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An Article in *Science* on Wet-Market Covid Origins is Unreliable

Michael B. Weissman[1]

LINK TO ABSTRACT

The Covid pandemic has been the largest exogenous shock to public health and the world economy of the twenty-first century. Minimizing the risk of future pandemics requires realistic comparisons of the risks from agricultural practices, wildlife trade, and research projects on potential pandemic pathogens. Since laboratory methods for enhancing pathogens have only recently become widespread, there is no historical record from which the research risk for novel pathogens can be easily extracted. If the SARS-CoV-2 (SC2) virus came from a research project, that would support prior estimates that risks from research on new pathogens are substantial (Klotz and Sylvester 2012; Butler 2015; Casagrande 2015; Lipsitch 2018; Feng et al. 2019; Johns Hopkins Center for Health Security 2019). If it were established that SC2 came from a more traditional source, then estimating the risks of new types of research would be more speculative.

In 2022, the leading journal *Science* published a pair of articles (Pekar et al. 2022; Worobey et al. 2022) (I'll call them W2022 and P2022) purporting to establish that SC2 first spilled over to humans from wildlife at the Huanan Seafood Market (HSM) in Wuhan. Michael Worobey, a coauthor on P2022 and the lead coauthor on W2022, conveyed the importance of these articles in a tweet (Worobey 2022) addressed to members of the press: "I said: OUR TWO RECENT PAPERS establish that a natural zoonotic origin is THE ONLY plausible scenario for the origin of the pandemic." P2022, largely concerning the number of spillovers, has now been shown to have reached a wrong conclusion via a series of coding and logic

[1] Department of Physics, University of Illinois at Urbana-Champaign, 1110 W. Green St. 61801, USA. Email: mbw@illinois.edu. Orcid 0000-0003-0081-4429. I thank Daniel Walker for preparing Figure 1, Jonathan Weissman for running the simulations shown in Figure 2, Andy Levin for useful conversations, Gilles Demaneuf for many helpful comments, especially some adversarial LLM reviews, and two anonymous referees.

errors (McCowan 2023; 2025). When a minimal repair of these errors is made, its result is reversed (Weissman 2026). That leaves W2022 as the most important remaining pillar of the HSM case, cited 629 times as of this writing, according to Google Scholar.

In this article, I integrate several previously published critiques of W2022, showing that several features of the statistics on which it is based are not easily consistent with an HSM origin of SARS-CoV-2, particularly now that the accompanying P2022 paper has been shown to be incorrect. The combined critiques will amount to a somewhat stronger case than the sum of the individual critiques, in particular because of incompatibility among possible responses to the criticisms of the W2022 interpretation of the data on case home address locations. Nevertheless, the analysis here concerns only the specific W2022 HSM origins zoonotic theory and has no direct relevance to other zoonotic theories. Comparison of generic zoonotic theories with lab theories requires several lines of evidence beyond the scope of this paper, although I have discussed such evidence informally elsewhere, concluding that a lab origin is much more probable (Weissman 2025).

Index Case Timing

For HSM to be the original spillover site of SC2, it is necessary that the first Covid cases linked to HSM not be substantially preceded by cases elsewhere. There are, however, numerous indications that cases had become fairly widespread before there were any known to be linked to HSM. Unless all these indications turn out to be spurious, there is almost no chance that the initial human cases were at HSM.

Not long before W2022 was written, a prominent paper sharing three senior authors with W2022 (Pekar et al. 2021) held that "this market cluster is unlikely to have denoted the beginning of the pandemic, as COVID-19 cases from early December lacked connections to the market." This view was supported by a reference to a *Nature* paper (Zhang et al. 2020) that relied on previous work from other Chinese research groups. Two early papers from these researchers (Huang et al. 2020; Li et al. 2020) report the earliest cases as not being linked to the market. The World Health Organization (WHO)-China report (WHO-China 2021b) continued to state, "The earliest cases had no history of exposure to the Huanan Market" in February 2021. The earliest unlinked case, however, was later redated to Dec. 16 (Ren et al. 2020), still leaving 8 of the first 11 cases in the WHO report unlinked to the market.

Further investigation of early cases in Wuhan has been impeded by a January 3, 2020, central government order that anyone in possession of the viral samples "should immediately destroy the samples on the spot or send them to the storage institutions designated by the state" (General Office of the National Health Com-

mission 2020). The WHO therefore had no access to patient samples from Wuhan and could not independently check for earlier cases.

Bloom (2021) describes other evidence of early cases. Quay (2026) lists even more lines of evidence indicating early cases, although I do not agree with his estimates of the reliability of some of those lines of evidence.

