

**From:** Peter Daszak <daszak@ecohealthalliance.org>  
**To:** Hongying Li <li@ecohealthalliance.org>, Tammie O'Rourke <torourke@metabiota.com>  
**Cc:** "Goldstein, Tracey" <tgoldstein@ucdavis.edu>, Aleksei Chmura <chmura@ecohealthalliance.org>, Christine Kreuder Johnson <ckjohnson@ucdavis.edu>, "Jonna Mazet (jkmazet@ucdavis.edu)" <jkmazet@ucdavis.edu>, "William B. Karesh" <karesh@ecohealthalliance.org>  
**Subject:** RE: China Genbank Sequences  
**Sent:** Tue, 28 Apr 2020 15:50:09 +0000

Cc'ing Jonna & Billy in.

Cheers,

Peter

**Peter Daszak**  
*President*

EcoHealth Alliance  
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Website: [www.ecohealthalliance.org](http://www.ecohealthalliance.org)  
Twitter: [@PeterDaszak](https://twitter.com/PeterDaszak)

*EcoHealth Alliance develops science-based solutions to prevent pandemics and promote conservation*

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**From:** Peter Daszak  
**Sent:** Tuesday, April 28, 2020 11:30 AM  
**To:** 'Hongying Li' <li@ecohealthalliance.org>; Tammie O'Rourke <torourke@metabiota.com>  
**Cc:** Goldstein, Tracey <tgoldstein@ucdavis.edu>; Aleksei Chmura <chmura@ecohealthalliance.org>; Christine Kreuder Johnson <ckjohnson@ucdavis.edu>  
**Subject:** RE: China Genbank Sequences  
**Importance:** High

All – It's extremely important that we don't have these sequences as part of our PREDICT release to Genbank at this point.

As you may have heard, these were part of a grant just terminated by NIH.

<https://www.politico.com/news/2020/04/27/trump-cuts-research-bat-human-virus-china-213076>

Having them as part of PREDICT will bring very unwelcome attention to UC Davis, PREDICT and USAID.

Cheers,

Peter

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**From:** Hongying Li <[li@ecohealthalliance.org](mailto:li@ecohealthalliance.org)>  
**Sent:** Tuesday, April 28, 2020 9:22 AM  
**To:** Tammie O'Rourke <[torourke@metabiota.com](mailto:torourke@metabiota.com)>  
**Cc:** Goldstein, Tracey <[tgoldstein@ucdavis.edu](mailto:tgoldstein@ucdavis.edu)>; Peter Daszak <[daszak@ecohealthalliance.org](mailto:daszak@ecohealthalliance.org)>; Aleksei Chmura <[chmura@ecohealthalliance.org](mailto:chmura@ecohealthalliance.org)>; Christine Kreuder Johnson <[ckjohnson@ucdavis.edu](mailto:ckjohnson@ucdavis.edu)>  
**Subject:** Re: China Genbank Sequences

Dear Tammie,

I have talked to local collaborators in China and EHA scientists who have been working on the analysis of these data. We would like to hold off the uploading because 1) many of the sequences have been analyzed, and some are ready for publication for which the sequences have been submitted to GenBank scheduled to be released, so we need time to double-check the data to avoid the duplicated submission; and 2) due to the COVID-19, any relevant data publication needs to be reviewed and approved by the institution in China, we have started the process, but the timeline is unpredictable at this moment

Please let us know if you have any questions. Thank you very much.

Best Regards,  
Hongying

**Hongying Li, MPH 李泓莹**  
Research Scientist

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On Fri, Apr 24, 2020 at 2:50 PM Hongying Li <[li@ecohealthalliance.org](mailto:li@ecohealthalliance.org)> wrote:  
Dear Tammie,

Thank you for the message, it's so efficient that we are planning to upload sequences for PREDICT 2 now!

I need to check with Peter and local collaborators before I can confirm with you. I also cc'ing Peter in this email in case he has the time to review this and comment.

UCDUSR0001052

Thank you, and hope all is well.  
Hongying

**Hongying Li, MPH 李泓莹**

Research Scientist

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On Fri, Apr 24, 2020 at 2:05 PM Tammie O'Rourke <[torourke@metabiota.com](mailto:torourke@metabiota.com)> wrote:  
Hi Hongying,

The attached PREDICT 2 virus sequences detected in China have been submitted to the GenBank sequence database. Each sequence has been assigned a GenBank accession number (please see attached excel file). These sequences are scheduled to be released in Genbank on April 30<sup>th</sup>, 2020. If sequences were not submitted, notes explaining why not are included in the file and are highlighted in yellow.

Please include the assigned GenBank accession number for all sequences you include in a publication. All sequences were edited prior to submission to GenBank. These clean sequences are attached and have been updated in EIDITH. Please use these edited and cleaned sequences for any analysis for publication.

Thank you, IM Team

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Tammie O'Rourke  
Metabiota  
Senior Information Management Developer  
Emerging Pandemic Threats - PREDICT Program  
tel **REDACTED**