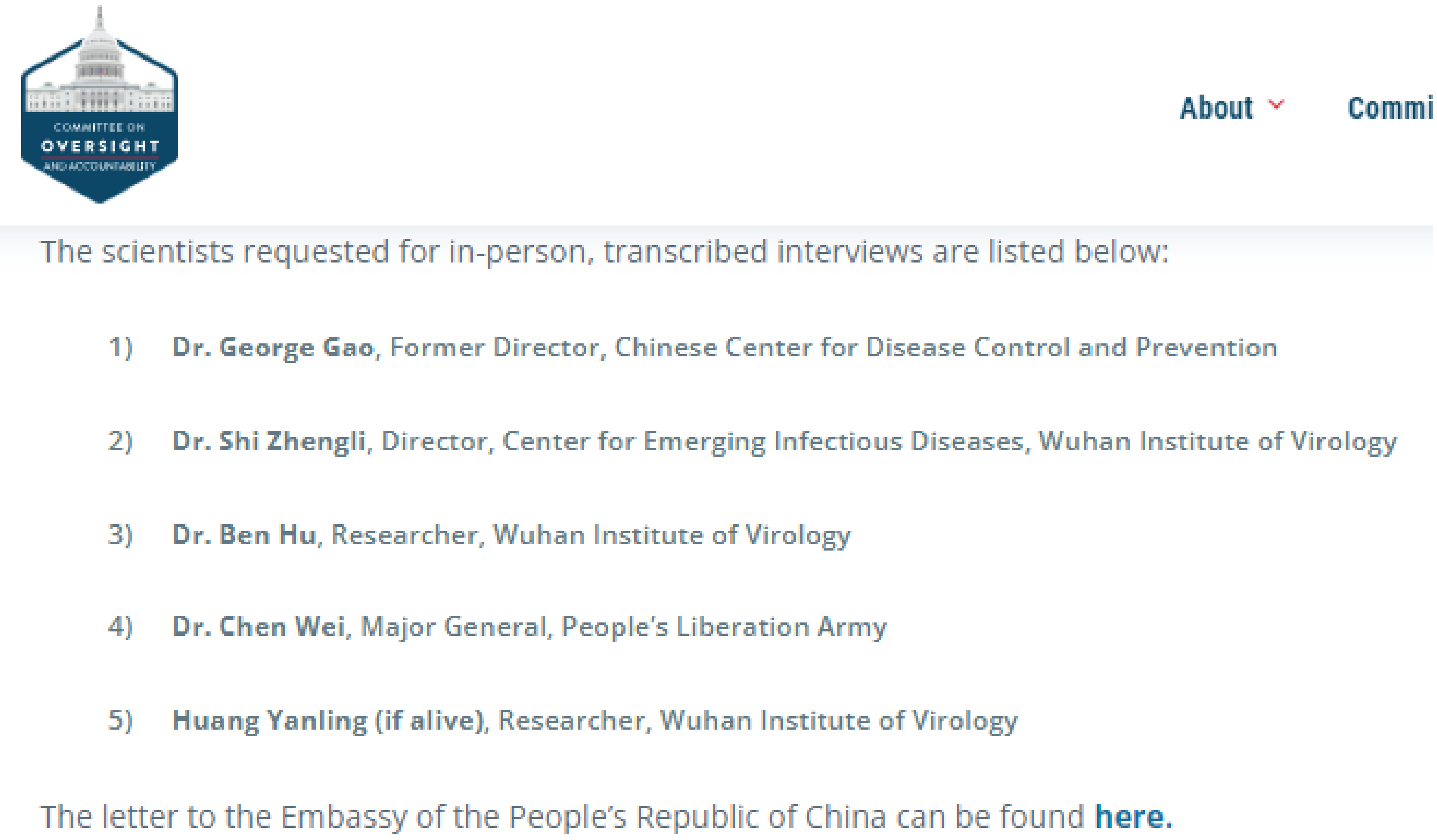
Recently, false information was circulated on the Internet, saying that our graduate Huang Yanling was the so-called "zero patient" who was first infected with the new crown virus. After verification, our solemn statement is as follows:

Huang Yanling graduated with a master's degree from our institute in 2015. During her studies, she studied the function of phage lyase and the broad-spectrum antibacterial activity. She has been working and living in other provinces since graduation. Infection, good health.

At this critical moment in the fight against epidemics, related rumors have greatly interfered with our scientific research work. We reserve the right to pursue legal responsibility according to law. Heartfelt thanks to all sectors of society for their care, support and help!

Wuhan Institute of Virology, Chinese Academy of Sciences
February 16, 2020

Almost all lab leak theories stopped talking about her,
but congressional Republicans did try to subpoena her in 2023:



The scientists requested for in-person, transcribed interviews are listed below:

1) **Dr. George Gao**, Former Director, Chinese Center for Disease Control and Prevention

2) **Dr. Shi Zhengli**, Director, Center for Emerging Infectious Diseases, Wuhan Institute of Virology

3) **Dr. Ben Hu**, Researcher, Wuhan Institute of Virology

4) **Dr. Chen Wei**, Major General, People's Liberation Army

5) **Huang Yanling (if alive)**, Researcher, Wuhan Institute of Virology

The letter to the Embassy of the People's Republic of China can be found **here.**

Trump made different claims about one sick researcher, back in April 2020, before his state department said it was 3 sick researchers:

Trump changed his story, in 2021:

David Asher, from the Trump state department, says he discovered this intelligence.

But he can’t keep his story straight.

He says the workers got sick in November. John Ratcliffe says they got sick in October.

When asked about the contradiction, David Asher refused to confirm which month it was.

In one interview, he received the intelligence from “2 foreign scientists working in Wuhan”

In another interview, he said the source was an Israeli newspaper.

In most versions, he said it was 3 sick researchers. In one case, he said that 3 researchers got sick and one of their wives died.

In one version, he said the pandemic was started in October by a monkey bite at the lab.

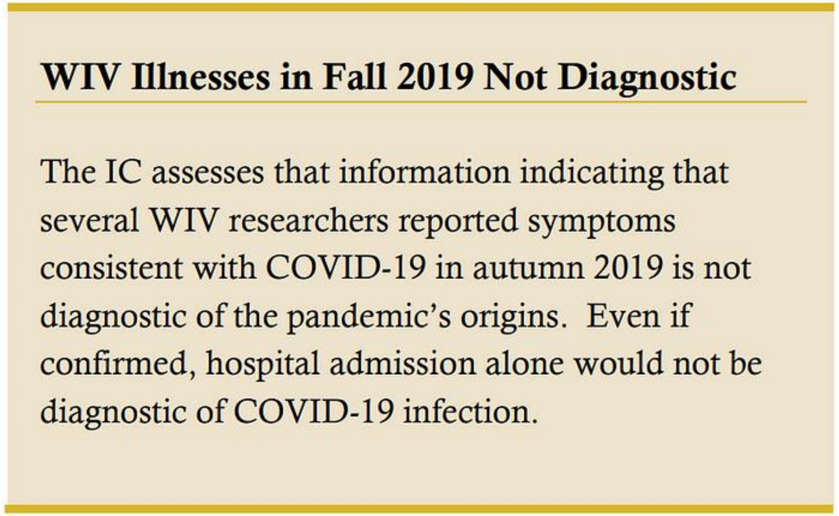
Other government reports can’t confirm 3 sick researchers:

The US senate report on covid doesn’t mention any such information.

The house GOP report on covid mentions it, but lists the WSJ article as the source.

This contradicts the other government reports that say Covid started in September.

Biden’s first intelligence report could not confirm it:



WIV Illnesses in Fall 2019 Not Diagnostic

The IC assesses that information indicating that several WIV researchers reported symptoms consistent with COVID-19 in autumn 2019 is not diagnostic of the pandemic’s origins. Even if confirmed, hospital admission alone would not be diagnostic of COVID-19 infection.

One writer of the Trump state department memo was asked for more details in a congressional hearing. He couldn’t give any more details, he said he wrote the memo to “raise interest in the subject”.

There was one foreign scientist working at the Wuhan lab in November 2019, Australian scientist Danielle Anderson. She says she was never sick, never had antibodies, and didn’t know of anyone else at the lab falling ill.

The WHO team’s investigation could not confirm that anyone got sick.

The hospitalization rate for covid is actually fairly low, let’s say 5%. For 3 people to end up in the hospital, you’d think that maybe 60 lab employees caught covid.

If the entire lab had gotten sick, it’s extremely unlikely that the first case cluster would be at a market across town, with no cases elsewhere.

One version of the “3 sick researchers” story says that the wife of one of the researchers died from covid.

It’s not impossible for a young person to die from covid, but it’s very unlikely. This detail has been omitted most other times that Asher told the story.

WIV scientists acted normally the whole time.

In December, Shi Zhengli travelled to Singapore for a conference about the Nipah virus.

In January, a month after the outbreak started, they all went out to dinner in Wuhan.

December 10th, Image from Dr Benhur Lee

January 15th, Image from this article

Who is Michael Gordon, the Wall Street Journal reporter?

He’s the guy who first announced that Iraq has WMD’s, back in 2002:

WORLD | THREATS AND RESPONSES: THE IRAQIS

THREATS AND RESPONSES: THE IRAQIS; U.S. SAYS HUSSEIN INTENSIFIES QUEST FOR A-BOMB PARTS

By MICHAEL R. GORDON and JUDITH MILLER SEPT. 8, 2002

MARCH 20, 2013

Looking Back at Iraq With...Michael Gordon?

PETER HART

Michael Gordon was the lead author on that infamous aluminum tubes article.

A few days into the U.S. bombing (3/25/13), Gordon appeared on CNN to endorse the bombing of Iraqi TV's offices, calling it "an appropriate target," since "we're trying to send the exact opposite message."

When U.S. politicians began to seriously consider a withdrawal of U.S. troops, Gordon criticized that policy, especially in one article (11/15/06) headlined, "Get Out of Iraq Now? Not So Fast, Experts Say"

He went on the Charlie Rose show (1/18/07) to endorse a troop surge. In 2007, Gordon wrote articles, relying heavily on anonymous U.S. sources, alleging that the Iranian government was sending weapons into Iraq (Action Alert, 2/16/07).

"if there is ever another moment that requires reporters to faithfully record the views of anonymous U.S. officials as they make their case for war, it's a safe bet that Michael Gordon will be there to do that job."

2023: Department of Energy announces a low confidence opinion that Covid is a lab leak.

First reported in the Wall Street Journal, by Michael Gordon.

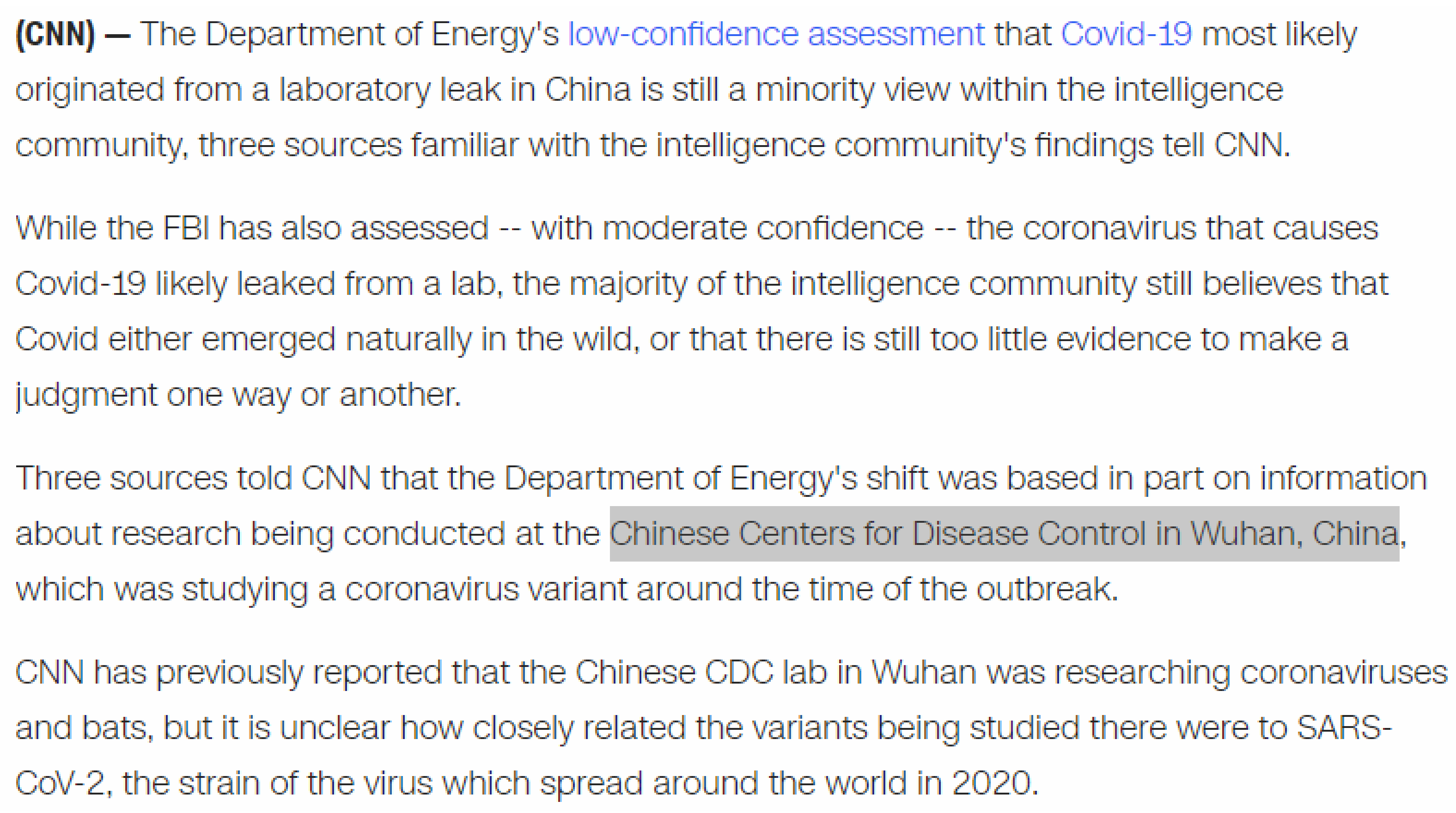
Lab Leak Most Likely Origin of Covid-19 Pandemic, Energy Department Now Says

U.S. agency's revised assessment is based on new intelligence

By Michael R. Gordon *and Warren P. Strobel*

Updated Feb. 26, 2023 4:29 pm ET

The 2023 article contradicts the 2021 article, it’s not even talking about the same lab.



