

Origin and cross-species transmission of bat coronaviruses in China

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This manuscript has been previously reviewed at another journal. This document only contains information relating to versions considered at Nature Communications.

This file contains all reviewer reports in order by version, followed by all author rebuttals in order by version.

Version 1:

Reviewer comments:

Reviewer #1

(Remarks to the Author)

Latinne and colleagues use bat coronavirus RdRP sequences to perform ancestral state reconstructions of both their geographic history and history of bat host switching. Since this is my fourth time reviewing I'll keep this review short.

I think the authors should make it very clear that some of their findings are substantially sensitive to data inclusion/exclusion. The differences in reconstruction between Fig 2B between the current version and previous are significant and I therefore feel like any statement that had to be modified between the previous version of the paper and the current version (e.g. precise rates, specific bat families) needs to be accompanied by a disclaimer along the lines of "but this can be sensitive to choice of data" along with a summary in the discussion of all the aspects that seem to depend strongly on data.

I feel like this is an easy and transparent way to inform the reader about the reproducibility of the findings and/or their statistical significance.

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Response to reviewer's comment:

We agree with the reviewer's suggestion and have added a section to the paragraph towards the end of the discussion that addresses limitations to the study, as follows:

Finally, it is important to note that some results were particularly sensitive to the data included in the analyses. The analyses reported here were conducted on a previous dataset that included 41 sequences from samples collected in Laos PDR, close to the border with China, a smaller number of sequences that were later found to be duplicates. Comparison of the results suggests that some findings (e.g. the relative involvement of specific bat families in the origin of Chinese β -CoVs) are sensitive to the data included. Further discovery of novel CoV sequences from bats in China, and across Southeast Asia, will likely provide a more robust understanding of origins and cross-species transmission for this important group of viruses.