

measures would prompt a secondary review to determine whether the research aims should be re-evaluated or new biosafety measures should be enacted.

EcoHealth failed to report this finding right away, as was required by the terms of the grant. EcoHealth is being notified that they have five days from today to submit to NIH any and all unpublished data from the experiments and work conducted under this award. Additional compliance efforts continue.

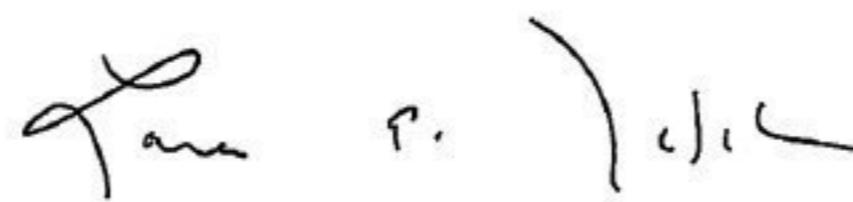
The second document is a genetic analysis demonstrating that the naturally occurring bat coronaviruses used in experiments under the NIH grant from 2014-2018 are decades removed from SARS-CoV-2 evolutionarily. The analysis compares the sequence relationships between:

- SARS-CoV-1, the cause of the SARS outbreak in 2003;
- SARS-CoV-2, the cause of COVID-19 pandemic;
- WIV-1, a naturally occurring bat coronavirus used in experiments funded by the NIH;
- RaTG13, one of the closest bat coronavirus relatives to SARS-CoV-2 collected by the Wuhan Institute of Virology; and
- BANAL-52, one of several bat coronaviruses recently identified from bats living in caves in Laos.

While it might appear that the similarity of RaTG13 and BANAL-52 bat coronaviruses to SARS-CoV-2 is close because it overlaps by 96-97%, experts agree that even these viruses are far too divergent to have been the progenitor of SARS-CoV-2. For comparison, today's human genome is 96% similar to our closest ancestor, the chimpanzee. Humans and chimpanzees are thought to have diverged approximately 6 million years ago.

The analysis attached confirms that the bat coronaviruses studied under the EcoHealth Alliance grant could not have been the source of SARS-CoV-2 and the COVID-19 pandemic.

If you or your staff have questions, NIH would be pleased to brief you on these documents.



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