

EXHIBIT 7

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National Institutes of Health
Bethesda, Maryland 20892

October 20, 2021

The Honorable James Comer
Ranking Member, Committee on Oversight and Reform
U.S. House of Representatives
Washington, D.C. 20515

Dear Representative Comer:

Thank you for your continued interest in the work of the National Institutes of Health (NIH). I am writing today to provide additional information and documents regarding NIH's grant to EcoHealth Alliance, Inc.

It is important to state at the outset that published genomic data demonstrate that the bat coronaviruses studied under the NIH grant to EcoHealth Alliance, Inc. and subaward to the Wuhan Institute of Virology (WIV) are not and could not have become SARS-CoV-2. Both the progress report and the analysis attached here again confirm that conclusion, as the sequences of the viruses are genetically very distant.

The fifth and final progress report for Grant R01AI110964, awarded to EcoHealth Alliance, Inc. is attached with redactions only for personally identifiable information. This progress report was submitted to NIH in August 2021 in response to NIH's compliance enforcement efforts. It includes data from a research project conducted during the 2018-19 grant period using bat coronavirus genome sequences already existing in nature.

The limited experiment described in the final progress report provided by EcoHealth Alliance was testing if spike proteins from naturally occurring bat coronaviruses circulating in China were capable of binding to the human ACE2 receptor in a mouse model. All other aspects of the mice, including the immune system, remained unchanged. In this limited experiment, laboratory mice infected with the SHC014 WIV1 bat coronavirus became sicker than those infected with the WIV1 bat coronavirus. As sometimes occurs in science, this was an unexpected result of the research, as opposed to something that the researchers set out to do. Regardless, the viruses being studied under this grant were genetically very distant from SARS-CoV-2.

The research plan was reviewed by NIH in advance of funding, and NIH determined that it did not fit the definition of research involving enhanced pathogens of pandemic potential (ePPP) because these bat coronaviruses had not been shown to infect humans. As such, the research was not subject to departmental review under the HHS P3CO Framework. However, out of an abundance of caution and as an additional layer of oversight, language was included in the terms and conditions of the grant award to EcoHealth that outlined criteria for a secondary review, such as a requirement that the grantee report immediately a one log increase in growth. These

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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.

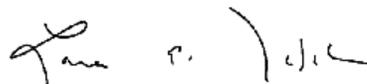
The second document is a genetic analysis demonstrating that the naturally occurring bat coronaviruses used in experiments under the NIH grant from 2014-2018 are decades removed from SARS-CoV-2 evolutionarily. The analysis compares the sequence relationships between:

- 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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