

**Daoyu**

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[archive.ph/MCqMS](https://archive.ph/MCqMS)

That data was based in Bias and Bias alone.

[archive.ph/VXtu9](https://archive.ph/VXtu9)

The CCP data they used to support “market spillover” is so unrealistic that there were evidence of global circulation at least 2 weeks before the first case at the Huanan market.

<https://archive.ph/MCqMS><https://archive.ph/VXtu9>

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[archive.ph/dmOXT](https://archive.ph/dmOXT)

Similarly, the genetics failed to support the Huanan market as the site of origin.

[archive.ph/A6cKN](https://archive.ph/A6cKN)

There are strains in the U.S. that are two mutations more early than even lineage A.

<https://archive.ph/dmOXT>

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[archive.ph/8thla](https://archive.ph/8thla)

[archive.ph/dsJ15](https://archive.ph/dsJ15)

Remember that the only cases that can be counted for the retrospective case list of the WHO report was cases that were extracted based on “several hospitals near the Huanan market and the neighborhood of the Huanan market”,

<https://archive.ph/8thla><https://archive.ph/dsJ15>

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And the only cases that may be counted for cases before 18/01/2020 are cases that [archive.ph/6LuXg](https://archive.ph/6LuXg)

[archive.ph/UIBkB](https://archive.ph/UIBkB)

have direct or indirect epidemiological link to the Huanan market. They suppressed diagnosis of cases so hard that in their official case counts a

### **[转载]卫健委曾规定：有海鲜市场接触史才能确诊**

發布於 2020 年 2 月 11 日 分布式入口

概要：12月26日，武汉某医院首先发现一家三口患病，29日上报卫健委；卫健委也发了一些常规的诊断标准，规定患者必须有华南海鲜市场接触史，以当时的苛刻条件，顶多只能有三分之一的病人才能申请核酸检测；1月16日国家卫健委制定新型肺炎诊疗方案，之前当地的诊疗标准才废止；1月16日，有海鲜市场接触史的占患者

而武汉市卫健委《入排标准》相比《试行诊疗方案》则要严苛不少。其开篇第一句就规定，同时具备流行病学史和临床表现者纳入。其中，临床表现要求与“国家专家组标准”病例定义列出的四条基本一致，仅对其中发热一条进一步定义为 $\geq 38$ 度；更大的改变是要求必须具有流行病学史，即2019年12月1日以来，长期在华南海鲜市场从事交易活动的商户、雇佣者和工作人员，或发病前两周内曾在海鲜市场从事加工、售卖、宰杀、处理和搬运等工作三小时以上者，或发病前两周内曾在海鲜市场有禽类、野生动物明确接触史（触摸或1米以内近距离观看等）者，以及与符合病例定义者共同生活、居住、学习、陪护、同病房的人员或未采用有效防护措施的诊疗、护理的医务人员。

<https://archive.ph/6LuXg>

<https://archive.ph/UIBkB>

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5 time jump of daily case counts can be seen at 01/01/2020. [archive.ph/uFlxC](https://archive.ph/uFlxC)

[archive.ph/9znGJ](https://archive.ph/9znGJ)

The bias in how the early cases were counted is not only well-present but was also well-documented. And the level of bias they enforce completely invalidated the “data”

<https://archive.ph/9znGJ><https://archive.ph/uFlxC>

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They provided to the WHO. [aljazeera.com/amp/news/2021/...](https://www.aljazeera.com/amp/news/2021/2/13/china-refuses-to-give-raw-data-to-who)

They were forbidden to take any independent investigation, or even try and obtain data to support or disprove the summary they were given—by none other than the Wuhan municipal CDC that ordered the destruction of all case samples



#### China ‘refused’ to give raw COVID data to WHO team

Investigator says China provided summary data on the 174 cases identified in the early phase of the outbreak in Wuhan.

[https://www.aljazeera.com/amp/news/2021/2/13/china-refuses-to-give-raw-data-to-w...](https://www.aljazeera.com/amp/news/2021/2/13/china-refuses-to-give-raw-data-to-who)

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Not already collected by them based on a connection to the Huanan market in 01-03/01/2020.