Although any small number of cases can be incorrectly identified, the interpretation by Pekar et al. (2021) was conventional until overturned by the pair of *Science* papers, W2022 and P2022. George Gao, then director of the Chinese Center for Disease Control and Prevention (Chinese CDC), concluded based on the many cases that he saw that "[a]t first, we assumed the seafood market might have the virus, but now the market is more like a victim. The novel coronavirus had existed long before" (Global Times 2020). A formal report from the WHO and the Chinese CDC (WHO-China 2021a; World Health Organization 2021) looking at the case location data concluded: "Many of the early cases were associated with the Huanan market, but a similar number of cases were associated with other markets and some were not associated with any markets….No firm conclusion therefore about the role of the Huanan Market can be drawn."

Many Western experts described hearing reports of the new coronavirus by mid-December 2019 or earlier, well before the few initially detected HSM cases could have provoked such reports. These experts included virologist Ian Lipkin (Birrell 2021) and global health policy expert Lawrence Gostin (Rainey and Feldman 2020). A report in *National Geographic* (Borrell 2020) also indicates that SC2 was becoming widespread in Wuhan by November 2019: "Michael Callahan, an infectious disease expert, was working with Chinese colleagues on a longstanding avian flu collaboration in November when they mentioned the appearance of a strange new virus. Soon, he was jetting off to Singapore to see patients there who presented with symptoms of the same mysterious germ." Likewise, the prominent viral gain-of-function researcher Ron Fouchier reported hearing of the new outbreak in the first week of December 2019, according to a Dutch documentary (Fouchier 2020).

The WHO-China (2021, 144) report says that "174 cases of COVID-19 were identified with onset date in 2019, including 100 laboratory confirmed cases and 74 clinically diagnosed cases." In contrast, the *South China Morning Post* (Ma 2021) published a story on May 10, 2021 claiming that unpublished Chinese government records showed 266 identified cases by December 31, 2019, including a first case with onset on November 17. That leaves a difference of 92 cases between Ma (2021) and WHO-China (2021b). Although hard to fully verify, some confirmation of those 92 missing cases, cleaned for possible duplicates using the patients' Chinese national IDs, can be found in other publications. Figure 1 of Wei et al. (2020) shows 146 laboratory-confirmed cases by December 29, recorded by the National

Notifiable Infectious Disease Information System as of February 27, 2020. Figure 2 of Annex E2 of WHO-China (2021b) shows a total of 19 lab-confirmed cases on December 30 and 31, so there is a discrepancy of 65 lab-confirmed cases by December 29 between Wei et al. (2020) and WHO-China (2021b). That discrepancy of 65 lab-confirmed cases agrees well with the somewhat larger discrepancy of 92 total 2019 cases between Ma (2021) and WHO-China (2021b) since many of the total cases are clinically diagnosed rather than lab-confirmed. As the *Washington Post* Editorial Board (2022) reported, Demaneuf (in arguments he later posted in detail (Demaneuf 2024)), infers from other peer-reviewed publications from China that the *South China Morning Post* numbers for 2019 onset cases are fully consistent with the process of retroactively back-filling and cleaning cases by the Chinese CDC. However, his analysis requires keeping track of that changing process in early 2020, which is not as simple as just looking directly at Wei et al. (2020). It is highly probable that the *South China Morning Post* numbers reflect the actual data cleaned and recorded at the end of February 2020 better than the numbers supplied to the WHO a year later, which seem anchored on numbers released by the CDC in mid-February 2020. Thus, it is likely but not certain that the *South China Morning Post* story also correctly reflects the case data for November 2019.

A systematic look at early cases using standard methods from conservation science to estimate endpoints of event times from sparse data sets (Roberts et al. 2021) finds that "results suggest that the virus emerged in China in early October to mid-November, 2019 and by January, 2020, had spread globally." The global spread by January 2020 suggests that if the pandemic started in Wuhan, the cases there would have been widespread before the first known HSM case.

Data from several search engines also indicate early spikes in interest in SARS-like infections. From December 1–3 of 2019, there was a particularly noticeable spike in searches for "SARS" on the Chinese WeChat site (Wang et al. 2020), apparently representing thousands of searches.

If the first human cases were at HSM, one would expect a significant time lag before much evidence of cases in remote locations turned up, consistent with the results of Roberts et al. (2021). Retroactive tests of wastewater in northern Italy show positive results at some sites starting on December 18, 2019, with consistently negative results before that and almost consistently positive results later (La Rosa et al. 2021). A subsequent report from the WHO (Scientific Advisory Group for the Origins of Novel Pathogens (SAGO) 2025) did not confirm the early positive results but indicated plans to follow up with more sensitive next-generation-sequencing tests, for which no results have yet been reported. Like any lab results, these positive results should not be taken to be definitely right, particularly since the date is earlier than other evidence would lead us to expect.

The timing of the first human cases can also be roughly estimated from the

genetic diversity of the early cases. Since it has become clear that the P2022 results supporting multiple successful introductions were erroneous, phylogenetic estimates of the probable timing should be based on the genetic diversity of the full set of early cases (Bloom 2021). Such estimates have substantial uncertainty, but some point roughly to October 2019 as when the first human case occurred, well before the earliest known market-linked cases (Caraballo-Ortiz et al. 2022).

