

Twitter Thread by [Daoyu](#)



Daoyu

[@Daoyu15](#)



<https://t.co/Sd9lslUCH5> a FCS need a FCS in the inoculum to exist. It can not arise de-novo as it will be destroyed instantly by the immune system.

[@franciscodeasis](#) <https://t.co/UgXygDjYbW> a fourth Sars-like CoV is live at the WIV. This fourth virus is an infectious clone, where engineering of the S1-S2 is used regularly as mean to generate a culturable virus in HAE cells. No VERO E6 here, and HeLa-hACE2 is the new VERO of the WIV

[@franciscodeasis](#) <https://t.co/DtjyycKy1v>

<https://t.co/PG7LVnHfsy>

Even with VERO E6, only half the time does passage lead to the loss of the FCS—smaller plaques need to be explicitly picked for that to be a certainty.

[@franciscodeasis](#) Marburg virus is a novel virus that escaped from the lab. <https://t.co/OGQM6qV27I> the only reason why it did not become a pandemic is due to it being too lethal to sustain asymptomatic transmission in humans.

[@franciscodeasis](#) The highest reported number of cases were in WuChang right on top of the old WIV headquarters, In contrast to the population density data of Wuhan—note that the place near the market had the highest population density in all of Wuhan, which make it the most optimal location for

[@franciscodeasis](#) Large-scale transmission and the first report of death in wuhan—which need substantial amount of active cases in order to begin getting reported. This mean that <https://t.co/cn4QuN4v6P> the highest population density area is most likely to report the first death—this is especially

[@franciscodeasis](#) True since an excess pneumonia death record in 01/2020 is already equilibrated, and <https://t.co/ZuWTPOW60b> it is found that when accounting for population density and aging degree, the JiangAn and the HanYang districts are the two locations with the largest absolute number of

[@franciscodeasis](#) Aged population in the entirety of Wuhan. SARS-CoV-2 mortality <https://t.co/SNnZjPvxuG> is strongly positively associated with age—the seafood market served as a superspreader, and <https://t.co/BU4ehyLHMm> raise to the major location of cases and the major lineage (B lineage) by

[@franciscodeasis](#) Jan 19th. This will of course skew the excess pneumonia deaths to the wrong side of the Yangtze river—after all, the districts that first showed an raise of excess pneumonia deaths were the districts where the majority of Wuhan’s aged population was located.

[@franciscodeasis](#) In fact, the highest absolute spacial density of aged population in Wuhan is also in the place near the market—those 3 districts had the highest number of retirement homes in the whole of wuhan—community transmission of SARS-CoV-2 lead to most <https://t.co/Rv81pEaEpE>

[@franciscodeasis](#) excess deaths in retirement homes. This is a far more parsimonious explanation than having the Huanan seafood market, which have no sequence of the ancestral A lineage, as the absolute origin of the SARS-CoV-2 index case.

[@franciscodeasis](#) <https://t.co/lb59PY7krz>

<https://t.co/s70jNlvUb4>

As for why “55% of the December 2019 cases were connected to the huanan seafood market”? “Contact history to the huanan seafood market” was literally written into the standard for reporting a case as SARS-CoV-2 infection in Wuhan

[@franciscodeasis](#) In the December 2019 standard. “██”

<https://t.co/sqsq5x3YRw>

In fact, they were still defending their claim of the seafood market as the absolute index case in Wuhan—they only admit “uncertainty” in the case reporting, while still attempt to defend

[@franciscodeasis](#) The market claim by using excess pneumonia deaths—while completely ignoring the fact that the districts near the market had the highest amount of retirement homes—the absolute biggest source of SARS-CoV-2 related deaths in the earliest stages of SARS-CoV-2.