- |        |   |
|--------|---|
| 29 Dec | <ul style="list-style-type: none"> <li>- Xinhua Hospital reported another four viral pneumonia cases, all of which were workers at the Huanan Market.</li> <li>- Wuhan CDC and Jiangnan CDC went to the hospital for throat swab sample collection.</li> <li>- Experts of Wuhan CDC, Jiangnan CDC and two other doctors did joint consultation.</li> <li>- The samples were transferred directly to Wuhan CDC laboratory.</li> <li>- All seven cases were transferred to Jinyintan Hospital.</li> <li>- In the afternoon at 5 pm, the Hubei Health Commission received a call about the seven viral pneumonia cases.</li> <li>- Hubei CDC visited Jinyintan Hospital in the evening at 7 pm together with Wuhan CDC.</li> </ul> |
| 30 Dec | <ul style="list-style-type: none"> <li>- A city-wide case screening was conducted targeting people with pneumonia of unknown origin, abnormal blood routine test (normal WBC, lymphocytopenia), and exposure history with Huanan market. More cases with similar symptoms were identified, traced and quarantined.</li> <li>- Wuhan CDC and Jiangnan CDC went to Huanan market for environment sample collection.</li> <li>- Hubei CDC verified the pathogen testing for all samples; all negative.</li> <li>- Hubei CDC reported to China CDC.</li> <li>- A test report showing SARS-like testing results was circulating on social media in the afternoon.</li> </ul>   |
| 31 Dec | <ul style="list-style-type: none"> <li>- Continued epidemiology surveillance at several hospitals (close to Huanan market), Huanan market and the neighbourhood of Huanan market.</li> <li>- China CDC experts arrived to launch a three-level joint taskforce. It was agreed that the identified cases were pneumonia of unknown etiology.</li> <li>- Jiangnan CDC together with a third-party organization disinfected Huanan market around midnight.</li> </ul>  |

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[archive.ph/GME5L](https://archive.ph/GME5L)

In addition, lineage A and B intermediate genomes are well supported by data and is present at levels that are well above the error rate for the experiments [archive.ph/JVFuc](https://archive.ph/JVFuc) performed, and is found even more abundantly as intra-host SNVs in human



<https://archive.ph/JVFuc>



<https://archive.ph/GME5L>

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Patients. There is no need for “two spillovers” and there were never “two spillovers”. 8782 and 28144 are in strong epistasis with each other but it does not stop intermediate genomes from popping up in 1/6 of all genomes sequenced from Sichuan.

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In addition, zero incidence or evidence of natural infection of either red foxes or raccoon dogs have ever been reported, indicating an absence of natural susceptibility outside the lab for any strain. No test using the ancestral D614 strain have ever been performed on

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Replying to @Daoyu15 @AntGDuarte and 19 others

Sorry, but your "raccoon dogs" claim does not hold up. [beiresources.org/Catalog/animal...](https://beiresources.org/Catalog/animal...) not only the WHO tested all raccoon dog samples they had and were left with all negatives, but the sole article with infection tests cited as "evidence" used the G614 isolate [biorxiv.org/content/10.110...](https://biorxiv.org/content/10.110...)

12:01 PM · Jul 2, 2021

25

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[ncbi.nlm.nih.gov/pmc/articles/P...](https://ncbi.nlm.nih.gov/pmc/articles/P...)

Raccoon dogs, where inoculation with G614 leads to an R0 of exactly 1. No evidence of either positive RT-PCR or S-reactive antibodies have ever been found in red foxes, either.

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Jun 2

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Time	Case Count	Status
17 Feb 2020 - 17 Feb 2020	1	Confirmed cases with no travel history
17 Feb 2020 - 17 Feb 2020	1	Confirmed cases with travel history
17 Feb 2020 - 17 Feb 2020	1	Confirmed cases with no travel history
17 Feb 2020 - 17 Feb 2020	1	Confirmed cases with travel history

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Jun 1

[@CD57227](https://archive.ph/vUy8n) [archive.ph/vUy8n](https://archive.ph/vUy8n) All hypothetical "predicted mechanisms" with not even a single actual FCS formed inside any of them—not even a single one of them or even as a minor fraction of them—they were below the error limits of the PCR and deep sequencing process confirming that

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May 29

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May 27

[archive.ph/BJguY](https://archive.ph/BJguY) Comparing evolution between a population of a billion hosts and 2+ years of continuous circulation with a population of <5000 hosts and each circulation event being less than two weeks in length, is like comparing apples to oranges due to the two Populations having orders of

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May 27

[@CharlesRixey](#) [@BallouxFrancois](#) [@BretWeinstein](#) It was forced to use aerosol transmission because only humans wear masks or isolate when an epidemic is reported. In order to be able to still transmit between masked and self isolated humans, the virus is forced to adapt to an aerosol-only transmission mechanism. In contrast,

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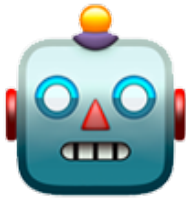


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May 25

[@scotub](#) These are actually not class II MHC epitopes—they are so-called "CTL epitopes" (or MHC class I epitopes) which are in fact dominated by pentapeptide and hexapeptide fragments. The long peptide view only hold for CD4 T cell epitopes, and even with that partial homology still

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