The earlier time estimated from these various lines of evidence is inconsistent with the account in which cases start with a spillover at HSM in early December 2019. But it is possible, if improbable, that all these lines of evidence are mistaken in various ways, so it is worth examining the multiple types of evidence W2022 cites to support the HSM account.

Contrast with the Beijing Market Outbreak

A simple empirical approach may be the best way to estimate how surprising the existence of a possible early cluster of cases at a market is if the introduction was elsewhere. After 56 days without detected local propagation of cases in Beijing, a propagating outbreak centered at the Xinfadi wet market occurred (Chen et al. 2021; Zhang et al. 2021). Similar market-centered outbreaks after periods of low transmission occurred at a fish market in Singapore (Ang 2021), a wet market in Thailand (Harmer 2020), and a vegetable market in Chennai, India (Alluri 2020). Thus, with several such examples in a few dozen major East Asian cities, we know empirically that an easily detected market epicenter can arise from existing scattered cases rather than from a market spillover. The non-market background for these other cases would be reduced, however, since they occurred during periods of partial lockdowns.

The main contrast between the Beijing outbreak and the early ascertained Wuhan cases is that Wuhan had a large fraction of early unlinked cases, 120 of the 155 total in W2022. According to Zhang et al. (2021) all 377 ascertained cases in the Beijing outbreak had known links to the Xinfadi market. A later paper (Dai et al. 2023) claims 344 Beijing cases with a parenthetical note seeming to indicate that 335 were linked. Only 35 of the 155 cases included in W2022 were linked to HSM.

The Beijing cases were detected at a much higher rate than were the early Wuhan cases, so ~350 Beijing cases would correspond to a much smaller number of early detected Wuhan cases. Nevertheless, even the earliest few reported cases from Wuhan show a roughly equal mixture of linked and unlinked cases, so the empirical contrast is real. The contrast supports the view that SC2 was circulating in Wuhan independently of HSM.

Market Case Lineage

If the original spillover from animals to humans occurred at HSM, one would expect cases at HSM to include the most ancestral sequences detected in the Covid-19 outbreak, i.e., sequences more closely resembling the natural virus relatives rather than sequences with more mutations distancing them from natural relatives. This is the opposite of what was found at HSM. The eleven cases that were directly linked to HSM and were sequenced well enough to identify the lineage were all lineage "B" (Pekar et al. 2022; Worobey et al. 2022). In contrast, many cases that had no known link to the market were lineage A, differing from B by two nucleotides (Bloom 2021). Lineage A shares those two nucleotides with all the closely related natural sequences. Although the earliest identified sequences in humans were lineage B, multiple groups have found that it is highly improbable that B is ancestral to A, with the only two mutations between them happening to be reversions to ancestral nucleotides (Pipes et al. 2020; Bloom 2021; Kumar et al. 2021; Caraballo-Ortiz et al. 2022; Lv et al. 2024; Bloom 2025). Bloom (2025) emphasizes that the outgroup sequences are less subject to missing-data problems than the early human sequences. Whether the most recent common ancestor of the human cases is lineage A or one of several possibilities that resemble the relatives at one more nucleotide than A is uncertain.

When Liu et al. (2024) examined nucleic acids on swabs taken from within HSM, they found one lineage A sample on a swab taken at HSM on January 1, 2020, but it had further mutations away from the relatives, indicating that it appeared shortly before the swabs were taken or even could have been introduced by lab contamination afterwards. As we have seen, by that point it is likely that both lineages of SC2 had spread widely around town. The team that did the sampling noted that, of relevant mammals, "only *Homo*, *Ovis*, *Bos*, and *Sus* reads but not species related to wildlife were found in the Env_0020 sample, the one with A lineage" (Liu et al. 2024). Of those genera, only *Homo* is a plausible host.

Market Vendor Cases

For SARS CoV-1 (Cyranoski and Abbott 2003) and MERS (Alshukairi et al. 2018), early cases were concentrated among people who had direct contact with the natural hosts. The SC2 cases at HSM included no identified wildlife vendor cases, but since a high fraction of cases were not identified, and some SC2 RNA was found in a wildlife vendor stall, we cannot confidently conclude that no such vendors caught it (WHO-China 2021b; Worobey et al. 2022). Nevertheless, serology studies of the SARS CoV-1 (Yu et al. 2003) and MERS (Khudhair et al. 2019) outbreaks found a high concentration of seropositive results among people who

handled the suspected intermediate host species, while no such SC2 serology studies have been reported.

RNA and DNA in the Market

Investigators collected 457 samples from 188 individual animals in HSM, including from a stray weasel (Liu et al. 2024). None contained detectable SARS-CoV-2.