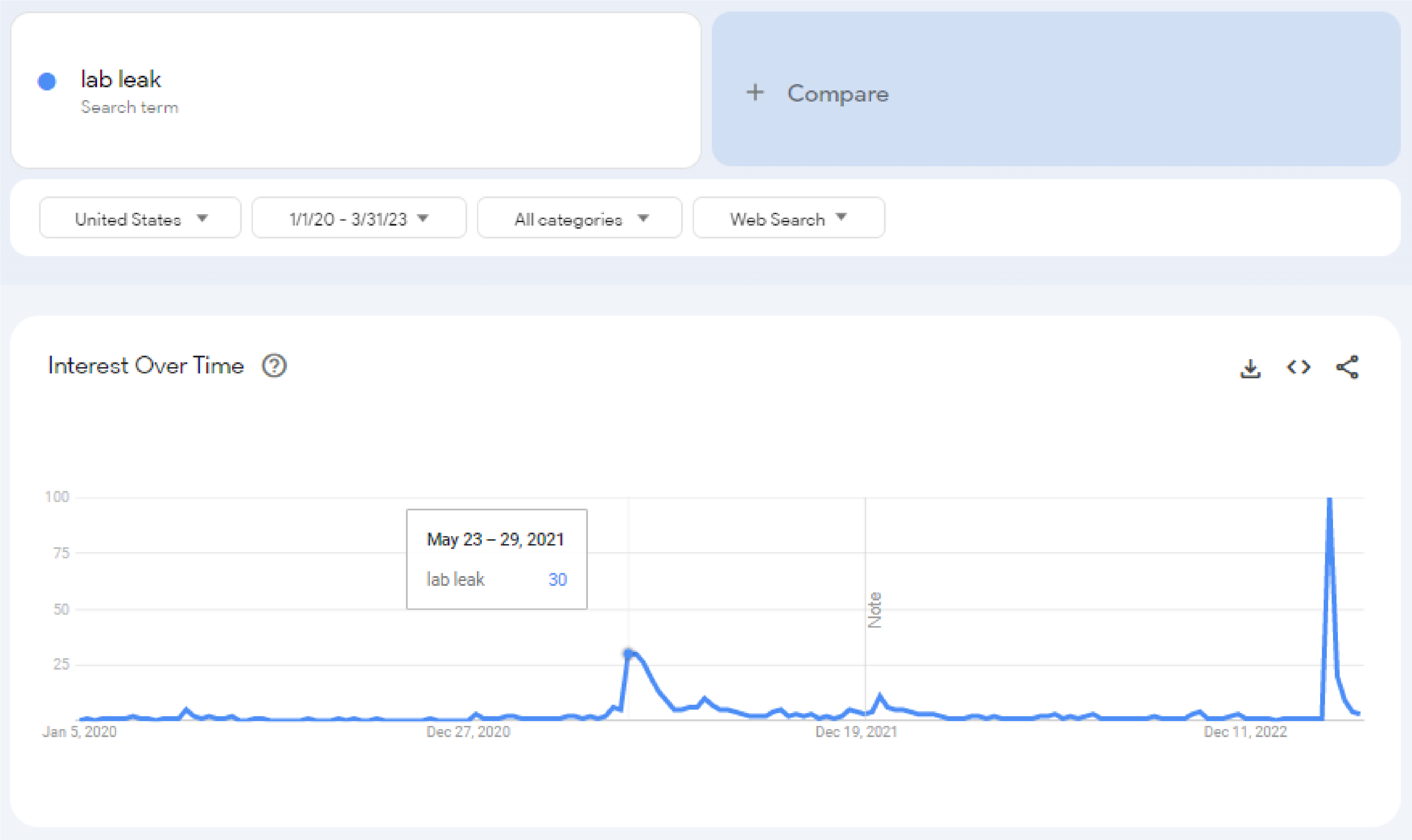
(CNN) — The Department of Energy's low-confidence assessment that Covid-19 most likely originated from a laboratory leak in China is still a minority view within the intelligence community, three sources familiar with the intelligence community's findings tell CNN.

While the FBI has also assessed -- with moderate confidence -- the coronavirus that causes Covid-19 likely leaked from a lab, the majority of the intelligence community still believes that Covid either emerged naturally in the wild, or that there is still too little evidence to make a judgment one way or another.

Three sources told CNN that the Department of Energy's shift was based in part on information about research being conducted at the Chinese Centers for Disease Control in Wuhan, China, which was studying a coronavirus variant around the time of the outbreak.

CNN has previously reported that the Chinese CDC lab in Wuhan was researching coronaviruses and bats, but it is unclear how closely related the variants being studied there were to SARS-CoV-2, the strain of the virus which spread around the world in 2020.

Google search trends for "lab leak" show 2 spikes of interest



lab leak
Search term

United States
1/1/20 - 3/31/23
All categories
Web Search

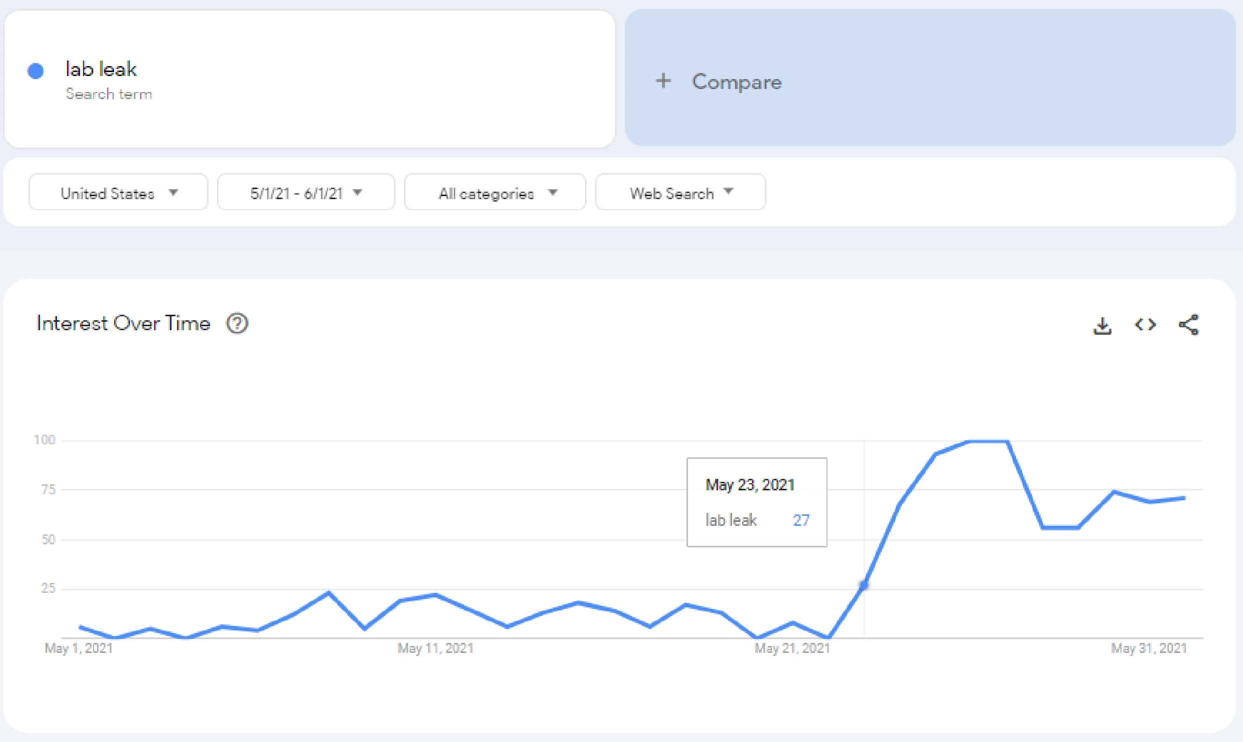
Interest Over Time

May 23 – 29, 2021
lab leak 30

In both cases, the uptick starts the day that Gordon wrote his articles.

His first article: May 23, 2021
His second: Feb 26, 2023

Other newspapers reported the same thing, citing the Wall Street Journal as the source.

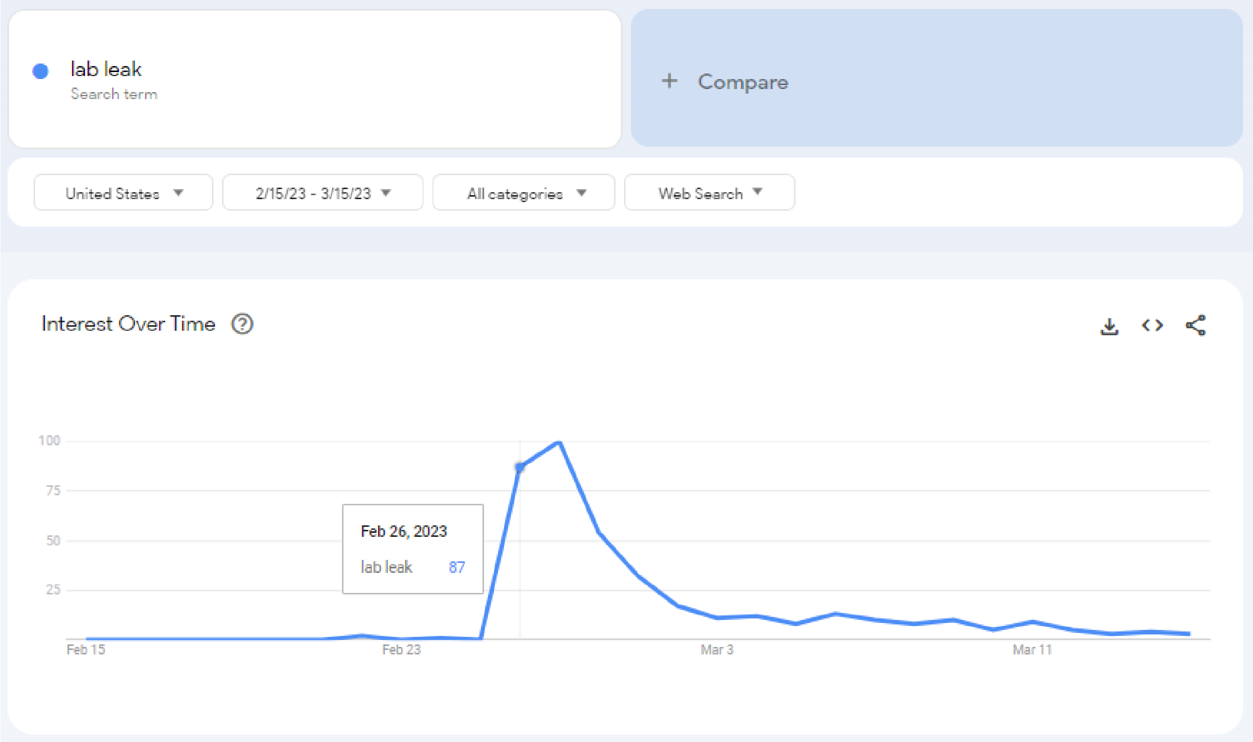


lab leak
Search term

United States
5/1/21 - 6/1/21
All categories
Web Search

Interest Over Time

May 23, 2021
lab leak 27



lab leak
Search term

United States
2/15/23 - 3/15/23
All categories
Web Search

Interest Over Time

Feb 26, 2023
lab leak 87

June 2023: substack article from Michael Shellenberger and Matt Taibbi named 3 scientists

First People Sickened By COVID-19 Were Chinese Scientists At Wuhan Institute Of Virology, Say US Government Sources

The three scientists were engaged in "gain-of-function" research on SARS-like coronaviruses when they fell ill

MICHAEL SHELLENBERGER, MATT TAIBBI, AND ALEX GUTENTAG
JUN 13, 2023

Ben Hu, one of threee "patients zero," and a researcher who led the Wuhan Institute of Virology's "gain-of-function" research on SARS-like coronaviruses, which increases the infectiousness of viruses.

Article cites "anonymous government sources".

It names Wuhan scientists Ben Hu, Yu Ping, and Yan Zhu, as the first patients infected with covid in November 2019.

One week earlier the same author reported this:

US Has 12 Or More Alien Spacecraft, Say Military And Intelligence Contractors

Military and intelligence agencies are withholding evidence from Congress, sources say

MICHAEL SHELLENBERGER
JUN 7, 2023

U.S.-Funded Scientist Among Three Chinese Researchers Who Fell Ill Amid Early Covid-19 Outbreak

Identification of three who worked at Wuhan Institute of Virology fuels suspicion for proponents of lab-leak theory

The Government Accountability Office noted last week that some coronavirus research at the Wuhan Institute of Virology in Wuhan, China, was funded by U.S. agencies.

PHOTO: HECTOR RETAMAL/AGENCE FRANCE-PRESSE/GETTY IMAGES

By Michael R. Gordon and Warren P. Strobel

June 20, 2023 10:00 am ET

One week later, a WSJ article reports the same 3 names.

Article is again written by Michael Gordon.

It also cites only anonymous sources.

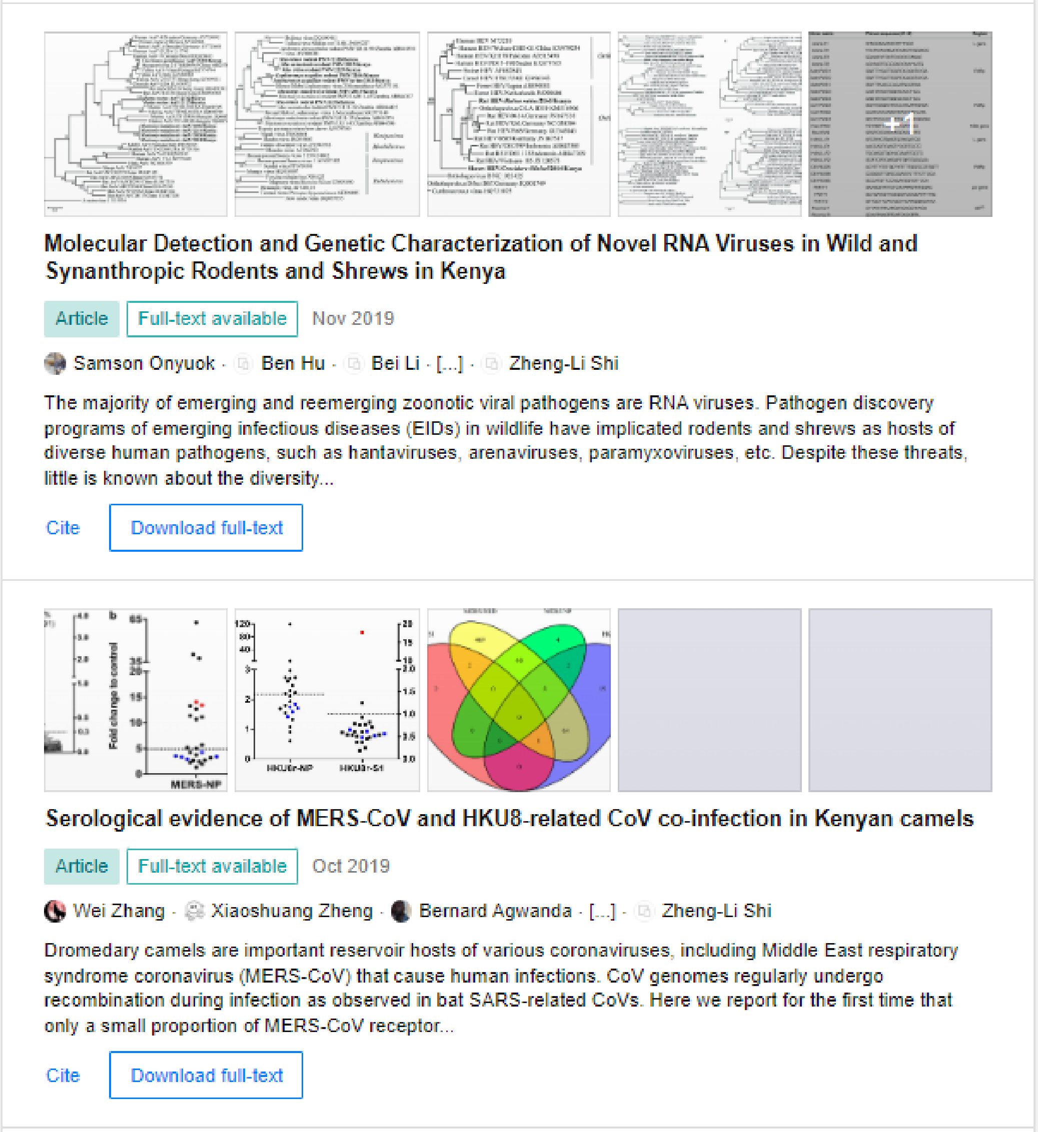
There are several reasons to doubt the names

Name ordering is inconsistent. It should be Ben Hu, Ping Yu, and Yan Zhu, for consistency.
That indicates someone just pulled the names off of papers written by the 3 -- Ping Yu
wrote a thesis that was popular among lab leak theorists.

Ben Hu, Ping Yu, and Shi Zhengli were asked for response by reporter Jon Cohen.
They stated they never got sick in fall 2019 and all tested negative for covid antibodies in March 2020.