[@franciscodeasis](#) On the index cases: <https://t.co/lZztF2siZq>

2/ Early MERS/CoV-1 spread showed a 50/50 rate of human versus animal transmission; lots of posterior diversity. With CoV-2, 1001 early Chinese genomes show No... ZERO posterior diversity. Flipping 1001 coins & getting heads every time? That’s a one in 10 with 84 zeros chance

— Dr Steven Quay (@quay_dr) [December 8, 2020](#)

[@franciscodeasis](#) <https://t.co/fPp0ihuQhZ>

WHO Report:
10,000 archived blood samples in Wuhan & no seroconversion
80,000 animals & no CoV-2
1.9 MM viruses in GISAID & no posterior diversity
All c/w lab origin

People keep saying we don't have evidence for the origin of CoV-2@[mattwridley](#) @[Ayjchan](#) @[AlexBerenson](#)
[#COVID19](#)

— Dr Steven Quay (@quay_dr) June 11, 2021

@franciscodeasis <https://t.co/4xtzGonSaB>

A zoonosis, whether community or laboratory acquired, have 3 elements in common: infected animal(s), viruses, and humans.

The differences are natural diversity versus a laboratory singularity.

What do the facts say?#COVID19 pic.twitter.com/K2kEAXGsR0

— Dr Steven Quay (@quay_dr) May 26, 2021

@franciscodeasis <https://t.co/YA9BShS9UF>

True but following data must be in the prediction: its not the market, not Hubei bats, not Hubei farmed animals, not pangolins, no Wuhan sero+ background as with SARS-1 & MERS, no post. diversity as with MERS, 1st 50 pts <15 km from world's expert on lab made chimeric CoVs

— Dr Steven Quay (@quay_dr) September 20, 2020

@franciscodeasis <https://t.co/dCO7hedYqG>

Given that the zoonoses, SARS1 and MERS, had >85% positive tests in markets, the likelihood CoV-2 is a zoonosis like SARS1 or MERS is less than 1 in a 1,000,000.

— Dr Steven Quay (@quay_dr) May 27, 2021

@franciscodeasis <https://t.co/LvAvsif4gk>

1/ A hallmark of a zoonotic epidemic is community undetected infection pre "Patient Zero." This is detected retrospectively with diagnostic tools looking at archived specimens.

Example: Of 7461 archived blood specimens from 2011-2016 in Saudi Arabia, 2.3% were positive for MERS

— Dr Steven Quay (@quay_dr) November 1, 2020

@franciscodeasis <https://t.co/id0RNxug8k>

CoV-1 v. CoV-2:

CoV-1: 91 civets & 15 raccoon dogs in wet markets tested: 106/106, 100% positive. <https://t.co/BKB4F3p7ev>

CoV-2: 0 of 336 specimens from wildlife sold at Hunan market are positive for CoV-2. [@gdemaneuf](https://twitter.com/gdemaneuf) 's nice annotation of the WHO ToR <https://t.co/k5r5Hnskbn>

— Dr Steven Quay (@quay_dr) December 12, 2020

@franciscodeasis <https://t.co/6yp9kCXKWm>

2/ 1271 nasal swab & 357 matched blood specimens from patients in Shanghai 1 Dec 2018 to 31 Mar 2020 were examined for CoV-2 by PCR. First positive is 25 Jan 2020.

This is not c/w a zoonotic epidemic but is consistent with a lab escape origin. <https://t.co/fE9WSpeXS4>

— Dr Steven Quay (@quay_dr) November 1, 2020

@franciscodeasis

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@franciscodeasis If "Most SARS-CoV-2 index case infections will not have resulted in sustained onward transmission" serological and PCR evidence before the outbreak should be present in Wuhan China. However no such evidence were present in either Wuhan or in other places in China.

@franciscodeasis As any local clusters will cause illness, and will be visible to the surveillance system, leading to sample collection and positive results. however, all 92 cases that were screened to be compatible with SARS-CoV-2 infection turned out to be negative.