W2022 described the presence of SC2 RNA in environmental swabs taken at HSM, but Bloom (2023) noted that the traces of SC2 RNA found in the swabs did not show a positive correlation with the mtDNA of suspected non-human potential hosts. In contrast, the RNA levels from the four actual animal coronaviruses that were detected in appreciable quantities all showed a distinct positive correlation with their known hosts' mtDNA (Bloom 2023). One other coronavirus, detected at very low levels, showed no distinct correlation with any potential host. Thus the market swabs with SC2 lacked the probable signature for a market animal coronavirus.

W2022 also argues that the distribution of the locations within HSM of the positive SC2 RNA swabs pointed to a spillover from some wildlife there. The positive SC2 RNA reads did tend to cluster in the general vicinity of some of the HSM wildlife stalls, the general region in which the sampling was most intense. But the number of samples collected per stall, with only one sample in several cases, is so small that one cannot confidently quantify and correct for sampling bias on a fine scale (Bloom 2023). The area with the most positive swabs, however, is also where bathrooms and a MahJong/cards room are located, both likely spreading sites (Courtier-Orgogozo and Ribera 2022). The space-time pattern of the vendor infections is consistent with spread via shared toilets, but does not show signs of spread from an infected stall (Levin 2025).

Potential Hosts

According to information given by Chinese authorities to the WHO and then reported by the *Lancet* commission, over 80,000 samples were taken from a variety of suspected animal hosts in China shortly after the pandemic started, but all were negative for signs of SC2 infection (Sachs et al. 2022). Although a broader survey of 461 deceased farmed and wild fur animals from multiple Chinese provinces found an alarming array of potential zoonotic viruses, none were SARS-related (Zhao et al. 2024). Thus there is no direct evidence pointing to any particular prior host, in contrast to most other recently emerged viral diseases, most notably the other important ones from coronaviruses, MERS and SARS (Schindell et al. 2022; Tang

et al. 2022).

Since it is possible that the host could have been missed, we can instead follow W2022 in investigating the wildlife sold at HSM. Fortunately, the wildlife sold at the markets in Wuhan happens to have been tracked in great detail (Xiao et al. 2021). Much of it was sourced locally, but a search for local sources of related viruses found nothing. As reported on page 2 of their paper, Wang et al. (2022, 2) "immediately performed a surveillance investigation in mammals in and around Wuhan…no SARS-CoV-2 or the close relatives of SARS-CoV-2 were found in these mammals." Likewise, environmental samples taken at HSM turned up a variety of pathogens including coronaviruses, but none that were SARS-related except for SC2 (Bloom 2023).

The virus might also have reached HSM, via a host sourced from the Yunnan area where the related bat viruses are found (Hassanin et al. 2024; Pekar et al. 2025), if it was sold at HSM in late 2019 and was able to sustain SC2 transmission. I shall argue that it is unlikely that any species meets all of these three criteria: source location near related viruses, timely market sales, and ability to sustain SC2 transmission.

Of the species sold in late 2019, only raccoon dogs are known to be susceptible to infection with SC2, at least when given large nasal inocula (Freuling et al. 2020) of a strain that has a mutation (D614G) that was not present in the initial cases and increases infectiousness. Levin (2025) has a good discussion of the Freuling et al. (2020) findings with helpful figures. Transmission was found between animals that could have direct physical contact, but the second generation of infections produced very low viral titers (Freuling et al. 2020). No third-generation cases were reported. No airborne transmission was observed between animals caged about 1.5 m apart. Luo et al. (2024, 10) find that SC2 binds poorly to raccoon dog ACE2, which they suggest explains why "[t]o date, while 45 species have been documented as naturally infected with SARS-CoV-2, there has been no confirmation of raccoon dogs being naturally infected with or carrying the virus."

W2022 uses the descriptor "live" in its table S5 for species that are directly known to be susceptible. Other than raccoon dogs, only mink (Bashor et al. 2021) and red fox are listed as such (muntjac also, but only via another species). W2022 also lists mink as not having been sold at HSM in late 2019. Jemeršić et al. (2021), the reference given for red fox being susceptible, states that "Based on the results of our study, we conclude that no spillover of SARS CoV-2 occurred in wild boars, red foxes and jackals in their natural habitat…" Several other species are described in W2022 as potentially susceptible, but none have been shown to be susceptible in any experiment of which I am aware.

Based on studies of SC2 binding to ACE2 receptor sites (Ou et al. 2023), civets and pangolins are also potential hosts (although not confirmed experimen-

tally), with binding not far behind the species with the best binding, humans. Neither civets nor pangolins were sold at HSM in late 2019 (Xiao et al. 2021). Pangolin coronaviruses were, however, apparently present in Wuhan. According to a June 4, 2021, diary entry from National Institute of Allergy and Infectious Diseases (NIAID) director Anthony Fauci (Fauci 2026), CIA intercepts had discovered "the transfer of Pangolin viruses from a group in Beijing two Wu Han. [sic] They felt that this was being used in a study using transgenic mice." Needless to say, transgenic laboratory mice would not have been sold at the market. Other species fall farther behind humans in ACE2 binding (Ou et al. 2023), although that does not flatly rule them out.