Ping Yu was a student at the lab who graduated summer 2019, it's not clear if she was even
at the WIV in November 2019. Her work was also computational, she didn't do lab experiments.

Ben Hu published papers in October and November 2019, It looks like he was working on MERS viruses in Kenyan camels and novel RNA viruses in rodents in Kenya, around the time he supposedly would have gotten sick.



Molecular Detection and Genetic Characterization of Novel RNA Viruses in Wild and Synanthropic Rodents and Shrews in Kenya

Nov 2019

Samson Onyuok · Ben Hu · Bei Li · [...] · Zheng-Li Shi

The majority of emerging and reemerging zoonotic viral pathogens are RNA viruses. Pathogen discovery programs of emerging infectious diseases (EIDs) in wildlife have implicated rodents and shrews as hosts of diverse human pathogens, such as hantaviruses, arenaviruses, paramyxoviruses, etc. Despite these threats, little is known about the diversity...

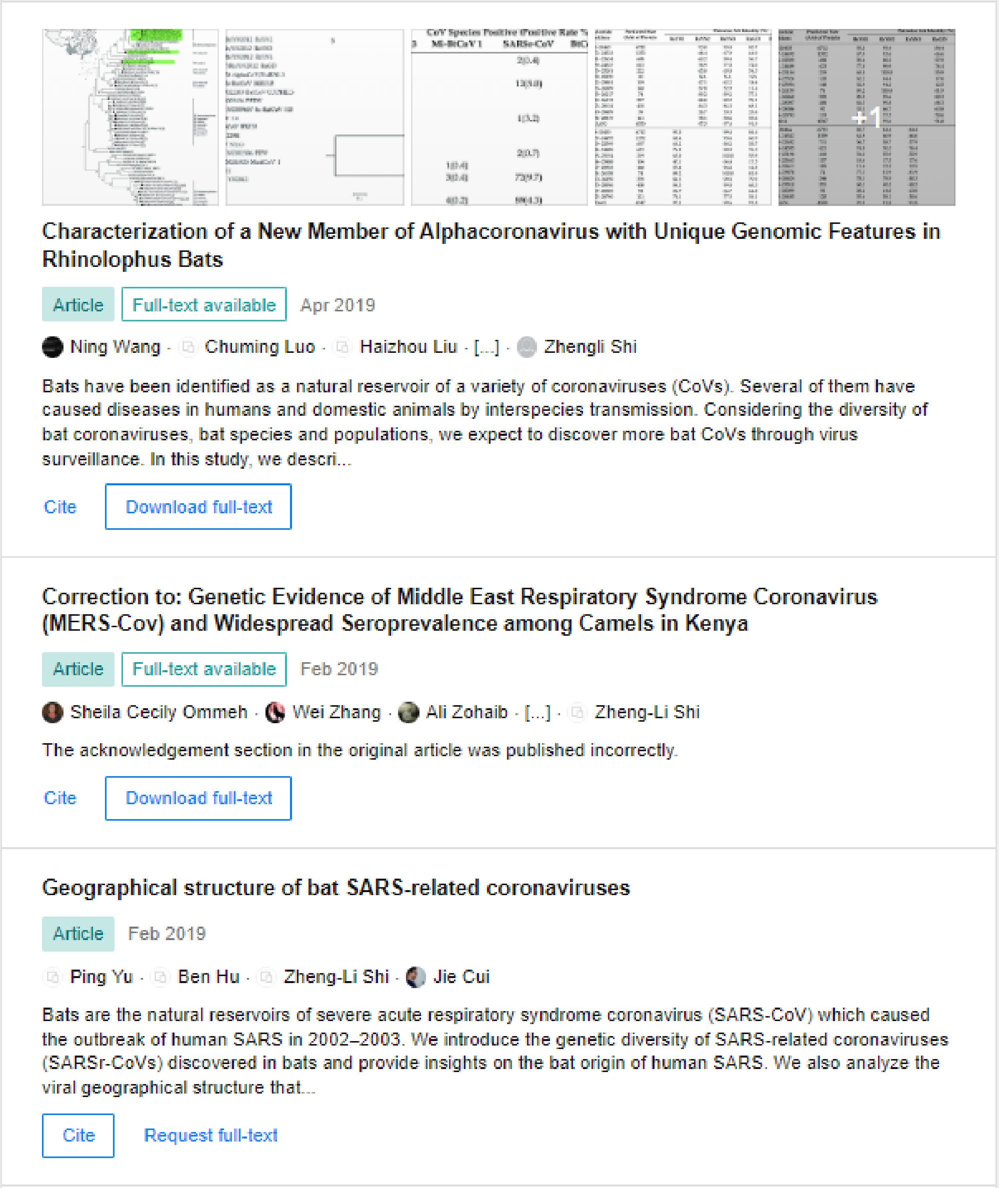
Serological evidence of MERS-CoV and HKU8-related CoV co-infection in Kenyan camels

Oct 2019

Wei Zhang · Xiaoshuang Zheng · Bernard Agwanda · [...] · Zheng-Li Shi

Dromedary camels are important reservoir hosts of various coronaviruses, including Middle East respiratory syndrome coronavirus (MERS-CoV) that cause human infections. CoV genomes regularly undergo recombination during infection as observed in bat SARS-related CoVs. Here we report for the first time that only a small proportion of MERS-CoV receptor...

Earlier in the year he was working on alphacoronaviruses. He is co-author of a paper on SARS viruses with Ping Yu from February. That paper just described their geography.



Characterization of a New Member of Alphacoronavirus with Unique Genomic Features in Rhinolophus Bats

Apr 2019

Ning Wang · Chuming Luo · Haizhou Liu · [...] · Zhengli Shi

Bats have been identified as a natural reservoir of a variety of coronaviruses (CoVs). Several of them have caused diseases in humans and domestic animals by interspecies transmission. Considering the diversity of bat coronaviruses, bat species and populations, we expect to discover more bat CoVs through virus surveillance. In this study, we descri...

Correction to: Genetic Evidence of Middle East Respiratory Syndrome Coronavirus (MERS-Cov) and Widespread Seroprevalence among Camels in Kenya

Feb 2019

Sheila Cecily Ommeh · Wei Zhang · Ali Zohaib · [...] · Zheng-Li Shi

The acknowledgement section in the original article was published incorrectly.

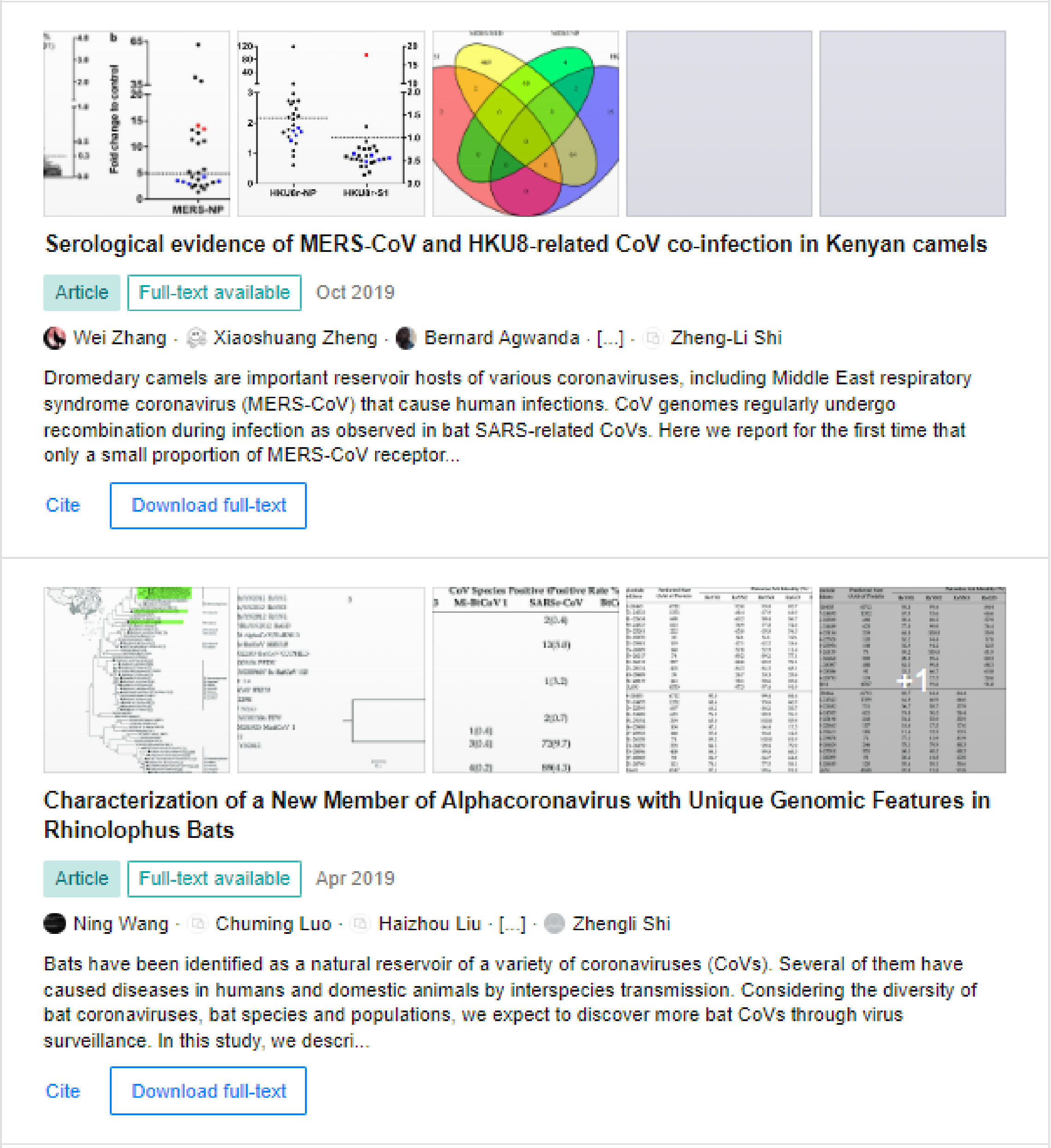
Geographical structure of bat SARS-related coronaviruses

Feb 2019

Ping Yu · Ben Hu · Zheng-Li Shi · Jie Cui

Bats are the natural reservoirs of severe acute respiratory syndrome coronavirus (SARS-CoV) which caused the outbreak of human SARS in 2002–2003. We introduce the genetic diversity of SARS-related coronaviruses (SARSr-CoVs) discovered in bats and provide insights on the bat origin of human SARS. We also analyze the viral geographical structure that...

Yan Zhu is co-author on 2 of those papers, and also worked on several other viruses earlier in 2019:



Serological evidence of MERS-CoV and HKU8-related CoV co-infection in Kenyan camels

Article · Full-text available · Oct 2019

Wei Zhang · Xiaoshuang Zheng · Bernard Agwanda · [...] · Zheng-Li Shi

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Cite · Download full-text

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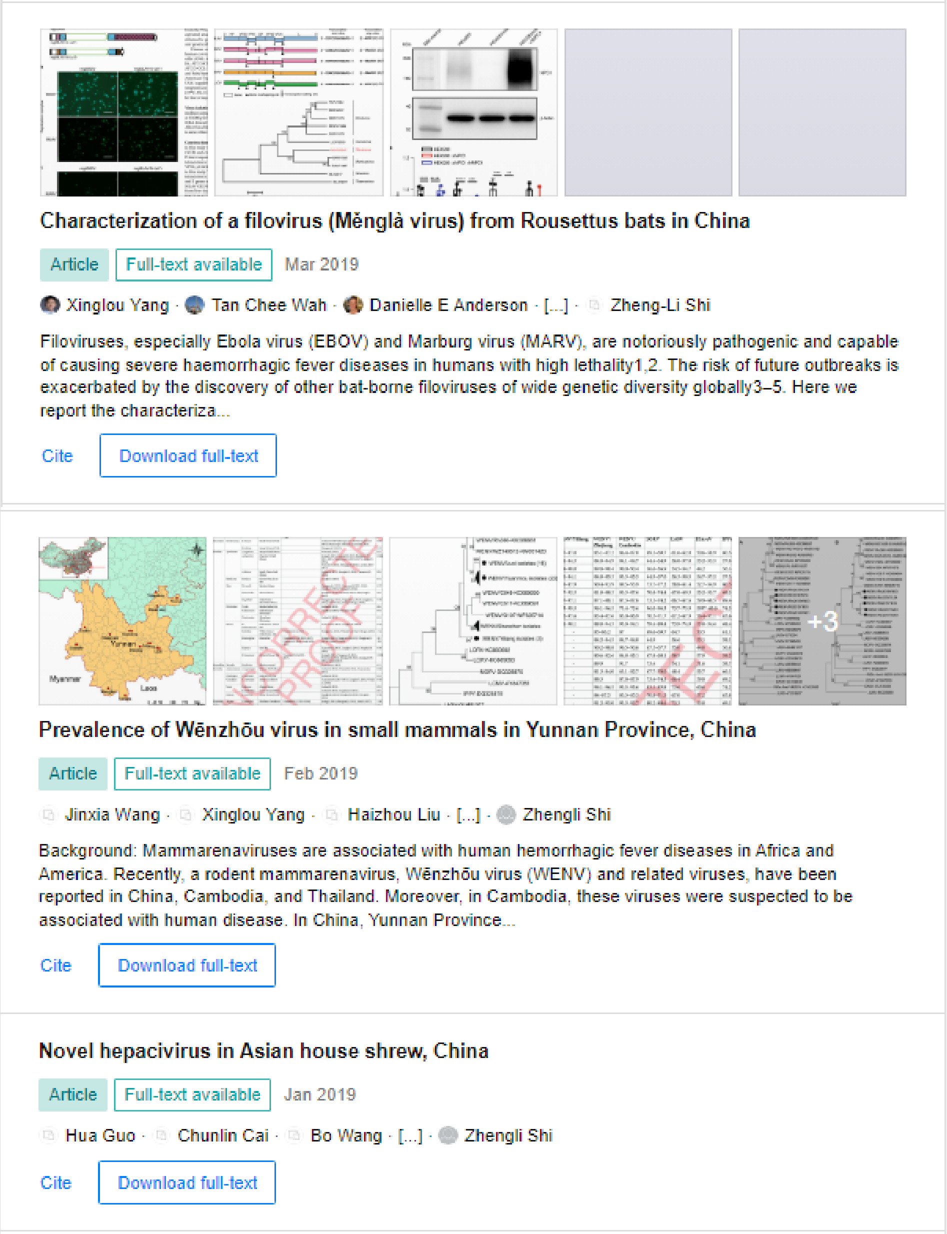


Characterization of a filovirus (Měnglà virus) from Rousettus bats in China

Article · Full-text available · Mar 2019

Xinglou Yang · Tan Chee Wah · Danielle E Anderson · [...] · Zheng-Li Shi

Filoviruses, especially Ebola virus (EBOV) and Marburg virus (MARV), are notoriously pathogenic and capable of causing severe haemorrhagic fever diseases in humans with high lethality1,2. The risk of future outbreaks is exacerbated by the discovery of other bat-borne filoviruses of wide genetic diversity globally3–5. Here we report the characteriza...

Cite · Download full-text

Prevalence of Wēnzhōu virus in small mammals in Yunnan Province, China

Article · Full-text available · Feb 2019

Jinxia Wang · Xinglou Yang · Haizhou Liu · [...] · Zhengli Shi

Background: Mammarenaviruses are associated with human hemorrhagic fever diseases in Africa and America. Recently, a rodent mammarenavirus, Wēnzhōu virus (WENV) and related viruses, have been reported in China, Cambodia, and Thailand. Moreover, in Cambodia, these viruses were suspected to be associated with human disease. In China, Yunnan Province...