@franciscodeasis <https://t.co/llMGTOJLx5> " Poliovirus is, however, strictly a human pathogen, and does not naturally infect any other species (although chimpanzees and Old World monkeys can be experimentally infected).[46]" <https://t.co/ZxJaD9sWn8>

@franciscodeasis Unfortunately, They got the entire basic of Polio wrong. Polio is a pathogen that is certified to exclusively infect humans. <https://t.co/BeDXMpLYUa>

@franciscodeasis "HCV has a narrow host range infecting only humans and chimpanzees." <https://t.co/BeDXMpLYUa> The same applies to Hepatitis C virus, which is also a certified human pathogen that exclusively infect humans.

@franciscodeasis "Hepatitis C virus displays a narrow host species tropism, naturally infecting only humans, although chimpanzees are also susceptible to experimental infection. To date, there is no evidence for an animal reservoir of viruses closely related to hepatitis C virus which may have

@franciscodeasis crossed the species barrier to cause disease in humans and resulted in the current pandemic. In fact, due to this restricted host range, a robust immunocompetent small animal model is still lacking,

[@franciscodeasis](#) hampering mechanistic analysis of virus pathogenesis, immune control and prophylactic vaccine development. "<https://t.co/tKFaQESIRn> Unfortunately, TWO exclusively human and decidedly non-zoonotic pathogens were defaulted as being of "zoonotic origin" in the holmes "article".

[@franciscodeasis](#) "Most of the genera in this family infect primarily humans and Old World anthropoids (Fig. 10), with nonprimate strains appearing to derive from their human counterparts (Rodrigo and Dopazo, 1995; Gromeier et al., 1999). "<https://t.co/eYwQmdnzKP> Polio and other Picornaviruses

[@franciscodeasis](#) infecting primates ORIGINATED in and COEVOLVED with humans--there will never be any animal origin for these.

[@franciscodeasis](#) <https://t.co/AYYICizVd4>

<https://t.co/wDDy1s6Tmk>

On SARS-CoV and MERS-CoV: Highly prevalent in Civets, Raccoon dogs in market, as well as in camel herds.

[@franciscodeasis](#) <https://t.co/UJQrANyLkE>

<https://t.co/Wel8UOx9R8>

On seroprevalence of SARS-CoV and MERS-CoV.

[@franciscodeasis](#) <https://t.co/mb8Rfwnhg6>

[@franciscodeasis](#) <https://t.co/Kp6qfNI5P6>

<https://t.co/18qKGTXn0y>

<https://t.co/Xx7GjNOiEc>

(And other clades of SARS-CoV-2)

Observation 4: All tested ACE2 favors H,Y or F on position 498 over Q498. The only RBD that is better with Q498 is Rs7327. However, it is not relevant to SARS-CoV-2, and carried a F498 by default, indicating that other constraints (folding) is at pic.twitter.com/e1WN3aFoXc

— Daoyu (@Daoyu15) [July 21, 2021](#)

[@franciscodeasis](#) <https://t.co/Egj9ZdAp1i> for everything else.

[@franciscodeasis](#) <https://t.co/dEbk3F3WjC>

On RaTg13.

[@franciscodeasis](#) <https://t.co/8kHw65luEH> Why a mutation in humans generated a RdRp that is more permissive to RDV binding than the original? <https://t.co/R0YmWMSOx3>

The RdRp had an anomalously high resistance to Remdesivir—best explained by passaging in the presence of RDV/RTP.

[@franciscodeasis](#) <https://t.co/jkdByR7Ia8>

Mojiang miners. This is why the oral serological claims made by the WIV can not be trusted in any way. No Data for the Shi addendum, or any of the claimed seronegativity of the WIV workers.

@franciscodeasis <https://t.co/0vmXzMDU0B>

SARS-CoV-2 LAI covered up for a year and a half.