A bamboo rat "product" (WHO-China 2021b), likely frozen meat, is the only product sold at HSM in late 2019 that was known to have been sourced in the region where the related viruses are found (WHO-China 2021b). Bamboo rats are known to be susceptible to some coronaviruses (Huong et al. 2020), but have not been shown to be susceptible to SC2.

Thus, it is unclear whether any species meets even one of the three criteria needed for a plausible host to carry SC2 from the region where related viruses are found to HSM. It is unlikely that any species will be found to meet all three criteria, although that cannot be ruled out based on current evidence.

Case Home Addresses

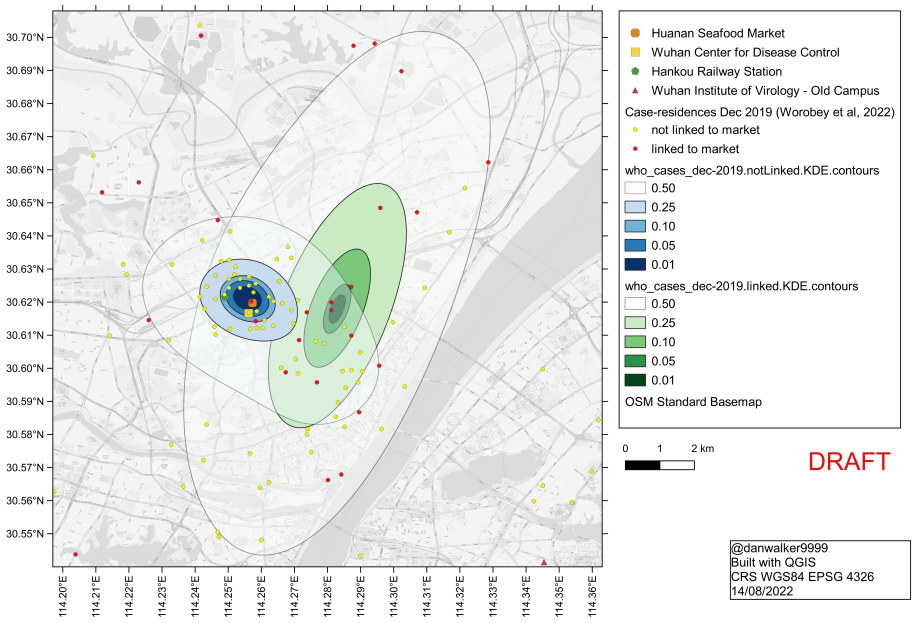
Although the factors discussed above could be enough to answer the substantive question of whether SC2 first entered humans at the HSM, it is worth looking at the W2022 analysis of the case home addresses, in part to clarify some methodology issues. In order to focus on those issues, I shall assume for this discussion that the cases used in the Worobey analysis are not missing a major group of preceding cases, although we have seen that they probably are. Figure 1 illustrates the case location data on which the W2022 argument was based.

Figure 1 is an overlay of two figures from W2022, prepared by Daniel Walker. The yellow dots and their accompanying blue heat map regions represent cases with no link to HSM, as shown in W2022. The red dots and their accompanying green heat map represent linked cases, as shown in a figure in W2022's online supplements.

W2022's analysis rests on an assumption that, as Worobey put it in a press interview, "We fully expect the cases that we don't sample to come from exactly the same geographic distribution as the ones that we do sample" (Washington Post Editorial Board 2022). Any violation of that assumption, i.e. any geographic dependence of the probability that a case would be included in the small fraction detected and used in the analysis, is called "ascertainment bias." The assumption was never

particularly plausible since, as one paper from a Chinese research group summarized it, "The initial epidemiological investigations targeted their search for early coronavirus disease 2019 (COVID-19) cases with a link to the Huanan Seafood market or its neighborhood in Wuhan" (Wang et al. 2022).

Figure 1: Case home-address locations and corresponding heat map



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Source: prepared by Daniel Walker from two maps given in W2022 and its supplementary material.

W2022 claims that "One of the key findings of our study is that 'unlinked' early COVID-19 patients, i.e., those who did not work at the market, did not know someone who did, and had not recently visited the market, resided significantly closer to the market than patients with a direct link to it." As Débarre and Worobey emphasized in a later follow-up, "[o]f the geographic findings…the most striking and consequential involved the early cases epidemiologically unlinked to the market" (Débarre and Worobey 2024a). The unlinked cases give the key part of the argument because the linked cases merely confirm that superspreading occurred from HSM. If the cases with no known link to HSM nevertheless also have some identifying property that points to HSM, in this case home address locations, that would at least suggest that HSM might have been more than a superspreading location for a virus that started elsewhere.