Cite · Download full-text

Novel hepacivirus in Asian house shrew, China

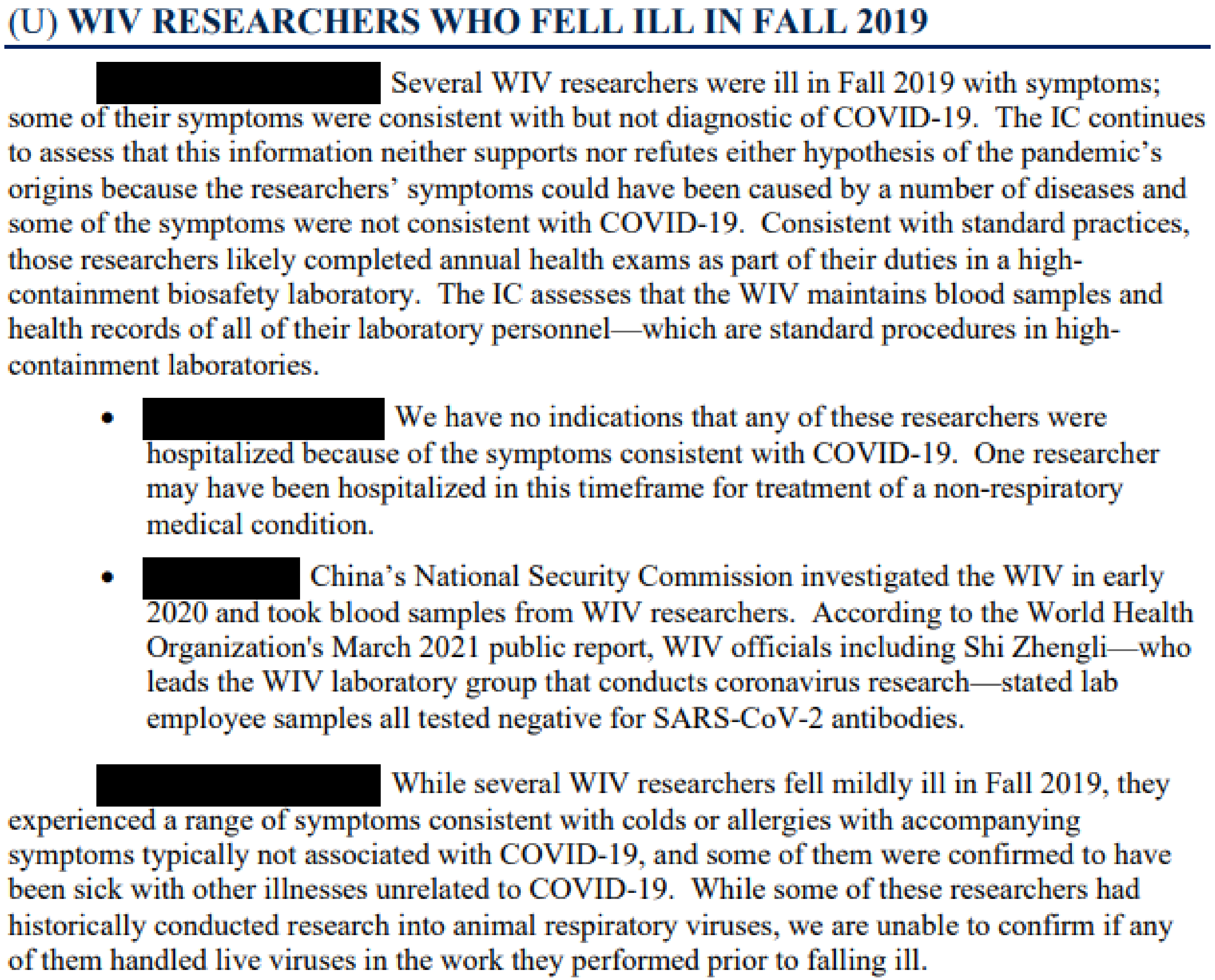
Article · Full-text available · Jan 2019

Hua Guo · Chunlin Cai · Bo Wang · [...] · Zhengli Shi

Cite · Download full-text

Jim Hines, the top ranking Democrat on the house intelligence committee, says he’s seen all the classified information, and there’s no conclusive evidence of a lab leak.

Declassified intelligence report on 6/23/2023 did not confirm the details about the 3 sick employees:



(U) WIV RESEARCHERS WHO FELL ILL IN FALL 2019

[redacted] Several WIV researchers were ill in Fall 2019 with symptoms; some of their symptoms were consistent with but not diagnostic of COVID-19. The IC continues to assess that this information neither supports nor refutes either hypothesis of the pandemic’s origins because the researchers’ symptoms could have been caused by a number of diseases and some of the symptoms were not consistent with COVID-19. Consistent with standard practices, those researchers likely completed annual health exams as part of their duties in a high-containment biosafety laboratory. The IC assesses that the WIV maintains blood samples and health records of all of their laboratory personnel—which are standard procedures in high-containment laboratories.

- [redacted] We have no indications that any of these researchers were hospitalized because of the symptoms consistent with COVID-19. One researcher may have been hospitalized in this timeframe for treatment of a non-respiratory medical condition.
- [redacted] China’s National Security Commission investigated the WIV in early 2020 and took blood samples from WIV researchers. According to the World Health Organization's March 2021 public report, WIV officials including Shi Zhengli—who leads the WIV laboratory group that conducts coronavirus research—stated lab employee samples all tested negative for SARS-CoV-2 antibodies.

[redacted] While several WIV researchers fell mildly ill in Fall 2019, they experienced a range of symptoms consistent with colds or allergies with accompanying symptoms typically not associated with COVID-19, and some of them were confirmed to have been sick with other illnesses unrelated to COVID-19. While some of these researchers had historically conducted research into animal respiratory viruses, we are unable to confirm if any of them handled live viruses in the work they performed prior to falling ill.

The “3 sick WIV researchers” story looks like an obvious misinformation campaign

It was spread by people involved with other misinformation campaigns.

Trump had his “stolen election” campaign at the same time the “3 sick researchers” story started.

Before becoming Trump’s Director of National intelligence, John Ratcliffe was criticized for following Qanon and 9/11 truther accounts on Twitter.

Michael Gordon was involved with starting the war in Iraq.

David Asher works with the Hudson Institute, which also advocated for the war in Iraq.

David Asher can’t keep his story straight.

In Conclusion:

Lab leak is highly politicized, with some bad actors supporting it.

All the evidence points to a natural origin at Huanan market, the most likely place for a natural virus to emerge in Wuhan.

There are many lab leak theories, most of them must be wrong.

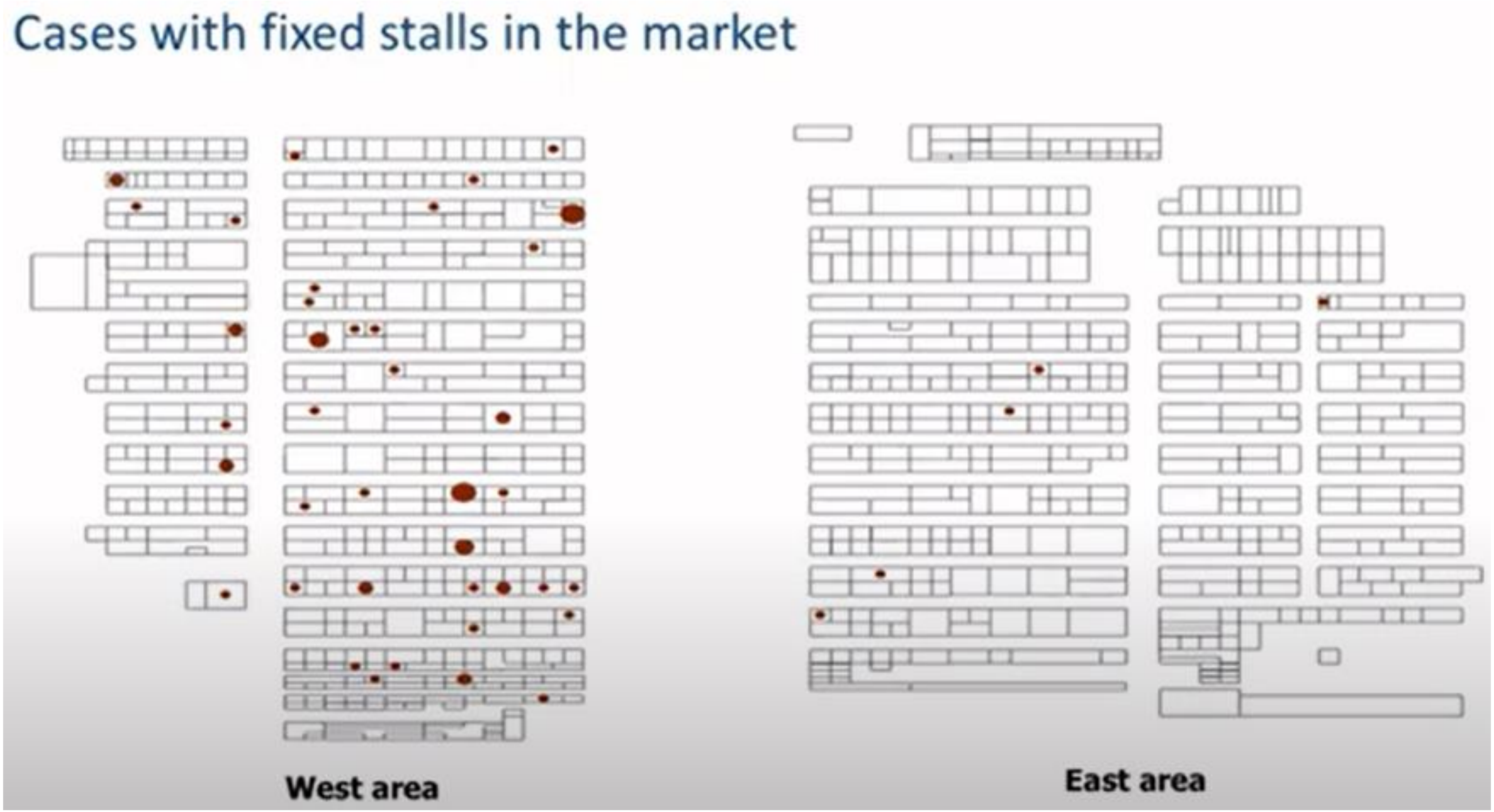
A November lab leak is still possible, with some low probability.

We still need to talk about genetics, to look for evidence there.

And let’s see how my opponent’s view differs on the evidence.

Supplemental information

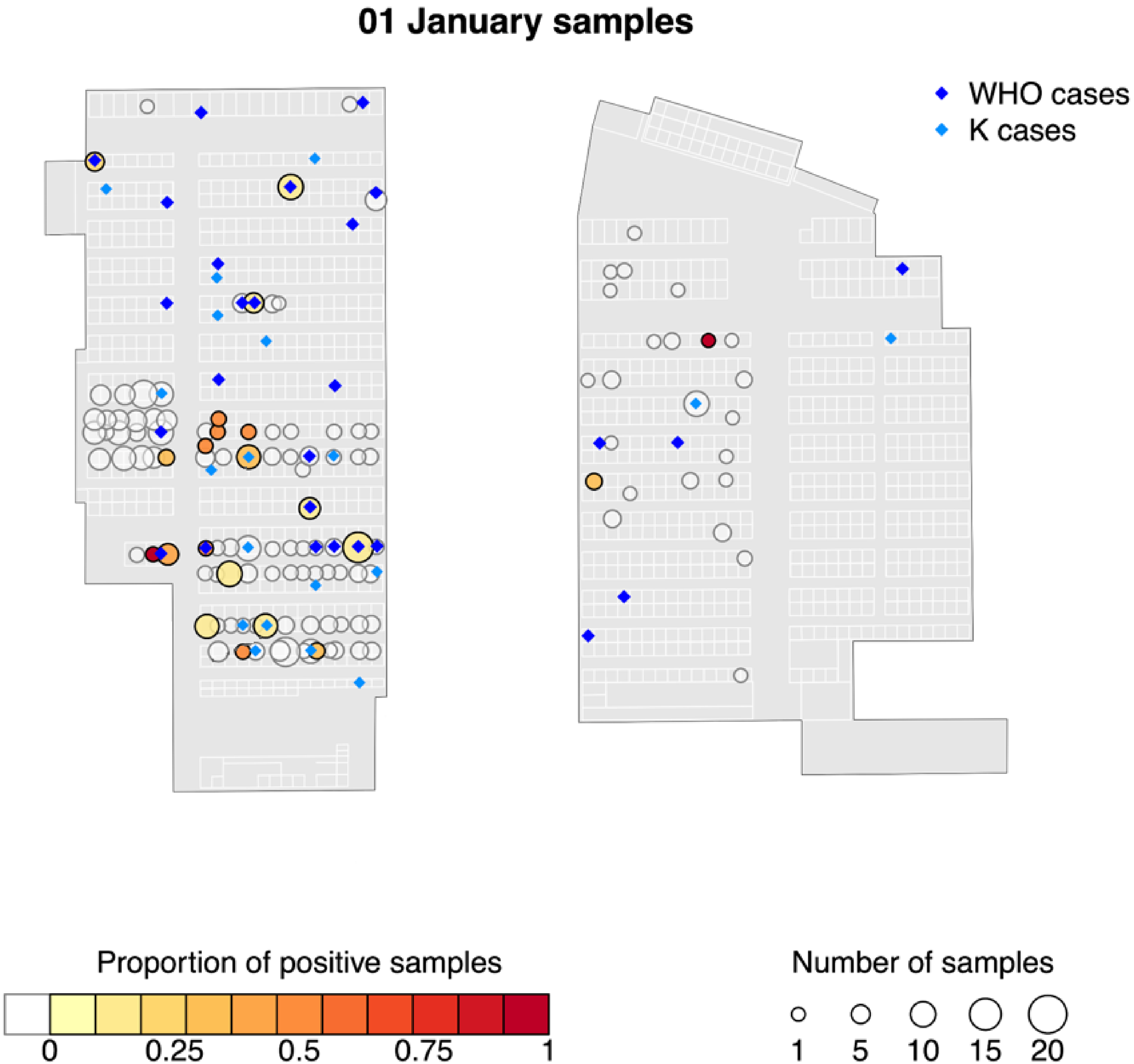
Marion Koopman’s map of all cases:



Cases with fixed stalls in the market

Liu et al 2023 data includes positive and negative sample numbers

Jan 1st sampling focused on stalls with known cases and blocks near these cases

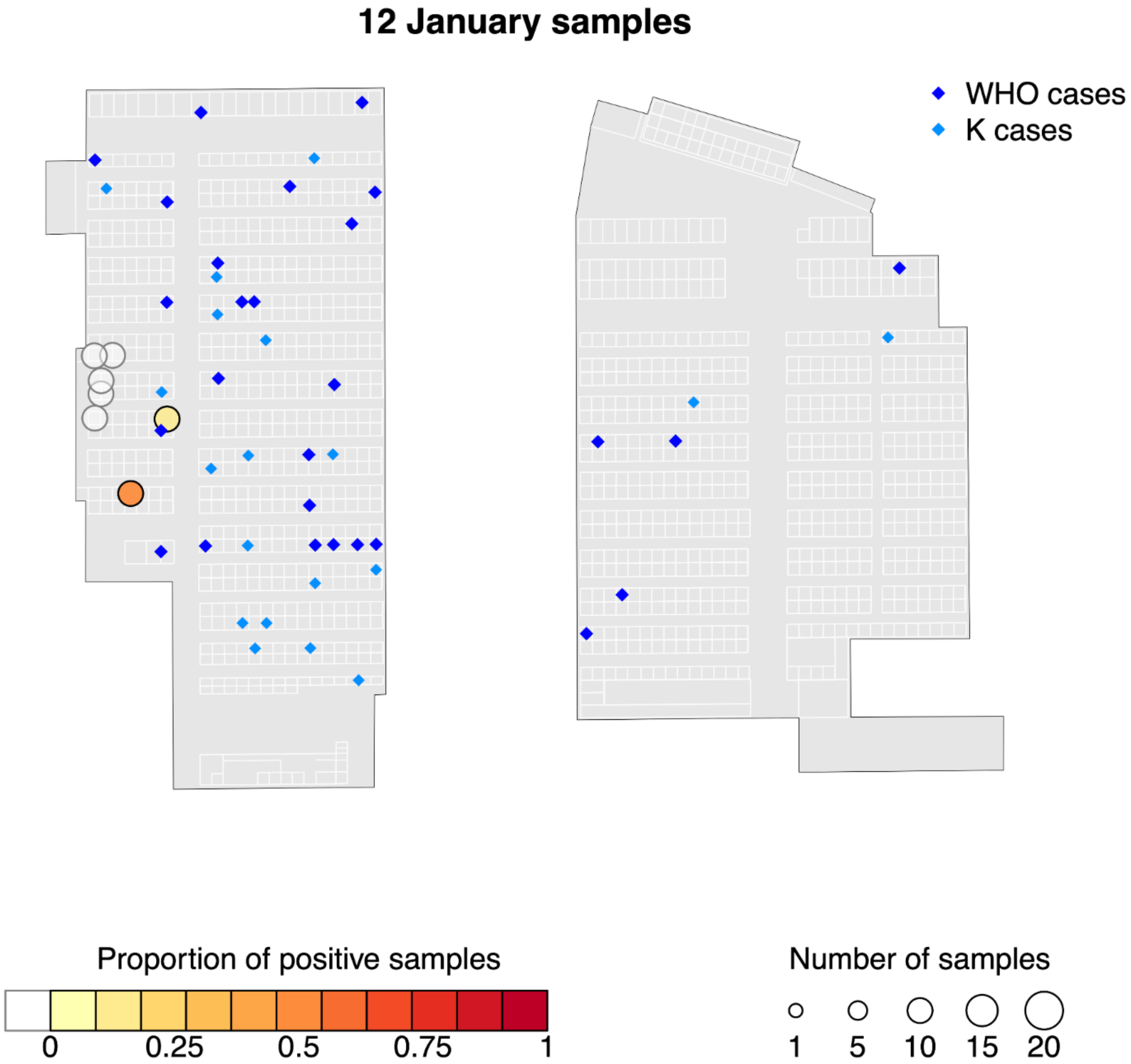


Jan 12th testing focused on the 7 wildlife shops

2 shops tested positive

6-29: raccoon dog shop,
5 positive samples. 2 positives taken later from water drains.

8-25: hedgehog shop, 1 positive sample this day.
More positive samples taken in February.
Positive warehouse samples associated with this shop.



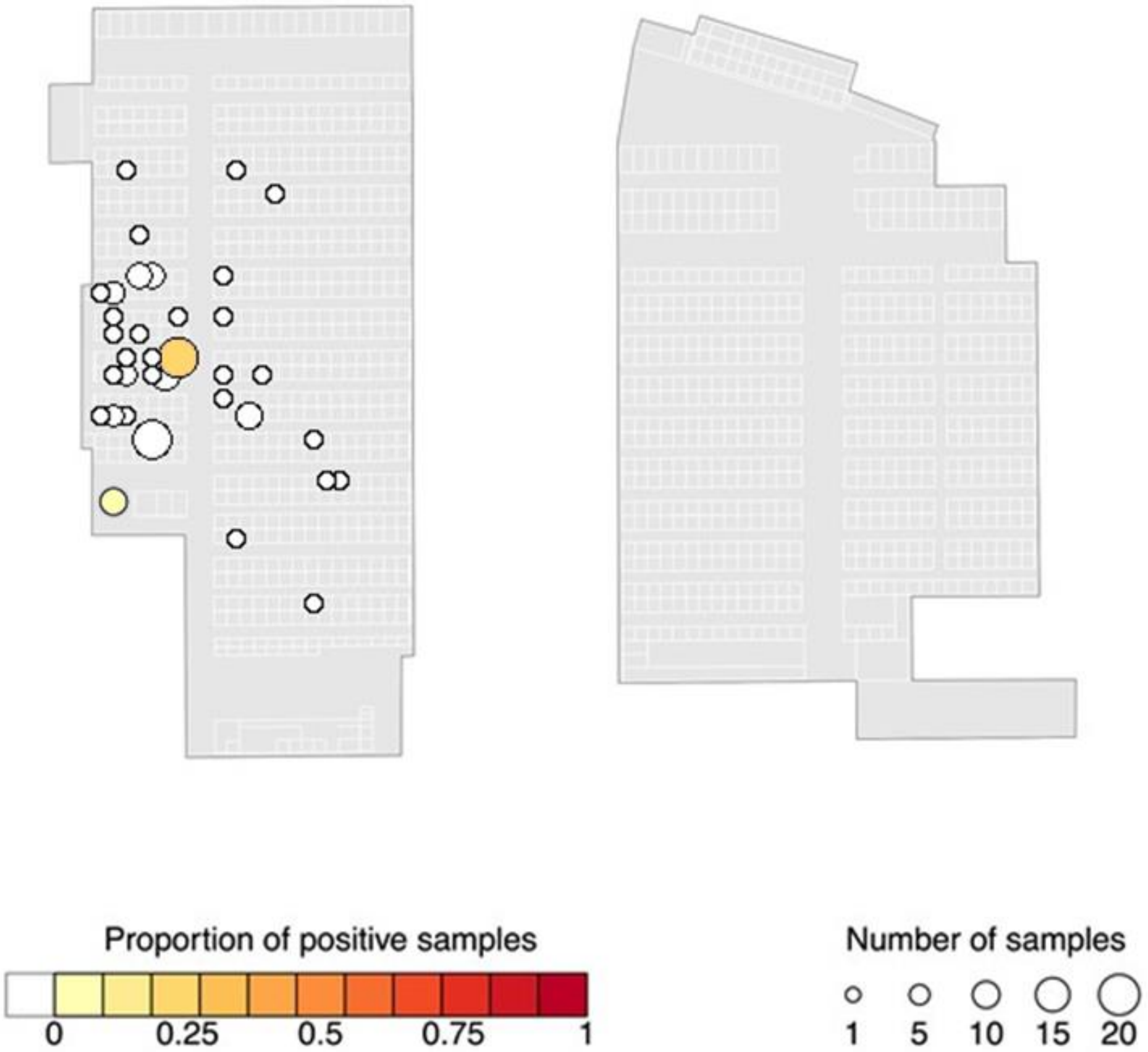
Jan 23rd to Mar 2nd

A number of shops were retested, with an emphasis on 6/29 and 8/25.

Shop 6/29 retests were negative after Jan 12th (but the 6/29 drains were still positive until February 15th)

6 positive samples in Shop 8/25. Tests were positive until Feb 15th.

One other positive test in the market: 5th street stairs between floor 1 and 2. That could be stairs up to other shops or it could be the stairs up to the Mahjong room. Samples within the Mahjong room itself were negative.



Market sampling data can be found in Liu et al, 2023

Market pictures and videos can be found on Babar’s website.

Jesse Bloom made a tool for looking up DNA by environmental sample.

Market analysis papers:
Worobey et al 2022
Bloom 2023
Crits Christoph et al 2023, first analysis
Crits Christoph et al 2023, second analysis

Full positive sample table, for comparing PCR values and dates:

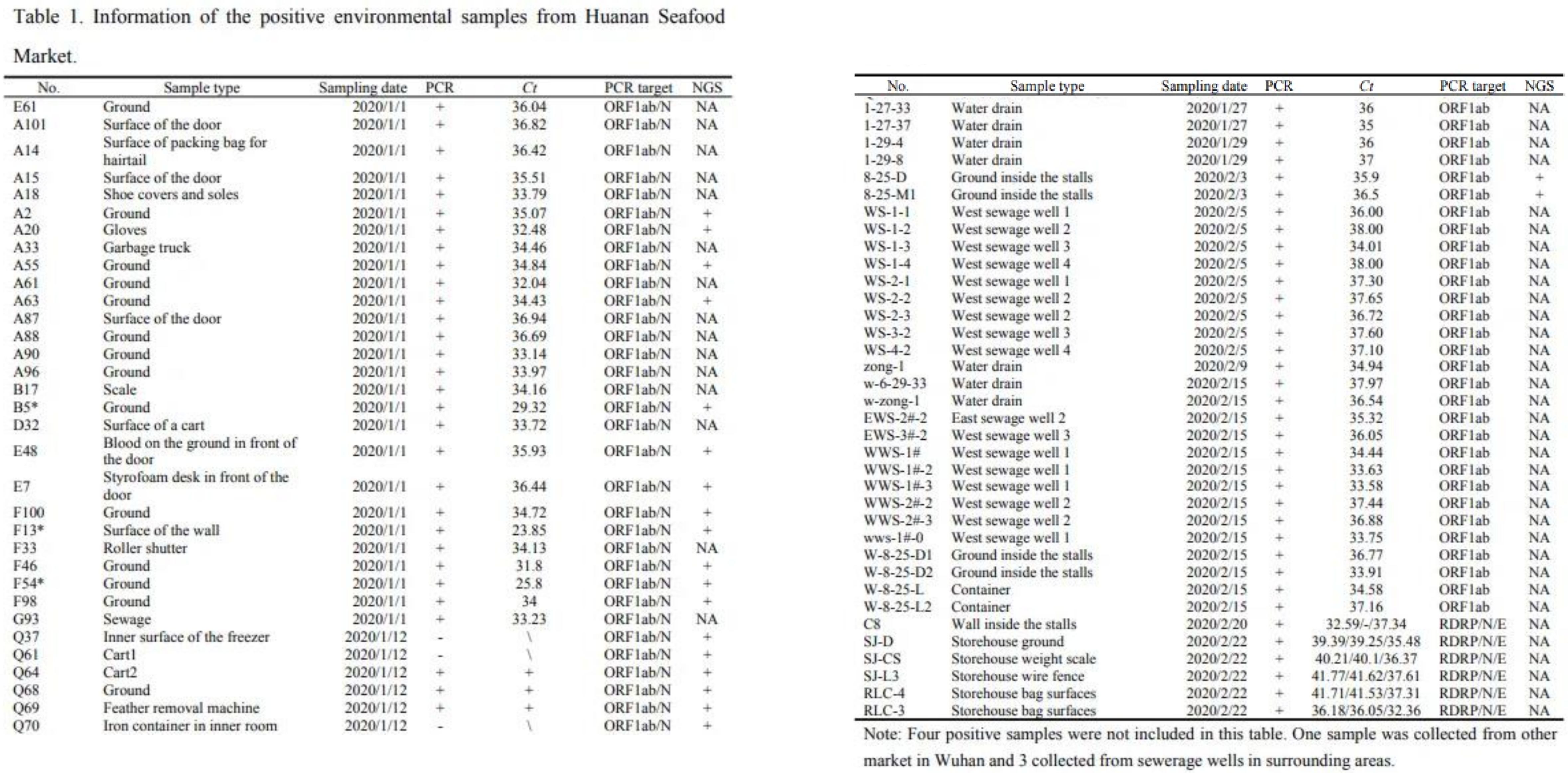
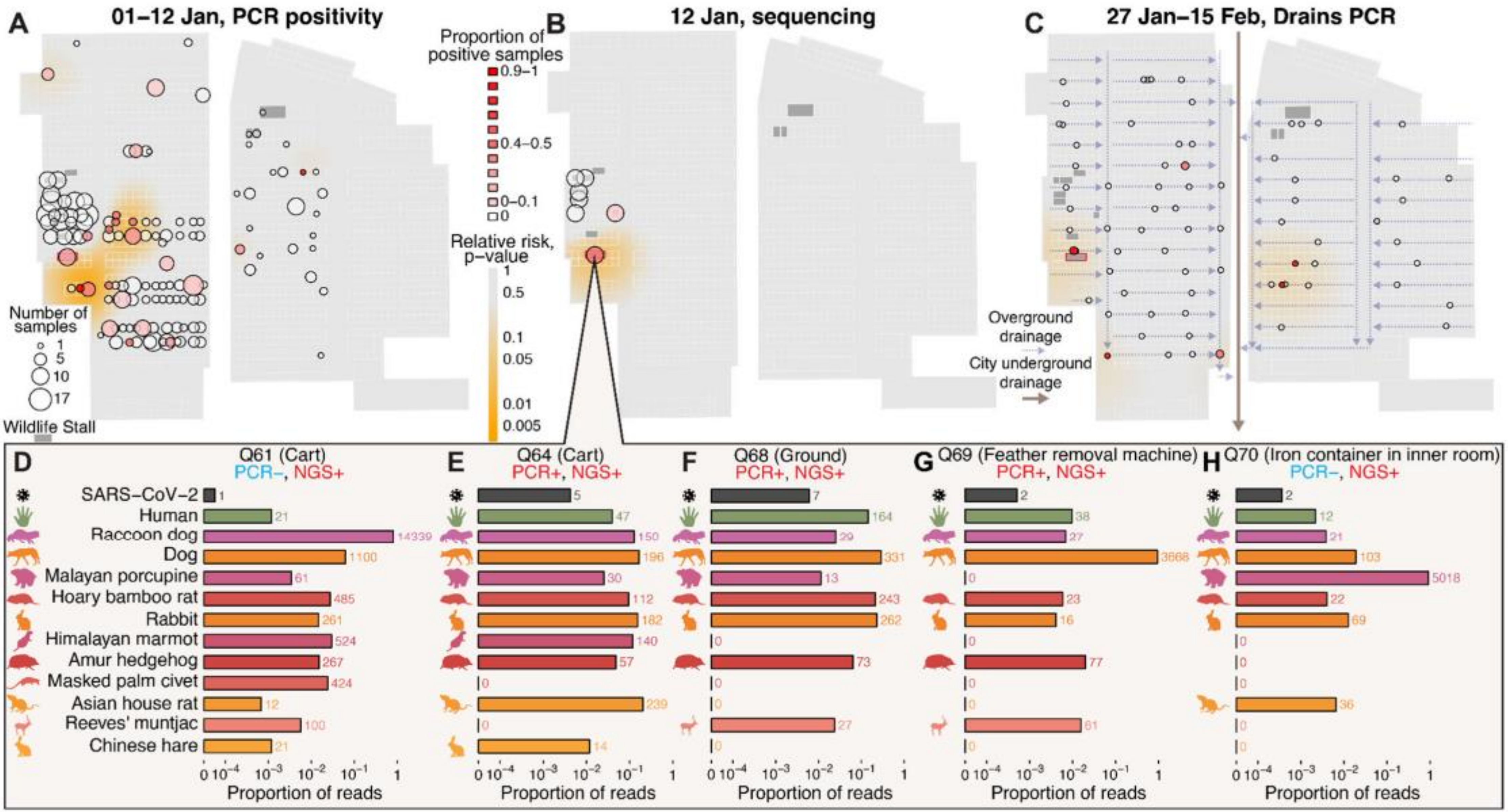


Table 1. Information of the positive environmental samples from Huanan Seafood Market.