@franciscodeasis Also important is that the cases that were found in the Huanan market was sampled about the same time as the lineage A genomes in Wuhan, and that at that time (December-January 2020, before 01/19/2020 where PCR testing kits becomes available), contact tracing to the wet market

@franciscodeasis (worked, entered, or have contacted others that have visited) was required for the diagnosis of SARS-CoV-2 infection--and only patients that had geological proximity to the market were sampled for sequencing before 19 January 2020. (as contact traced history to the Huanan market

@franciscodeasis was required for diagnosis of the "unknown pneumonia cases" in wuhan at that time, making the sampling of the earliest lineage A genomes necessarily biased to cases that just happened to have geographic proximity to the market. <https://t.co/clKNfnJnZ5>

@franciscodeasis The first official case had an symptom onset date that is consistent with the incubation period of SARS-CoV-2 Wuhan strain, which is approximately one week after initial exposure, indicating that he was in fact exposed in 08/Dec/2019. <https://t.co/D85r2bHHNR>

@franciscodeasis Neither the March 2020 interview nor the WHO interview indicate contact history that are closely related to the Huanan seafood market, which "■■■■" was in fact way outside of Wuhan, with visit time that was way in the beginning of November 2019, and zero contact history to the

@franciscodeasis market in any way. there is no "travel to the north of the huanan seafood market shortly before symptoms begin". Notably, at time of the case tallying by RT-PCR have begun, the distribution of cases have already fully matched that of the population density pattern for Wuhan.

@franciscodeasis And the density pattern of elderly people in Wuhan. A serological survey indicate that <https://t.co/SIxHjAHFh7> the highest amt of asymptomatic PCR positivity was detected in Wuchang, <https://t.co/Ua7FQdqHNv> which is consistent with the location being the highest amt of

@franciscodeasis SARS-CoV-2 positivity based on past Influenza prevalence data and COVID-19 positivity (symptomatic)/influenza positivity rates. remember that the only patient samples that hit the sequencers in December 2019 are the samples that were connected (epidemiology, contact tracing)

@franciscodeasis To the Huanan seafood market--in order to be even diagnosed as a case of COVID-19 and have your sample sequenced before 19/01/2020, you must either be in direct contact or be geographically near the Huanan seafood market, within reasonable contact tracing ranges.

@franciscodeasis The Jiangxia case have also denied any contact or travel history to the location where the Huanan seafood market was located at, 15 days before symptom onset. This makes contact with the Huanan market extremely unlikely.

@franciscodeasis In addition, as both of the "earliest A lineage genomes" sampled near, but not actually contacting, the Huanan seafood market (only cases near the market gets to be sequenced. <https://t.co/XDqdgLxn70> some hospital sequenced cases from the same period, again right atop the

@franciscodeasis WIBP dormitories, have lineage A genomes as well as other highly diverse genomes. samples were Dec-Jan 2020), were sampled at the same time as the actual cluster case in the Huanan seafood market, the temporal range of these samples overlap in the same course of human SARS-CoV-2

@franciscodeasis infection, Should A lineage be actually present in the market within community transmission time range (market to community), necessary to assign a market origin for these 2 A lineage cases, then there is no reason that the lineage was not present in the market samples--since

@franciscodeasis they would have been sampled within the range of viral persistence in the human body considering their overlapping sampling dates. In stead, despite all the cases within the market being sequenced, even including environmental isolates, none of the genomes were lineage A,

@franciscodeasis which would have been wholly inconsistent with an origin in the Huanan seafood market. as lineage A genomes were also found in the RenMin hospital approximately the same time, it rules out the seafood market as the source of the ancestral A lineage genomes.

@franciscodeasis <https://t.co/BZykqhlwu6>

Note that there were 2 genomes in Wuhan and 15 out of the 91 genomes from Sichuan before 2021 carrying intermediate between A and B lineage, with sampling outside the market generally returning much greater diversity than inside the market.