The time-dependent way in which cases were identified affects any modeling that assumes that ascertainment is independent of either case location or on case timing (Tsang et al. 2020). Several researchers (e.g. Bahry 2023 and, with much detail, Demaneuf 2024) suggested that the case location data had been seriously skewed by ascertainment bias based on detailed reports of how cases were found. The support for their claim is clear on page 125 of WHO-China (2021b):

> "30 Dec - 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…..
>
> 31 Dec - Continued epidemiology surveillance at several hospitals (close to Huanan market), Huanan market and the neighbourhood of Huanan market."

Thus both direct linkage to HSM and proximity to HSM were pathways to being identified as an early case. When the HSM-linked criterion for identifying cases was dropped on January 18, 2020 (Tsang et al. 2020), retroactive identification of unlinked cases would have been impeded by the sample destruction ordered on January 3 (General Office of the National Health Commission 2020).

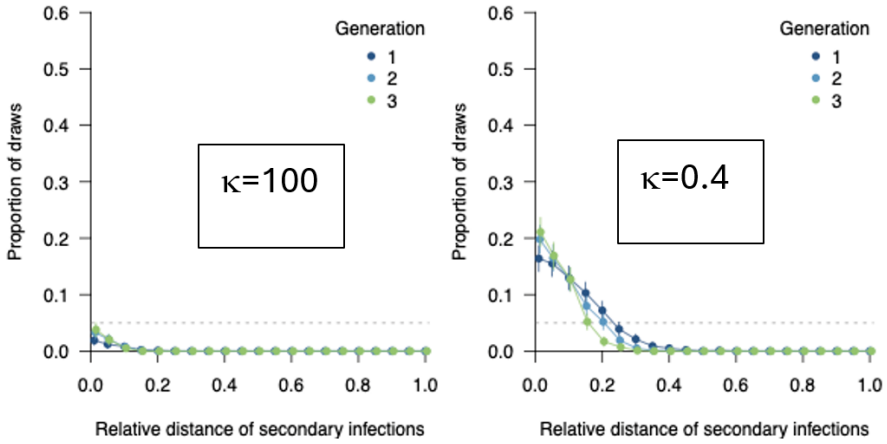
I pointed out in Weissman (2024a) that this situation, where either direct HSM-linkage or near-HSM location provides probable paths to ascertainment, would give a classic case of bias due to stratification on a collider (Greenland et al. 1999), with the collider here being ascertainment and the colliding causes being linkage and proximity to HSM. Stratification creates a negative correlation between these variables beyond whatever correlation would be present in an unbiased sample. The negative correlation between proximity and linkage that W2022 observed had the sign expected for collider stratification bias.

I also pointed out that in the simple, unstructured W2022 model of viral transmission, one would expect a correlation of the *opposite sign*, since for unlinked cases there would be at least one transmission step and probably several before the final step from an infection site to a home address (Weissman 2024a). Adding steps would generally tend to *increase* distances rather than decrease them.

Débarre and Worobey (2024b) responded with an arXiv post presenting a model for how cases spread geographically. In their model, unlike W2022, the transmission is (realistically) over-dispersed, i.e. most cases lead nowhere but a few lead to many new cases. That overdispersion tends to create less predictable outcomes and allows a reasonable chance that the unlinked cases would have accidentally been slightly more tightly clustered around HSM than the linked ones. In particular, they showed that, even if one includes extra steps contributing plausibly to the distance of the home location of the case from the hypothetical HSM source, the chance that the unlinked cases would be closer than the linked cases was not so low as to require statistical attention.

The Débarre and Worobey argument was flawed because it did not test whether the unlinked cases could be *as much closer* to HSM as W2022 had reported, 70% of the distance of the linked cases. The standard frequentist method is to calculate a p-value from the observed result rather than from an arbitrarily chosen value. With help from Jon Weissman, I showed that the Débarre and Worobey model would be unlikely to give that substantial observed distance contrast unless the unlinked transmissions had some special properties (Weissman 2024b).

Figure 2: P-values for the small ratio (0.70) of linked to unlinked distances from the Débarre and Worobey model.



(Weissman 2024b) Source code from (Débarre and Worobey 2024b)

Figure 2 shows how probable (i.e. frequentist one-sided p-value) it would be for the Débarre and Worobey transmission model to produce as large a contrast as W2022 reported between distances from HSM to linked and to unlinked cases. The low-dispersion model (κ=100) corresponds to the model used in W2022. The high dispersion model (κ=0.4) suggested by Débarre and Worobey (2024b) is more realistic. Except for the dispersion labels, this figure was generated simply by using the Débarre and Worobey code with the observed 0.70 ratio of linked to unlinked typical distances rather than the arbitrary 1.0 they used.