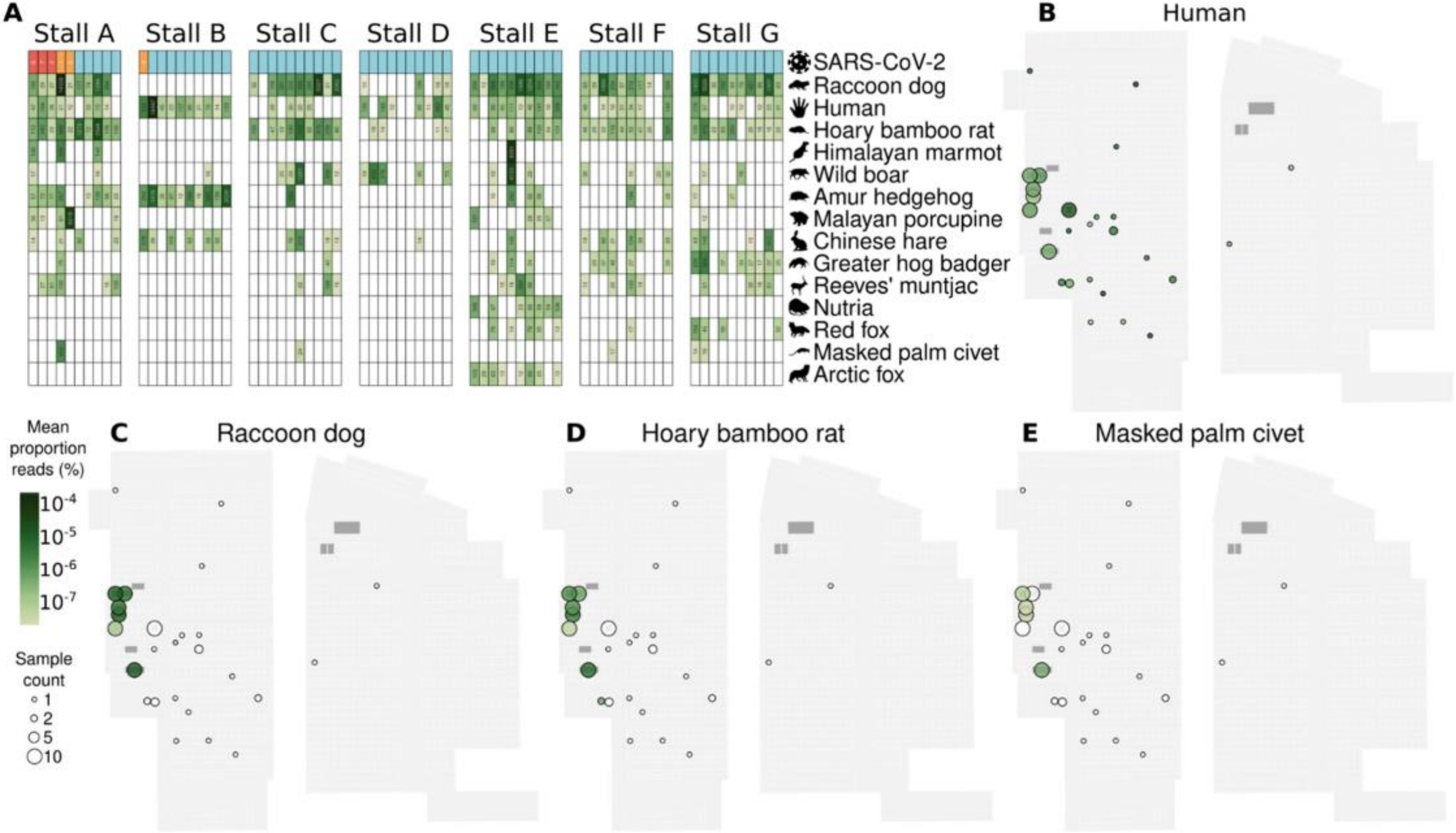
No.	Sample type	Sampling date	PCR	*Ct*	PCR target	NGS
E61	Ground	2020/1/1	+	36.04	ORF1ab/N	NA
A101	Surface of the door	2020/1/1	+	36.82	ORF1ab/N	NA
A14	Surface of packing bag for hairtail	2020/1/1	+	36.42	ORF1ab/N	NA
A15	Surface of the door	2020/1/1	+	35.51	ORF1ab/N	NA
A18	Shoe covers and soles	2020/1/1	+	33.79	ORF1ab/N	NA
A2	Ground	2020/1/1	+	35.07	ORF1ab/N	+
A20	Gloves	2020/1/1	+	32.48	ORF1ab/N	+
A33	Garbage truck	2020/1/1	+	34.46	ORF1ab/N	NA
A55	Ground	2020/1/1	+	34.84	ORF1ab/N	+
A61	Ground	2020/1/1	+	32.04	ORF1ab/N	NA
A63	Ground	2020/1/1	+	34.43	ORF1ab/N	+
A87	Surface of the door	2020/1/1	+	36.94	ORF1ab/N	NA
A88	Ground	2020/1/1	+	36.69	ORF1ab/N	NA
A90	Ground	2020/1/1	+	33.14	ORF1ab/N	NA
A96	Ground	2020/1/1	+	33.97	ORF1ab/N	NA
B17	Scale	2020/1/1	+	34.16	ORF1ab/N	NA
B5*	Ground	2020/1/1	+	29.32	ORF1ab/N	+
D32	Surface of a cart	2020/1/1	+	33.72	ORF1ab/N	NA
E48	Blood on the ground in front of the door	2020/1/1	+	35.93	ORF1ab/N	+
E7	Styrofoam desk in front of the door	2020/1/1	+	36.44	ORF1ab/N	+
F100	Ground	2020/1/1	+	34.72	ORF1ab/N	+
F13*	Surface of the wall	2020/1/1	+	23.85	ORF1ab/N	+
F33	Roller shutter	2020/1/1	+	34.13	ORF1ab/N	NA
F46	Ground	2020/1/1	+	31.8	ORF1ab/N	+
F54*	Ground	2020/1/1	+	25.8	ORF1ab/N	+
F98	Ground	2020/1/1	+	34	ORF1ab/N	+
G93	Sewage	2020/1/1	+	33.23	ORF1ab/N	NA
Q37	Inner surface of the freezer	2020/1/12	-	\	ORF1ab/N	+
Q61	Cart1	2020/1/12	-	\	ORF1ab/N	+
Q64	Cart2	2020/1/12	+	+	ORF1ab/N	+
Q68	Ground	2020/1/12	+	+	ORF1ab/N	+
Q69	Feather removal machine	2020/1/12	+	+	ORF1ab/N	+
Q70	Iron container in inner room	2020/1/12	-	\	ORF1ab/N	+
1-27-33	Water drain	2020/1/27	+	36	ORF1ab	NA
1-27-37	Water drain	2020/1/27	+	35	ORF1ab	NA
1-29-4	Water drain	2020/1/29	+	36	ORF1ab	NA
1-29-8	Water drain	2020/1/29	+	37	ORF1ab	NA
8-25-D	Ground inside the stalls	2020/2/3	+	35.9	ORF1ab	+
8-25-M1	Ground inside the stalls	2020/2/3	+	36.5	ORF1ab	+
WS-1-1	West sewage well 1	2020/2/5	+	36.00	ORF1ab	NA
WS-1-2	West sewage well 2	2020/2/5	+	38.00	ORF1ab	NA
WS-1-3	West sewage well 3	2020/2/5	+	34.01	ORF1ab	NA
WS-1-4	West sewage well 4	2020/2/5	+	38.00	ORF1ab	NA
WS-2-1	West sewage well 1	2020/2/5	+	37.30	ORF1ab	NA
WS-2-2	West sewage well 2	2020/2/5	+	37.65	ORF1ab	NA
WS-2-3	West sewage well 2	2020/2/5	+	36.72	ORF1ab	NA
WS-3-2	West sewage well 3	2020/2/5	+	37.60	ORF1ab	NA
WS-4-2	West sewage well 4	2020/2/5	+	37.10	ORF1ab	NA
zong-1	Water drain	2020/2/9	+	34.94	ORF1ab	NA
w-6-29-33	Water drain	2020/2/15	+	37.97	ORF1ab	NA
w-zong-1	Water drain	2020/2/15	+	36.54	ORF1ab	NA
EWS-2#-2	East sewage well 2	2020/2/15	+	35.32	ORF1ab	NA
EWS-3#-2	West sewage well 3	2020/2/15	+	36.05	ORF1ab	NA
WWS-1#	West sewage well 1	2020/2/15	+	34.44	ORF1ab	NA
WWS-1#-2	West sewage well 1	2020/2/15	+	33.63	ORF1ab	NA
WWS-1#-3	West sewage well 1	2020/2/15	+	33.58	ORF1ab	NA
WWS-2#-2	West sewage well 2	2020/2/15	+	37.44	ORF1ab	NA
WWS-2#-3	West sewage well 2	2020/2/15	+	36.88	ORF1ab	NA
wws-1#-0	West sewage well 1	2020/2/15	+	33.75	ORF1ab	NA
W-8-25-D1	Ground inside the stalls	2020/2/15	+	36.77	ORF1ab	NA
W-8-25-D2	Ground inside the stalls	2020/2/15	+	33.91	ORF1ab	NA
W-8-25-L	Container	2020/2/15	+	34.58	ORF1ab	NA
W-8-25-L2	Container	2020/2/15	+	37.16	ORF1ab	NA
C8	Wall inside the stalls	2020/2/20	+	32.59/-/37.34	RDRP/N/E	NA
SJ-D	Storehouse ground	2020/2/22	+	39.39/39.25/35.48	RDRP/N/E	NA
SJ-CS	Storehouse weight scale	2020/2/22	+	40.21/40.1/36.37	RDRP/N/E	NA
SJ-L3	Storehouse wire fence	2020/2/22	+	41.77/41.62/37.61	RDRP/N/E	NA
RLC-4	Storehouse bag surfaces	2020/2/22	+	41.71/41.53/37.31	RDRP/N/E	NA
RLC-3	Storehouse bag surfaces	2020/2/22	+	36.18/36.05/32.36	RDRP/N/E	NA

Note: Four positive samples were not included in this table. One sample was collected from other market in Wuhan and 3 collected from sewerage wells in surrounding areas.

Crits Christoph paper lists sampling numbers for less common species:



6/29 8/25


A
Stall A
Stall B
Stall C
Stall D
Stall E
Stall F
Stall G
SARS-CoV-2
Raccoon dog
Human
Hoary bamboo rat
Himalayan marmot
Wild boar
Amur hedgehog
Malayan porcupine
Chinese hare
Greater hog badger
Reeves' muntjac
Nutria
Red fox
Masked palm civet
Arctic fox
B
Human
C
Raccoon dog
D
Hoary bamboo rat
E
Masked palm civet
Mean proportion reads (%)
10^-4
10^-5
10^-6
10^-7
Sample count
1
2
5
10

Most likely intermediate hosts for Covid-19:

	Arguments for:	Arguments against:
Raccoon Dog 	Can catch and transmit Covid. Were also carriers of SARS. No spike mutations seen on covid infection. Sold in shop 6/29.	Other shops sold them and tested negative.
Civet 	Carriers of SARS. Found sick in Hubei during SARS. Sold in shop 6/29 and not in most shops.	Sold in low numbers. Not enough studies to conclude how susceptible they are – one study says covid grows very well in civet cells, one says covid binds well to civet ACE2, another disagrees.
Bamboo Rat 	Animals came from Yunnan. Found to carry bat coronaviruses. 1 computational study says Covid binds better to bamboo rat ACE2 than human. Sold in shop 6/29.	Other shops sold them and tested negative. Not enough studies to conclude how susceptible they are to Covid. 3 bamboo rats were tested from shop 6/29.

Most likely intermediate hosts for Covid-19:

	Arguments for:	Arguments against:
Malayan Porcupine 	From Southeast Asia. 6/29 porcupine cage sample tested positive. Highest correlation between covid RNA and animal DNA (in Jesse Bloom study) Associated with another coronavirus spillover.	Covid susceptibility unknown.
Amur Hedgehog 	Sold in shop 6/29 and 8/25. One 8/25 positive warehouse sample had hedgehog DNA. Good DNA correlation (Bloom study). Carry betacoronaviruses and MERS family viruses.	Covid susceptibility unknown (poor ACE2 binding in some studies). 14 hedgehogs were tested from shop 6/29, all tested negative (but no live animals) Too cute to blame the pandemic on.

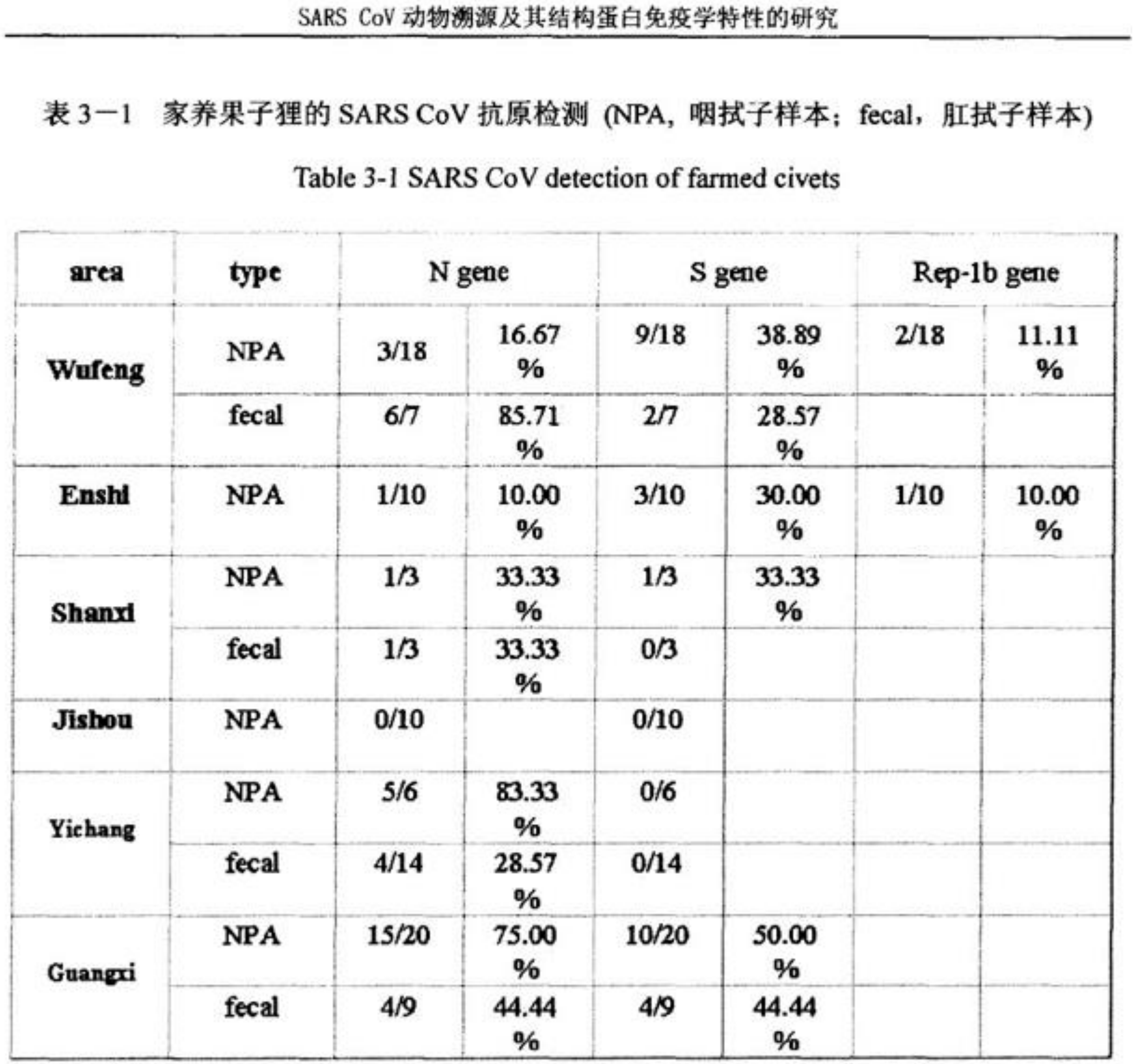
Less likely intermediate hosts:

	Arguments for:	Arguments against:
Hog Badger	Sold in 6/29 Susceptible to SARS Other badgers susceptible to Covid.	Not much DNA in covid positive market samples Not much DNA in 6/29.
Siberian Weasel	Similar to mink, which catch and transmit covid very well. Sold in 8/25.	Weasel DNA rare in the market, not sold in 6/29. Mink with covid have spike mutations that early covid strains do not, maybe weasels would have the same.
Foxes	Can catch and transmit Covid.	Not sold in 6/29 or 8/25

Unlikely intermediate hosts:

Muntjac	Sold in shop 6/29. Same ACE2 residues as white tailed deer, which catch covid.	Truncated ACE2 gene without signal peptide may show lack of covid susceptibility.
Marmot	Sold in 6/29	High elevation native range means they’re unlikely to be naturally exposed to bats.
Dogs, rabbits, boar	Can catch covid.	Can’t transmit covid well.

