



Sainath Suryanarayanan <sainath@usrtk.org>

**PLOS Pathogens: Reply to your inquiries regarding
doi: 10.1371/journal.ppat.1008421**

PLOS Pathogens <plospathogens@plos.org>

Mon, Nov 2, 2020 at 4:22 PM

To: "sainath@usrtk.org" <sainath@usrtk.org>

Dear Sainath,

I am writing in reply to the emails you have sent to PLOS Pathogens and the PLOS Pathogens Editors-in-Chief over the past few days, regarding the article, "Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?" (doi: 10.1371/journal.ppat.1008421)

Please be assured that we take the concerns about this article seriously and are committed to the integrity of work published by PLOS. I am a Senior Editor on PLOS Publication Ethics team, and we are in the midst of following up on questions that have been raised about this article, including the issues that you mentioned in your emails. PLOS abides by the guidance of the Committee on Publication Ethics (COPE) in following up on issues raised to our journals. Our investigation and follow-up discussions for this case are ongoing, but we will update you as to its resolution when we conclude this work.

In the future, if you have questions or additional information that is relevant to this case/investigation, please contact me directly by replying to this email (plospathogens@plos.org); please cc rhoch@plos.org and reference Case 06647502 in the Subject line of any messages about this case. Please note, however, that our investigation and information received in follow-up discussions are held as confidential and we will not be able to provide any substantive updates until we conclude our work on this case.

Thank you for your interest in this article and for relaying to us your concerns and the information you have received in regard to this matter.

Kind regards,
Renee

Renee Hoch, Ph.D.
Senior Editor, Team Manager Publication Ethics

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Case Number: 06647502
ref:_00DU0lfis._5004P1ABOET:ref

----- Original Message -----

From: Sainath Suryanarayanan [sainath@usrtk.org]

Sent: 11/2/2020 2:08 AM

To: khalidar@nd.edu; plospathogens@plos.org; jheber@plos.org; michael.malim@kcl.ac.uk

Cc: stanley-perlman@uiowa.edu; gary@usrtk.org

Subject: PLoS Pathogens investigation of Liu et al. (2020)

Dear PLoS Pathogens Editors-in-Chief:

I work with the non-profit public interest group [U.S. Right to Know](https://www.usrighttoknow.org/), and am following up on the email (attached) I sent on October 29, 2020 regarding significant concerns with Liu P, Jiang J-Z, Wan X-F, Hua Y, Li L, Zhou J, et al (2020) "Are

pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?" PLoS Pathogens 16(5): e1008421. I have since been in further correspondence with senior author Dr. Jinping Chen (attached), who shared with me Liu et al's RT-PCR primer data (.xlsx file) and RT-PCR product sequence data (.fas file). I indicated to Dr. Chen that these are not the raw data, and raw chromatograms are what other scientists need in order to independently assemble the genome. Dr. Chen insists that the .fas data he sent are the unchanged amplicon sequencing and raw chromatogram data. Obviously, we cannot rely on sequence-only files to determine whether particular base calls are accurate or resolve situations where multiple reads disagree with each other. It could be that someone other than Dr. Jinping Chen is in possession of the raw chromatogram files or the amplicon sequences used to assemble the full genome of Pangolin coronavirus. **PLOS Pathogens should make Liu et al. publicly release their amplicon data and the missing pangolin sample (F9) data immediately.**

I cannot overemphasize the importance of urgently investigating Liu et al. **Please know that U.S. Right to Know would like to fairly represent the actions of PLoS Pathogens in any information we publish regarding this case.** I would appreciate your acknowledgement of my emails and an explanation of what exactly PLoS Pathogens is doing about investigating Liu et al.

Thanks for your consideration.

Sincerely,
Sainath
Sainath Suryanarayanan, PhD
Staff Scientist, U.S. Right to Know
usrtk.org/about/

CC:
Stanley Perlman, Editor of Liu et al. (2020)
Gary Ruskin, Executive Director, U.S. Right to Know

From: Sainath Suryanarayanan <sainath@usrtk.org<mailto:sainath@usrtk.org>>
Date: Thursday, October 29, 2020 at 2:27 AM
To: "khaldar@plos.org<mailto:khaldar@plos.org>" <khaldar@plos.org<mailto:khaldar@plos.org>>, "mmalim@plos.org<mailto:mmalim@plos.org>" <mmalim@plos.org<mailto:mmalim@plos.org>>
Cc: "Perlman, Stanley" <stanley-perlman@uiowa.edu<mailto:stanley-perlman@uiowa.edu>>, PLOS Pathogens <plospathogens@plos.org<mailto:plospathogens@plos.org>>, Joerg Heber <jheber@plos.org<mailto:jheber@plos.org>>
Subject: Information to advance an urgent investigation of Liu et al. (2020) in PLoS Pathogens