For the original W2022 model (κ=100), the chance that the unlinked/linked distance ratio would be as small as observed is significantly low, as W2022 claimed. Unless the typical unobserved transmission step distance is a very small fraction of the typical distance from HSM to home for a linked case, the probability of seeing that extreme unlinked/linked ratio becomes negligible.

Even for the more realistic overdispersed (κ=0.4) Débarre and Worobey

model, if the distance from infection to home were similar in both types of cases, the results would be highly improbable, unless each previous unlinked step were less than about 20 percent of the typical HSM to home distance of the linked cases. Débarre and Worobey (2024b) propose a way this could occur: HSM workers mainly spread the infection just outside HSM, and unlinked transmission in that neighborhood proceeded by small steps. Spread inside HSM gives linked cases by definition. Spread near the homes of the sort of cases that were linked would already start with distances comparable to the linked cases and then add further spread (Weissman 2024b). Spread commuting to and from work seems likely to give larger steps than are compatible with the tight clustering.

Thus the unlinked distance feature that played such a prominent role in the W2022 interpretation requires some major changes from their simple model. The most obvious change that would produce the observed distance contrast is the previously hypothesized collider stratification bias from the effect of proximity on ascertainment, known to exist from the WHO report (WHO-China 2021b). An alternative would be that the HSM neighborhood is special with the occasional spread from HSM to it creating a highly localized cluster.

These hypothetical special properties of the local transmission leading to the unlinked home addresses cannot be ruled out. They do, however, require an intense population structure in the transmission, i.e. different groups of people in different neighborhoods would spread the infection quite differently. That sort of population structure also breaks the assumptions underlying the W2022 argument because it means that such a local cluster can easily arise regardless of how the cases got to the neighborhood.

Of the statistical issues that Stoyan and Chiu (2024) raised concerning W2022, probably the most important was that W2022 incorrectly took rejection of an unrealistic null model of random case locations to imply that an HSM-based model was correct. The null model that W2022 had rejected ignores not only overdispersion but also ascertainment bias and population structure, some combination of which is required to explain the anomalous linked/unlinked distance contrast, as we have seen. Thus the main analysis of W2022 assumes the absence of the ingredients that are required to explain the statistic that it describes as "one of the key findings" and that Débarre and Worobey describe as "the most striking and consequential." It is not possible retroactively to disentangle the effects of ascertainment bias and the effects of population structure, but either effect undermines the W2022 interpretation of the distribution of ascertained unlinked cases. That effects not included in the W2022 analysis are large enough to flip the sign of a key statistic does not show that there was no HSM spillover, but does show that the unlinked clustering cannot provide strong evidence of an HSM spillover.

Levin (2025) reanalyzed the various types of observations used in W2022

by more conventional Bayesian methods, comparing the likelihoods of different hypotheses rather than just ruling out an *a priori* unrealistic null. He uses both case location and timing, rather than just location, for modeling the initial spread. He includes some population structure in the form of a dependence of the transmission rate on local population density, and uses a conventional distribution of transmission step distances. He makes no allowance for any ascertainment bias. Unsurprisingly, Levin finds that the unlinked home location distribution over time strongly disfavors the original unstructured W2022 model of spread from HSM (ibid.).

Levin then compares a structured model that includes enhanced probability of transmission on the southeast side of the Yangtze (across the river from HSM, on the same side as the Wuhan Institute of Virology) with a model with the same number of adjustable parameters, including one favoring especially short-range transmission on the northeast side (ibid.). He obtains a Bayes factor of 27 favoring the model that includes enhanced probability of transmission southeast of the Yangtze. His model looks for transmission from recent cases, not just overall locations, so that Bayes factor is driven primarily by the timing of the unlinked cases southeast of the river that do not look like they derive from preceding linked cases. The WHO map used by Levin appears to omit an HSM-linked case southeast of the river, included on the map in Figure 6 of (WHO-China 2021a). Inclusion of that point would shift the Bayes factor toward an HSM account by an amount that I cannot estimate. Inclusion of some allowance for ascertainment bias would shift the factor toward favoring a source other than HSM. Levin interprets the geospatial Bayesian likelihood factor as favoring a spillover on the southeast side of the Yangtze.

No specific factor from such formal modeling should be taken too seriously, since the model details are somewhat arbitrary. For example, Levin does not include the existence of a superspreading event at HSM as a feature for which to calculate likelihoods. Since a spillover at HSM would be more likely to start an early superspreader event at HSM than would a spillover elsewhere, this omitted factor would tend to favor an HSM spillover. Nevertheless, since we have seen empirically that superspreader events in large cities are often centered at wet markets, that factor would not be huge. The spread of ascertained cases around Wuhan thus does not provide much evidence either for or against an original HSM spillover.