2004 infection rates in Wufeng, Hubei farmed civets:



SARS CoV 动物溯源及其结构蛋白免疫学特性的研究

表 3－1　家养果子狸的 SARS CoV 抗原检测 (NPA，咽拭子样本；fecal，肛拭子样本)

Table 3-1 SARS CoV detection of farmed civets

area	type	N gene		S gene		Rep-1b gene	
Wufeng	NPA	3/18	16.67 %	9/18	38.89 %	2/18	11.11 %
	fecal	6/7	85.71 %	2/7	28.57 %		
Enshi	NPA	1/10	10.00 %	3/10	30.00 %	1/10	10.00 %
Shanxi	NPA	1/3	33.33 %	1/3	33.33 %		
	fecal	1/3	33.33 %	0/3			
Jishou	NPA	0/10		0/10			
Yichang	NPA	5/6	83.33 %	0/6			
	fecal	4/14	28.57 %	0/14			
Guangxi	NPA	15/20	75.00 %	10/20	50.00 %		
	fecal	4/9	44.44 %	4/9	44.44 %		

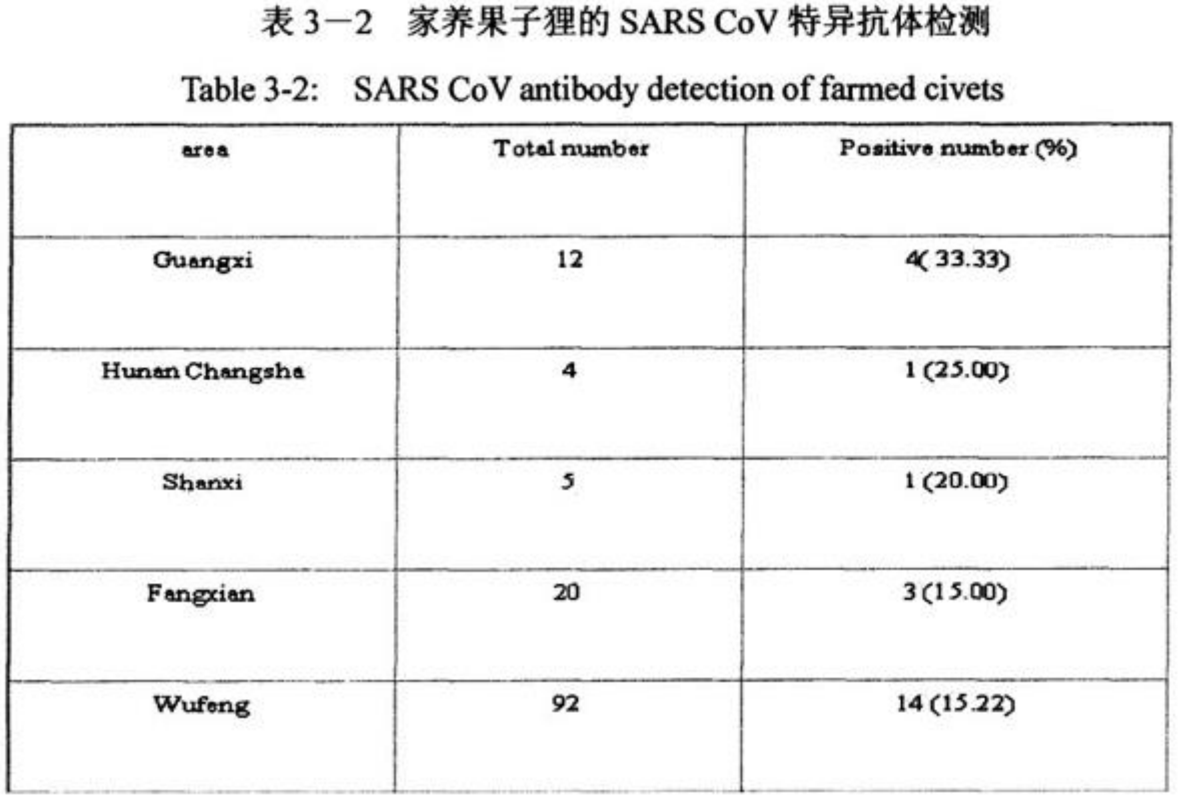


表 3－2　家养果子狸的 SARS CoV 特异抗体检测

Table 3-2:　SARS CoV antibody detection of farmed civets

area	Total number	Positive number (%)
Guangxi	12	4(33.33)
Hunan Changsha	4	1 (25.00)
Shanxi	5	1 (20.00)
Fangxian	20	3 (15.00)
Wufeng	92	14 (15.22)

Table 1. Full list of animals sold at the market (Xiao et al., 2021) and their susceptibility to SARS-CoV-2.

Animal (mammals)	SARS-CoV-2 susceptibility	Context	Refs
Raccoon dog (*Nyctereutes procyonoides*)	Yes	Experimental animal SARS-CoV-2 infection; can transmit to other animals.	Freuling et al. (2020)
Amur hedgehog (*Erinaceus amurensis*)	No data but likely yes	Found to carry beta-CoVs MERS-related CoVs.	Delogu et al. (2020); Li et al. (2021)
Siberian weasel (*Mustela sibirica*)	No data but likely yes	Found to carry CoVs.	Dong et al. (2007)
Hog badger (*Arctonyx albogularis*)	No data but likely yes	Another badger species (Meles meles) was found to be SARS-CoV-2-positive.	Davoust et al. (2022)
Asian badger (*Meles leucurus*)	No data	Found to carry influenza A virus H9N2.	He et al. (2022)
Chinese hare (*Lepus sinensis*)	No data	-	-
Pallas's squirrel (*Callosciurus erythraeus*)	No data with mixed inferences from other species.	Fox and Wyoming ground squirrel species not susceptible to SARS-CoV-2 in animal experiments.	Bosco-Lauth et al. (2021)
		Computational modelling predicts strong binding between red squirrel ACE2 receptor with SARS-CoV-2.	Pach et al. (2021)
		Eastern gray squirrel was found to be SARS-CoV-2-positive.	Goldberg et al. (2023)
Masked palm civet (*Paguma larvata*)	Likely yes	Experimental in vitro SARS-CoV-2 infection.	Li et al. (2023); Zhou et al. (2020)
Chinese bamboo rat (*Rhizomys sinensis*)	No data but likely yes	Found to carry CoVs, including bat CoVs.	Huong et al. (2020); Wang et al. (2022); He et al. (2021)
		Computational modelling predicted strong binding between SARS-CoV-2 and ACE2 of another bamboo rat species (*R. pruinosus*).	Chen et al. (2022)
Malayan porcupine (Hystrix brachyura)	No data but likely yes	Found to carry CoVs, including bat CoVs.	Huong et al. (2020); He et al. (2022)
Chinese muntjac (*Muntiacus reevesi*)	No data but likely yes	Found to have the same ACE2 key residues as white-tailed deer (Odocoileus virginianus), with reported human-to-deer SARS-CoV-2 transmission and back.	ACE2: Lopes (2023) Deer susceptibility: Chandler et al. (2021); Hale et al. (2022); Kuchipudi et al. (2022); Marques et al. (2022)
Coypu (*Myocastor coypus*)	No data	Found to carry bovine parainfluenza virus 3 and rotavirus.	He et al. (2022)
Marmot (*Marmota himalayana*)	No data but likely yes	Found to carry CoVs.	Zhu et al. (2021)
		Found to exhibit flu-like symptoms	He et al. (2022)
Red fox (*Vulpes vulpes*)	Yes	Experimental SARS-CoV-2 infection; can shed infectious viruses.	Porter et al. (2022)
		Found to be SARS-CoV-2-positive.	Jemeršić et al. (2021); The WHO (2022); Goldberg et al. (2023)
Mink (*Neovison vison*)	Yes	Human-to-animal transmission and back	Oude Munnink et al. (2021); Rabalski et al. (2021)
Red squirrel (*Sciurus vulgaris*)	Likely yes	Computational modelling predicts strong binding between red squirrel ACE2 receptor with SARS-CoV-2.	Pach et al. (2021)
Wild boar (*Sus scrofa*)	Likely yes	Found to be SARS-CoV-2-positive.	Jemeršić et al. (2021)
		Experimental SARS-CoV-2 animal infection showed no susceptibility.	Schlottau et al (2020); Vergara-Alert et al. (2021)
		Experimental SARS-CoV-2 animal infection showed susceptibility, with transmission possible.	Pickering et al. (2021); Meekins et al. (2020)
		Experimental in vitro SARS-CoV-2 infection possible.	He et al. (2022)
Complex-toothed Flying Squirrel (*Trogopterus xanthipes*)	No data	-	-

Animals tested for Covid in China

The WHO report states: “More than 80 000 wildlife, livestock and poultry samples were collected from 31 provinces in China and no positive result was identified for SARS-CoV-2 antibody or nucleic acid before and after the SARS-CoV-2 outbreak in China.”

BUT ONLY 0.57% (n = 457, Table 3) and another 0.77% (n = 616, Table 5.1) of the 80,000 animal samples were related to the Huanan market tested between 1st Jan and 2nd March 2020:

- From Huanan market (n = 327).
- From warehouses related to the Huanan market (n = 32)
- From vector animals like stray cats and dogs in the Huanan market (n = 92).
- From animal products sold in other markets in Wuhan (n = 6).
- From suppliers of the Huanan market (n = 616).

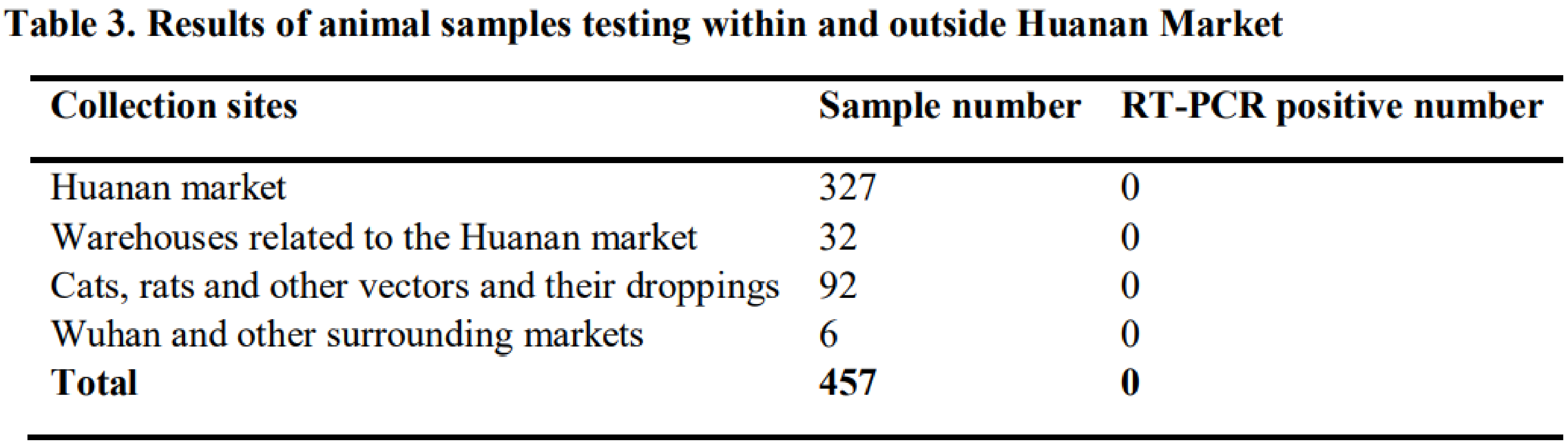


Table 3. Results of animal samples testing within and outside Huanan Market

Collection sites	Sample number	RT-PCR positive number
Huanan market	327	0
Warehouses related to the Huanan market	32	0
Cats, rats and other vectors and their droppings	92	0
Wuhan and other surrounding markets	6	0
Total	**457**	**0**

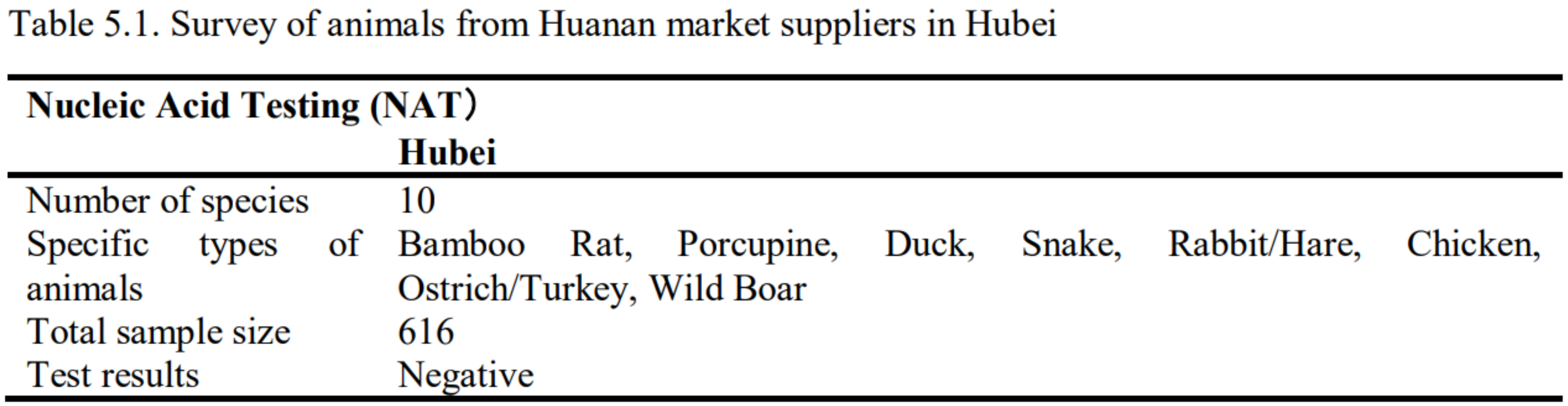


Table 5.1. Survey of animals from Huanan market suppliers in Hubei

Nucleic Acid Testing (NAT)	**Hubei**
Number of species	10
Specific types of animals	Bamboo Rat, Porcupine, Duck, Snake, Rabbit/Hare, Chicken, Ostrich/Turkey, Wild Boar
Total sample size	616
Test results	Negative

Of the 0.57% (n = 457) samples, ONLY 0.3% (n = 237) were from potentially relevant animals, such as cats (n = 80), hedgehog (n = 67), muntjac (n = 18), bamboo rat (n – 15), weasel (n = 2), etc. (Table 4).

NONE were from prime suspects, such as raccoon dogs and civets.