October 29, 2020

Kasturi Haldar and Michael Malim
Editors in Chief
PLoS Pathogens

CC: Stanley Perlman, PLoS Pathogens Editor of Liu et al. (2020)
Joerg Heber, Editorial Director, PLOS

Re: Liu P, Jiang J-Z, Wan X-F, Hua Y, Li L, Zhou J, et al (2020) "Are pangolins the intermediate host of the 2019 novel coronavirus (SARS-CoV-2)?" PLoS Pathogens 16(5): e1008421.

Dear Drs. Haldar and Malim:

I emailed Liu et al.'s senior author Dr. Jinping Chen on October 28, 2020 with questions and concerns about the veracity of their core dataset, and Dr. Chen responded immediately with information (attached) that I believe PLoS Pathogens should be aware of, and act upon, as soon as possible.

Most noteworthy among the comments made by Dr. Chen is his admission regarding a crucial coronavirus sample supposedly collected from a pangolin individual that was part of a batch of smuggled pangolins intercepted in July 2019. The sequence read archive (SRA) data for the July 2019 sample, which Dr. Chen identifies as F9, remains missing from NCBI and unverifiable despite it being used by Liu et al. for assembling their pangolin coronavirus genome sequence that is published in PLoS Pathogens. Upon being questioned regarding this missing sample, Dr. Chen stated: "individual (F9) from different batch was also positive, the raw data can be seen in NCBI SRA SUB 7661929, which will be released soon for we have another MS (under review) and RT-PCR was amplified for all gaps in our PLOS pathogens paper" (my emphases). Not only is Liu et al. missing data that was used to assemble a coronavirus genome sequence, but this missing data is being used to submit another manuscript in a different journal. PLoS Pathogens should tell Liu et al. to (1) immediately release the SRA of F9, properly attributing it to the PLoS Pathogens paper, (2) correct the PLoS Pathogens

paper to link to the F9 SRA once it is released, (3) immediately notify the journal where their new MS is under review to avoid data duplication and misattribution.

Dr. Chen denied that Liu et al. have had any relationship with Xiao et al.'s (2020) Nature study titled, "Isolation of SARS-CoV-2-related coronavirus from Malayan pangolins." Here, it is worth noting Liu et al.'s full pangolin coronavirus genome is 99.95% identical to the full pangolin CoV genome published by Xiao et al. However, both Liu et al. and Xiao et al. have yet to publish the amplicon data they used to assemble the pangolin coronavirus genome sequence. It should also be noted that Liu et al. and Xiao et al. shared two authors, and that Xiao et al. "renamed pangolin samples first published by Liu et al. [2019] Viruses without citing their study as the original article that described these samples, and used the metagenomic data from these samples in their analysis" (Chan and Zhan, bioRxiv<<https://www.biorxiv.org/content/10.1101/2020.07.07.184374v2.full.pdf>>). Significantly, contrary to the contents of Dr. Chen's emails, we have separately obtained evidence that Xiao et al. were in communication with Liu et al. about these metagenomic datasets shortly before the publication of each manuscript at Nature and PLoS Pathogens in May. PLoS Pathogens should ask Liu et al. to produce their amplicon sequencing data for independent verification right away. This is essential to understanding how they could have produced a whole genome that is 99.95% identical to Xiao et al. (only ~15 nucleotides difference).

Beyond this, given the significant connections between Liu et al. and Xiao et al., I urge you to share Dr. Chen's emails (attached) and any other relevant information about your investigation of Liu et al. with the appropriate Nature editor responsible for scrutinizing research integrity issues in Xiao et al.'s paper. Please do not hesitate to email me if you have any questions or clarifications. Thanks so much for your consideration of the issues I have raised.

Sincerely,
Sainath

Sainath Suryanarayanan, PhD
Staff Scientist, U.S. Right to Know
usrtk.org/about/<<http://usrtk.org/about/>>

Attachments (PDF):

1. Email reply #1 by Dr. Jinping Chen
2. Email reply #2 by Dr. Jinping Chen
3. Email reply #3 by Dr. Jinping Chen