Summary

The cluster of cases at HSM shows that there was a major spreading event there. The unusually tight cluster of case home addresses near HSM for cases without any known link to HSM is just what would be expected for the proximity

ascertainment bias inferred from the documented ways in which cases were found (WHO-China 2021b; Bahry 2023; Demaneuf 2024), as confirmed by the head of China's CDC (Global Times 2020). It is highly improbable this tight cluster could arise from the simple unstructured model used by W2022 to reject the possibility that those cases descended from a source outside the market. Levin's (2025) modification of the simple model to be compatible with the tight clustering of the unlinked cases removes the statistical support for the claim that the case locations showed that HSM was the probable spillover site.

The rest of the data in W2022 point away from an HSM spillover. The HSM account runs into the following difficulties.

The cases:

1. appear to occur at the wrong time, i.e. too late compared to probable earlier cases indicated by many independent lines of evidence. W2022 in effect assumes without evidence that cases before the ascertained ones must have been at HSM.

2. have the wrong lineage, i.e. the less ancestral lineage B rather than the more ancestral versions spreading elsewhere. W2022 assumes that lineage A spilled over separately at HSM, although the companion P2022 analysis from many of its authors indicates that separate spillovers were unlikely, once its basic logic error is repaired (Weissman 2026).

3. are found in the wrong people, i.e. do not include wildlife handlers, in contrast to SARS and MERS, the other major recently emerged coronaviruses (Cyranoski and Abbott 2003; Alshukairi et al. 2018). W2022 in effect assumes that there must be missing wildlife vendor cases without presenting any of the serological evidence found for known zoonotic spillovers (Yu et al. 2003; Khudhair et al. 2019).

The wildlife sold in HSM in the relevant period includes:

4. no animals known to be infected (Liu et al. 2024).

5. no species in which the initial SARS-CoV-2 virus is known to sustain propagation (Luo et al. 2024).

6. no potential host species with mtDNA found to be positively associated with SARS-CoV-2 in swab samples, in contrast to known animal coronaviruses found in HSM swabs (Bloom 2023).

7. no sample with any detected sarbecoviruses, unlike what would be expected if wildlife sourced from rural areas known to harbor sarbecoviruses was sold there.

Another point, not directly addressed in W2022, is also needed to evaluate the probability that any Wuhan wet market would be the path for SC2 to get into humans. Although Wuhan has ~1% of China's population, it has a much lower fraction of the live-mammal trade, less than 10,000 animals per year (Xiao et al. 2021). In contrast, the province of Guangxi had 36,000,000 animals of a single species (bamboo rats), most destined to be sold before reaching 10 months of age (Lin 2020). Thus, the Wuhan location of the outbreak not only tends to tilt the odds for the origin toward a lab leak compared to some generic zoonosis (which would more likely occur among the other 99% of China's population) but shifts the odds especially far away from Wuhan wet markets, since those carry such a tiny fraction of the wildlife trade.

These points should suffice to invalidate the widely accepted idea that the W2022 evidence points toward HSM as the spillover site. To reiterate, that conclusion has no relevance to possible zoonotic scenarios that do not involve HSM. That conclusion is consistent with the most recent CIA report (National Intelligence Council 2023), prepared under the Biden administration and tending to support a lab-leak account. The report particularly downgraded the market account, concluding that evidence "both reinforced CIA's concerns about the potential for a laboratory associated incident and led CIA to focus on isolated animal encounters in secluded environments as the most plausible natural origin scenarios" (ibid.).

Reflections

Although it required rather detailed examination to see some of the problems with W2022, many readers could have noticed at least two reasons to take it as less than conclusive. Data outside the W2022 set that contradicted its model, e.g. multiple lines of evidence indicating cases preceding the HSM cases, were already widely available. The centerpiece of the W2022 results themselves, that the unlinked cases clustered even closer to the HSM than did the linked cases, also could have struck readers as statistically peculiar rather than as strong evidence for the HSM account. We see that with W2022, as with P2022, much of the scientific community accepted an important conclusion without sufficient scrutiny. It is past time for an unclassified re-examination of Covid origins without distractions from invalid papers.

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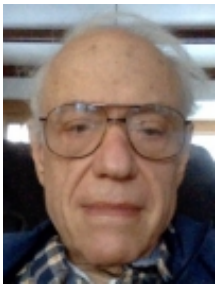
About the Author



Michael B. Weissman is a Professor Emeritus of Physics at the University of Illinois at Urbana-Champaign and a Fellow of the American Physical Society. He has worked mostly on condensed matter experiments, especially on low-frequency noise in disordered materials. He has worked in botany and chemistry departments. His undergrad degree is in math. Since retirement he has used statistical forensics to help catch a couple of fake pollsters and has written papers on numerous errors in causal reasoning in physics education research publications. He did time for Vietnam draft resistance and was an originator of the scientists' boycott of the Strategic Defense Initiative. He thinks that libertarian philosophy is factually detached from the realities of our species, implicitly cruel, and will lead to environmental catastrophe. He supports unions and is considering changing his opposition to the designated-hitter rule. That change may be the result of neurological sequelae to Covid. His email is mbw@illinois.edu.

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