

1 Circular arguments on the origin of SARS-CoV-2

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6 Two recent papers argue that SARS-CoV-2 emerged from wildlife sold in the Huanan Seafood
7 Market (HSM) with lineages A and B spilling over separately,^{1,2} against alternatives such as a
8 research lab accident.³ Yet they give circular arguments, by relying on data itself non-randomly
9 ascertained under local authorities' initial—understandable—assumption of a HSM spillover.

10 It remains plausible that HSM was not the origin of SARS-CoV-2, but only an early
11 super-spreader event for lineage B, “due to the high number of visitors every day.”⁴ Lineage A
12 shares its ‘T/C’ haplotype with outgroup cousins such as RaTG13, and so is plausibly ancestral,
13 whereas lineage B with its ‘C/T’ haplotype has dominated the pandemic including most of the
14 known early HSM-centered cases and HSM environmental samples, and emerging variants.⁵

15 Worobey et al. argue: “Early cases lived near to and centered on the Huanan market”;
16 and within HSM, “Positive environmental samples [were] linked ... to live mammal sales”;
17 both claims dismiss ascertainment bias.¹ However, after only *four* reported HSM-linked cases,
18 Wuhan CDC initiated “a retrospective search for pneumonia patients potentially linked to the
19 market,”⁶ including “epidemiology surveillance at several hospitals (close to Huanan market),
20 Huanan market and the neighborhood of Huanan market.”⁷ HSM sampling concentrated on
21 the south-western corner, where wildlife was sold, with most other stalls not sampled at all.⁴

22 On cases clustering around HSM, Worobey et al. claim: “We tested the robustness of
23 our results to the possibility of ascertainment bias.”¹ However, their test only considered false
24 positives near the market, testing robustness to this possibility by dropping the cases nearest
25 the market from the data. Yet the issue was not false positives, but false negatives: cases missed

26 for *not* being near HSM. Their test is like surveying New Yorkers; dropping the 68% of New
27 Yorkers nearest to Central Park; and concluding from the other 32% of New Yorkers that most
28 of humanity lives near to Central Park, a result robust to the possibility of ascertainment bias.

29 On linking HSM environmental samples to live mammal sales, Worobey et al. claim
30 that they “investigate the robustness of these findings to ... over-sampling of live mammal and
31 unknown meat stalls”; yet their Table S10 shows this only meant considering 2× sampling of
32 these stalls.¹ This potentially far underestimates sampling bias, given the initial assumption of
33 a HSM zoonosis. Without details of the sampling process—which Worobey et al. do not
34 have—there is no basis for assuming so little focus on wildlife stalls, given early assumptions.

35 Worobey et al. also claim: “seroprevalence in Wuhan was highest in the districts around
36 the market.”¹ This misleads about their source, which found *lower* seroprevalence in Jiangnan
37 district, the HSM district, than in three other downtown districts [note: data for April 2020].⁸

38 Against the possibility that HSM was a super-spreader, which would be lineage-specific,
39 Worobey et al. claim: “Both early lineages of SARS-CoV-2 were geographically associated with
40 the market.” Yet they base this on only three data points—two of them spurious. The single
41 lineage A sample found in HSM (out of 1,380 samples, 73 positive⁴), after both lineages were
42 already circulating in Wuhan, was likely introduced by a human. The man who stayed in a
43 hotel near HSM was likely included in their source,⁹ together with its nine HSM-linked cases,
44 *because* the hotel was near HSM: more ascertainment bias. Nothing can be concluded from
45 the remainder: one man with lineage A, living in downtown Wuhan, 2.31 km south of HSM.

46 Pekar et al. argue: “the inability to reconcile the molecular clock ... with a lineage A
47 ancestor without information from related sarbecoviruses (e.g., the recCA [recombinant
48 common ancestor]) requires us to question the assumption that both lineages A and B resulted
49 from a single introduction.”² Yet it requires no such thing. Pekar et al. themselves consider
50 the recCA-constrained root plausible, later using it to date the alleged two spillovers. We also

51 have a straightforward explanation for the molecular clock's rejection of a lineage A ancestor.
52 Molecular clock rooting by design assumes the root to be near the earliest-sampled genomes:
53 in this case, lineage B genomes sought and found because they were linked to or near HSM.¹⁰

54 This comment is not intended to be exhaustive.

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