@franciscodeasis As the consensus sequence in animals is that of lineage A, T8782/C28144, And since there exist a statistically significant fraction of genomes (1/4 out of all genomes in Sichuan, 2 in Wunan) that matches the exact intermediate lineage from A to B using a rooted tree based on

@franciscodeasis USA/WA-1, Guangdong/HKU/SZ or Shandong/Ly005/2, and that intermediate genomes between A and B lineages are found abundantly within the stool samples of children sick with SARS-CoV-2 and respiratory samples of SARS-CoV-2 patients, A is the ancestor of B and there are no need for

@franciscodeasis "two spillovers" to happen at all. all happened in humans. Also there is another issue with the early SARS-CoV-2 case data--as contact tracing to the Huanan seafood market is necessary for the initial (between 20/Dec to 04/Jan) recognition of SARS-CoV-2 cases for sequencing and

@franciscodeasis for the recognition and archival of early cases of SARS-CoV-2(which, as per the deleted SRR dataset that were found right atop the dormitories of the WIBP, a lot of SARS-CoV-2 cases, especially A lineage genomes, w/mutations indicative of substantial diversity in early Jan 2020)

@franciscodeasis , and given the effort of obfuscating and destruction of case records and sequence data outside of the Huanan seafood market for samples that were taken before 04/Jan/2020, and the fact that <https://t.co/WiGSze3POM> there exist french patients that have no travel history to China

@franciscodeasis , whose throat swab have a positive PCR test in 27/Dec/2019 (requiring at least 1 round of community transmission from a person that recently traveled abroad, pushing the date of first wuhan case onset to at least two weeks before that at ~10 Dec 2019 in case of travel)

@franciscodeasis <https://t.co/UyZkEJktqF>, as well as some swab PCR positivity in Italy with a date of collection of 05 December, which is before the first Huanan seafood market case, indicate that cases exist in China before the official first case in the Huanan seafood market.

@franciscodeasis <https://t.co/QiCSDcKeCD>

Then, there is an increase in the amt of S seropositivity in sera collected in France in December 23 2019, which would have required the first widespread transmission of SARS-CoV-2 in france beginning at 09/2019--with substantial amt of infection well

@franciscodeasis past patient zero at that time. <https://t.co/FU8RKB1052>

Another clue came from italy, which have shown consistent qRT-PCR positivity from wastewater (this is not the november claim with just one sample. this is consistent PR-PCR positivity) since 18/12/2019, which once again

@franciscodeasis would have required that the beginning of transmission (substantial amount of infection, take about two weeks to achieve from patient zero) in both cities to begin well before the claimed 11 December symptom onset of the first Huanan seafood market vendor in 2019.

@franciscodeasis These aggregated data all suggest that SARS-CoV-2 transmission have begun in Europe in the same time as, or even before, the Huanan seafood market cluster, which as international travel for pathogen spread requiring even more time than domestic spread, would be consistent

@franciscodeasis with the lineage A of SARS-CoV-2 emerging before Lineage B and spread to high diversity in Wuchang, and Lineage B emerging in humans in Wuhan (with samples suggesting intermediate lineage in Wuchang) and entering europe at the same time or before the Huanan seafood market.

@franciscodeasis <https://t.co/Gq6qPDPaak>

Similarly, consistent detection of SARS-CoV-2 have been reported in Brazil between 27/11/2019 and 11/12/2019. Note that A lineage have been found just south of the location being sampled, and is found in South america in general.

@franciscodeasis A lineage also exist in Italy and Spain where the detection of SARS-CoV-2 have been reported that would have pushed the initial outbreak date in Wuhan far before that of the Huanan seafood market, indicating that clade A have in deed been circulating at that time.

@franciscodeasis <https://t.co/ButKs5Hoc7>

In deed, this would have been consistent with SARS-CoV-2 having a tMRCA in November 17 2019, which is consistent with WIV and WIBP as the origin, with the first outbreak happening in Wuchang, in stead of with the Huanan market as the origin.