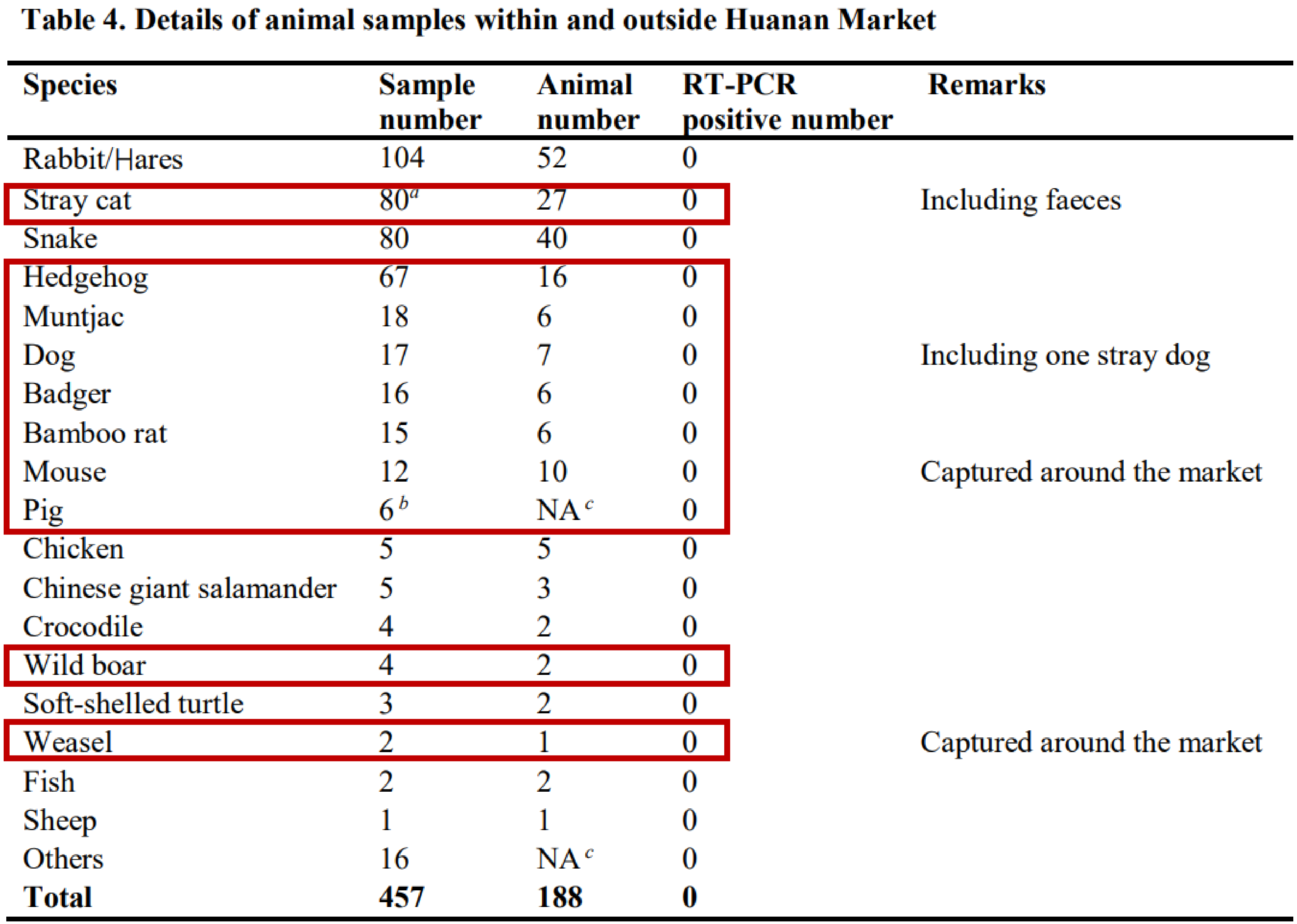


Table 4. Details of animal samples within and outside Huanan Market

Species	Sample number	Animal number	RT-PCR positive number	Remarks
Rabbit/Hares	104	52	0	
Stray cat	80[a]	27	0	Including faeces
Snake	80	40	0	
Hedgehog	67	16	0	
Muntjac	18	6	0	
Dog	17	7	0	Including one stray dog
Badger	16	6	0	
Bamboo rat	15	6	0	
Mouse	12	10	0	Captured around the market
Pig	6[b]	NA[c]	0	
Chicken	5	5	0	
Chinese giant salamander	5	3	0	
Crocodile	4	2	0	
Wild boar	4	2	0	
Soft-shelled turtle	3	2	0	
Weasel	2	1	0	Captured around the market
Fish	2	2	0	
Sheep	1	1	0	
Others	16	NA[c]	0	
Total	**457**	**188**	**0**	

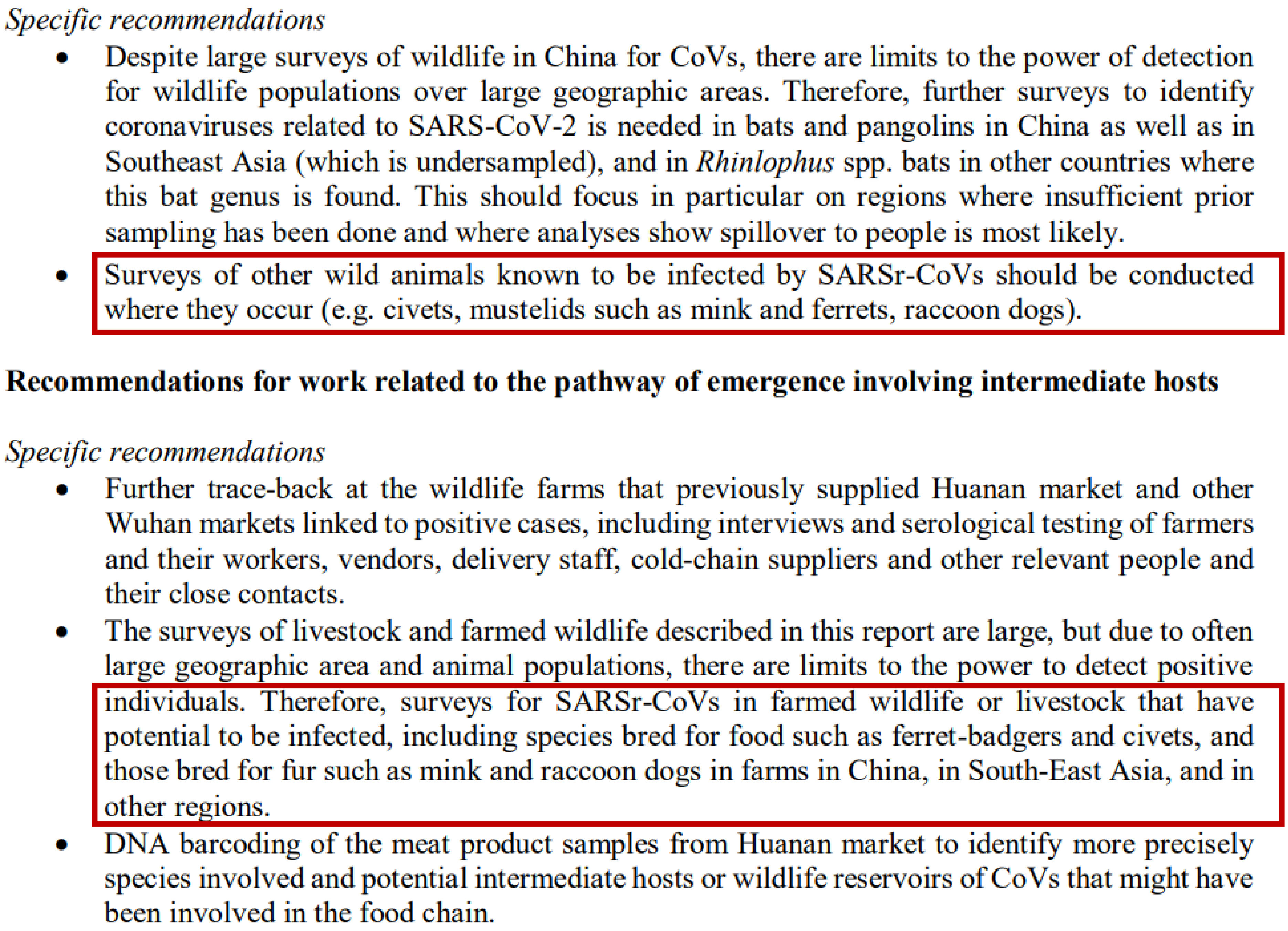
Basically, only 1.34% (n = 457 + 616 = 1,073) of the 80,000 animal samples tested were related to the Huanan market.

Now, where did the remaining 98.7% of the animal samples came from?

- 1,287 (1.6%) samples were from wild animals (e.g., pangolin, civet, bat, bamboo rat, macaque, porcupine, fox, etc.) collected between Feb and Mar 2020 from 3 provinces.
- 5,638 (7%) samples were from livestock and poultry samples (e.g., pig, bovine, sheep, chicken, duck, and goose) collected in 2019 from 31 provinces.
- 6,070 (7.6%) samples were from livestock and poultry samples collected in 2020 from 31 provinces.
- 12,092 (15.1%) samples were from livestock and poultry samples collected in 2018-2019 from 26 provinces and regions.
- 26,807 (33.5%) samples were from domesticated animals stored in 2019-2020 from 24 provinces and regions.
- 1,914 (2.4%) samples were from livestock, domesticated, and captive wildlife animals collected from Nov 2019 to Mar 2020.
- 648 (0.81%) samples were from 9 captive animals species (e.g., red pandas, white foxes, badgers, civets, bamboo rats, porcupines, guinea pigs and macaques) collected between 8 Feb and 11 Mar 2020 in several provinces.
- 2,995 (3.7%) samples of 37 species of captive or farmed wildlife (e.g., bamboo rats, porcupines, guineapigs and macaques) collected after 8 April 2020 in 14 cities in Hubei Province.
- 27,000 (33.8%) samples of wild animals (e.g., primates, lagomorphs, artiodactyls, chiropterans, rodents and many kinds of wild birds) were collected between May and Sept 2020 in China.
- 6,811 (8.5%) samples of livestock and captive wildlife animals were collected from several provinces from 2015 to 2019.
- 2,328 (2.9%) samples of captive wildlife animals (e.g., macaque, deer, tigers, camels, bamboo rats, goats, racoon dog, and guinea pigs) were collected in Dec 2019 from tourist areas, zoos and artificial breeding sites in Hubei.

Total: 93,590 samples,
but % is out of 80,000

The WHO report admits that important animals like civets, mink, ferrets, and raccoon dogs were barely tested or should be investigated further.



Specific recommendations

- Despite large surveys of wildlife in China for CoVs, there are limits to the power of detection for wildlife populations over large geographic areas. Therefore, further surveys to identify coronaviruses related to SARS-CoV-2 is needed in bats and pangolins in China as well as in Southeast Asia (which is undersampled), and in *Rhinlophus* spp. bats in other countries where this bat genus is found. This should focus in particular on regions where insufficient prior sampling has been done and where analyses show spillover to people is most likely.
- Surveys of other wild animals known to be infected by SARSr-CoVs should be conducted where they occur (e.g. civets, mustelids such as mink and ferrets, raccoon dogs).

Recommendations for work related to the pathway of emergence involving intermediate hosts

Specific recommendations

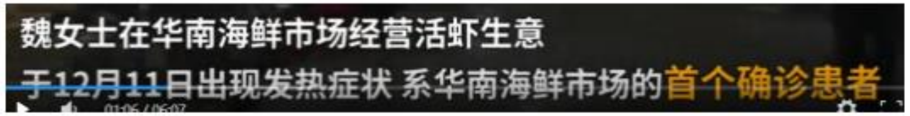
- Further trace-back at the wildlife farms that previously supplied Huanan market and other Wuhan markets linked to positive cases, including interviews and serological testing of farmers and their workers, vendors, delivery staff, cold-chain suppliers and other relevant people and their close contacts.
- The surveys of livestock and farmed wildlife described in this report are large, but due to often large geographic area and animal populations, there are limits to the power to detect positive individuals. Therefore, surveys for SARSr-CoVs in farmed wildlife or livestock that have potential to be infected, including species bred for food such as ferret-badgers and civets, and those bred for fur such as mink and raccoon dogs in farms in China, in South-East Asia, and in other regions.
- DNA barcoding of the meat product samples from Huanan market to identify more precisely species involved and potential intermediate hosts or wildlife reservoirs of CoVs that might have been involved in the food chain.

Chinese video interviewing Wei Guixian

There's a short summary translation of the video here, from Michael Worobey.

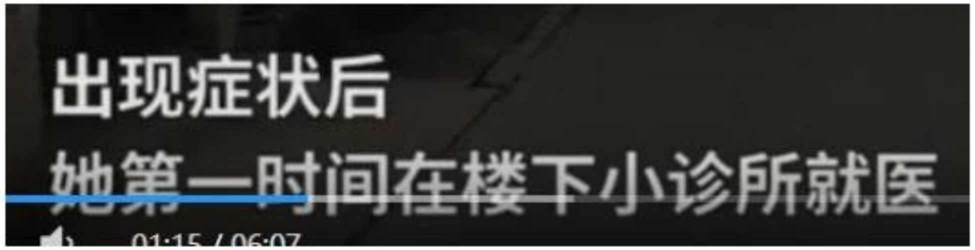
Worobey also posted a 30 minute long full translation of the video.

I also had someone translate parts of the video:


魏女士在华南海鲜市场经营活虾生意

于12月11日出现发热症状 系华南海鲜市场的首个确诊患者

This part says Ms Gui was selling live shrimp at HuaNan Seafood Market when on 11 Dec (2019), she developed a fever - making her one of the first patients.

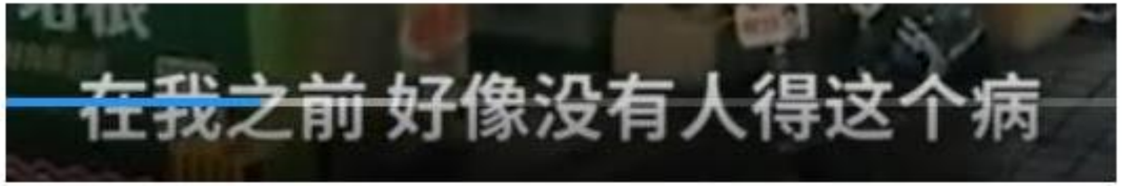

出现症状后

她第一时间在楼下小诊所就医

(earlier dialogue not shown) she lives 500m away from the market; the moment she developed fever, she went to the clinic below her housing area.

就去（小诊所）打针 打了两针之后没有反应

"so I went to this clinic (name: Wuhan Zhong Sheng Clinic) to get 2 shots (vaccine), which usually helps, but this time, there was no effect. I felt very sick."

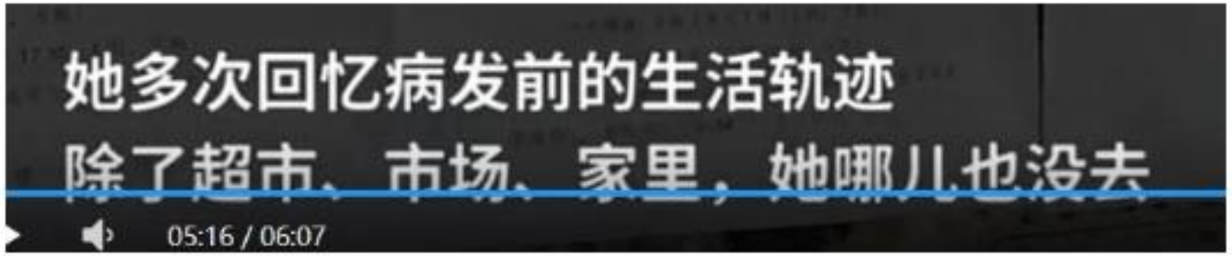


在我之前 好像没有人得这个病

she went to a different hospital on the 11th, coz she still wasn't feeling better, doctor gave her some tablets (content unknown); as she needs to earn money, she got back to work on 15th. here, she mentions "before my case, I don't think anyone has this (disease)"

你们华南的还有几个人

on the 16th, she went to the bigger hospital, and the doctor said, "it's from HuaNan Market (meaning that there are other patients like her from the market)"



她多次回忆病发前的生活轨迹
除了超市、市场、家里，她哪儿也没去

well, in this segment they're finding out the places she's been, which stated that aside from the super market, market, home, she's not been anywhere else

声音来源：
华南海鲜市场首位确诊病例 魏女士

好像没去哪里 我这个人又不打牌

At 5:23 mark: "I've not been anywhere, I don't even play mahjong" (after this: "after work at the market, I go home right away)