

Peer Review

# Review of: "The Contentious Origins of SARS-CoV-2: A Comprehensive Review of Current Knowledge"

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I commend the author for their prompt and diligent efforts in refining the manuscript in response to the initial review. The second version was produced swiftly and effectively addresses several key issues I previously noted. I appreciate the dedication to enhancing the quality of the work. Below, I offer a few additional comments for the author's consideration should they wish to further strengthen the manuscript.

**1) Cite and use the best standards and guidelines for literature review:** A number of methods exist for producing literature reviews, such as Cooper et al. (2018; DOI: <https://doi.org/10.1186/s12874-018-0545-3>). There are also specific guidelines for reporting systematic reviews, such as the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA), which are also published (for example, see Page et al. 2020; DOI: <https://doi.org/10.1136/bmj.n71>). The current manuscript would certainly benefit from citing and following those standards and guidelines.

**2) Consider broadening the search:** Not necessarily would the best or most detailed studies on the origins of SARS-CoV-2 contain the sentence "origin of SARS-CoV-2" or include originally generated data. During the COVID-19 pandemic, it was common to have fast publication of new SARS-CoV-2 genomes that would only be analyzed in the context of other sequences in future publications. The author should review and clarify whether original analyses using publicly available data in novel ways were included in the review.

**3) Fix typos and other grammar mistakes:** There are some typos and grammar issues that are easy to spot and correct. For example, see the sentence [sic.] "Preprints were excluded., being studies published in English prioritized."

**4) Polish the language about phylogenetic support to avoid conceptual errors:** The author states that “relevant branches in the phylogenetic trees (linking SARS-CoV-2 to bat coronaviruses) typically exhibit high bootstrap support values (e.g., >70%).” However, bootstrap is not a direct measure of support (i.e., it does not directly measure or correlate to the amount of evidence supporting a branch) and it is also not a measure of confidence, statistical accuracy, or significance. For example, see Jacob Machado et al. (2021; DOI: <https://doi.org/10.1111/cla.12496>) and Grant & Kluge (2008; DOI: [10.1111/j.1096-0031.2008.00231.x](https://doi.org/10.1111/j.1096-0031.2008.00231.x)). Since this is not a phylogenetic paper, perhaps this could be fixed simply by editing the language and calling bootstrap a support metric or comparing it to posterior probabilities (which is a support metric, just like likelihood ratio tests or Goodman-Bremer values).

**5) Improve on the discussion about the need for an intermediary host:** The author is correct in stating that the absence of a confirmed intermediate host could be attributed to several factors, but one of those factors should be that there were no other non-bat hosts involved in the zoonosis of SARS-CoV-2, which could have been transmitted directly from bats to humans.

## **Declarations**

**Potential competing interests:** No potential competing interests to declare.