@franciscodeasis <https://t.co/QKfMWWuljR>

In deed, before the more widespread control on the narrative for SARS-CoV-2 origins were established in China, there were reports of contact tracing for first case as early as in 17 November 2019, which is once again earlier than the market, but

would have

@franciscodeasis coincided perfectly with the calculated global MRCA of SARS-CoV-2. As samples of SARS-CoV-2 before 18/Jan/2021 was only diagnosed, archived and sequenced if they had geographical or epidemiological link to the Huanan seafood market, It shouldn't be surprising that

@franciscodeasis "the earliest patient of SARS-CoV-2 onset was in the Huanan seafood market"--that will be the first case that meets the criterion of documentation in that time. <https://t.co/0BPmegrJwc>
Considering the extreme censorship of early cases in China, and the existence of consistent

@franciscodeasis PCR and serological evidence of SARS-CoV-2 circulation in Italy, France and Brazil at the same time or before the beginning of circulation at the Huanan seafood market, between the end of November 2019 and the beginning of December 2020, The idea that SARS-CoV-2 started in the

@franciscodeasis Huanan seafood market is still inconsistent with actual epidemiological data, and may have willingly precipitated in the CCP's cover-up of earlier cases of SARS-CoV-2 in Wuhan.
In deed, much higher diversity exist outside of the market than inside the market for the earliest

@franciscodeasis Wuhan cases, which would be consistent with another source in Wuhan generated the first SARS-CoV-2 human genomes much earlier than the Huanan seafood market, and only one of the branches then entered the seafood market and triggered the monophyletic B lineage outbreak.

@franciscodeasis <https://t.co/Y6qK4FoVjR>
Certain Florida cases also have an onset date at Jan 1 2020.

@franciscodeasis <https://t.co/T6QJXgqxvq>
There are other possible points before, but they are dubious at best. The first confirmed PCR positivity in Italy and Brazil pushes the arrival date of SARS-CoV-2 at these 2 countries (A, possibly A or B) at 27/11/2019.
<https://t.co/nUBbhZxisU>

@franciscodeasis This would have been more than a week before the beginning of the first case at the Huanan seafood market--but would have been perfectly fit the 17 November 2019 global TMRCA of SARS-CoV-2 indicated at time before censorship on early contact-tracing and origin-tracing of Wuhan

@franciscodeasis SARS-CoV-2 have took place in China. circa April 2020.

@franciscodeasis another proof that only cases that were market-traced were registered before <https://t.co/ZognD2v2jb> the beginning of 01 Jan 2020, is that there is a huge gap in the amt of confirmed cases before and after 01/2020, as per the report from CDC. With this in mind, up to

@franciscodeasis 6 times as many cases that weren't associated with the Huanan seafood market were simply erased from the record--they were simply never registered, should they have an epidemiology that is inconsistent with a market-derived origin--if they came before the onset date of the first

@franciscodeasis case in the Huanan seafood market, if they did not contact any person that have visited the market, if they does not live close enough to the market should condition 1 and condition 2 weren't met. You can't just look at data that have been carved out from <https://t.co/xLNR9tyJ5J>

@franciscodeasis a larger set of (6 times as much!) data based on the connection to the market, and then relying on the coincidence that the HSWM is also where the densest population of people, especially aged people, was located, after that date, to justify your claim of "market origin".

@franciscodeasis <https://t.co/yrcb9ki0ke>

Very similarly, this happened as well. as many as 4/5 times the active cases were simply removed (not recognized) before the beginning of 2020, simply because they are not epimediologically linked to the Huanan seafood market--you aren't going to find

@franciscodeasis anything that were inconsistent with a plausible "contact traced" epidemiological link with the Huanan seafood market from data that derived before that date--given that epidemiological link to the market was used as the criterion of diagnosis before successful symptom- and PCR-

@franciscodeasis testing were conducted. The CCP feeds you manipulated data, and you will always derive manipulated result from it!

@franciscodeasis