# Re: Fw: JVI00116-18 Decision Letter

From: Fang Li <lifang@umn.edu>
To: 石正丽 <zlshi@wh.iov.cn>
Cc: Chuming Luo <chumingluo1989@gmail.com>
Sent: February 21, 2018 8:10:52 PM CST
Received: February 21, 2018 8:10:52 PM CST

Dear Zhengli,

Yes, we have the antibodies and Chuming will start testing them.

Cheers,
Fang

On Wed, Feb 21, 2018 at 7:24 PM, 石正丽 <zlshi@wh.iov.cn> wrote:

> Dear Fang, Chuming,
>
> Please see the following email from JVI editor. It is a very positive decision. The major comment is on the pseudovirus and we need to conduct additional experiments. I suppose your have MERS-CoV antibody and can do it easily.
>
> @Chuming, please address the comments appropriately, thanks.
>
> Best regards,
> Zhengli,
>
> > -----原始邮件-----
> > **发件人:**asm@msubmit.net
> > **发送时间:**2018-02-22 00:18:42 (星期四)
> > **收件人:** zlshi@wh.iov.cn
> > **抄送:**
> > **主题:** JVI00116-18 Decision Letter
> >
> > Prof. Zheng-Li Shi
> > Wuhan Institute of Virology, Chinese Academy of Sciences
> > 44 Xiao Hong Shan
> > Wuhan, Hubei 430071
> > China
> >
> > Re: JVI00116-18 (Discovery of novel bat coronaviruses in south China that use the same receptor as MERS coronavirus)
> >
> > Dear Prof. Zheng-Li Shi:
> >
> > Below you will find the comments of the reviewers. Both reviewers viewed your findings as significant to the field and worthy of publication in JVI. Yet they did have several comments aimed at improving your manuscript. Notably, reviewer #1 had questions about whether pseudoviruses adequately reflect authentic virus entry processes, and suggested that the limitations of the pseudovirus approaches be further discussed. Additionally, reviewer #1 suggested that some additional experiments involving anti-spike neutralization of pseudovirus transduction be completed, so that statements might be made about the antigenic similarities (or differences) amongst the bat MERS-CoV spikes. I agree that these experiments might generate valuable results that improve the manuscript. As it is likely that these

recommended experiments, as well as the suggested modifications to the text and figures, can be completed with the next 60 days, my recommendation is for modification of your manuscript.

To submit your modified manuscript, log onto the eJP submission site at https://jvi.msubmit.net/cgi-bin/main.plex. If you cannot remember your password, click the "Can't remember your password?" link and follow the instructions on the screen. Go to Author Tasks and click the appropriate manuscript title to begin the resubmission process. The information that you entered when you first submitted the paper will be displayed. Please update the information as necessary. Provide point-by-point responses to the issues raised by the reviewers in a file named "Response to Reviewers," not in your cover letter. Specify with page and line numbers where in the revised manuscript the revisions have been made. If you perform additional experiments in response to the reviewers' comments, we expect that the results of those experiments will be incorporated into the body of the manuscript and NOT submitted as supplemental data, except as allowed by the Instructions to Authors.

Please return the manuscript within 60 days; if you cannot complete the modification within this time period, please contact me. If you do not wish to modify the manuscript and prefer to submit it to another journal, please notify me of your decision immediately so that the manuscript may be formally withdrawn from consideration by Journal of Virology.

To avoid unnecessary delay in publication should your modified manuscript be accepted, it is important that you upload all of your native files (i.e., not a single PDF) and that all elements meet the technical requirements for production. I strongly recommend that you check your digital images using the Rapid Inspector tool at http://rapidinspector.cadmus.com/RapidInspector/zmw/

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**If you are interested in providing an illustration, related to this manuscript, for the cover of JVI, contact Dr. Stacey Schultz-Cherry at Stacey.Schultz-Cherry@StJude.org for details.**

Thank you for submitting your paper to JVI.

Sincerely,
Tom Gallagher
Editor, Journal of Virology

Reviewer comments:

Reviewer #1 (Comments for the Author):

General Comments:
The manuscript describes results from metagenomic analysis of 2C coronaviruses currently in bat populations across multiple sites in south China. The work identified 90 strains and went on to further characterize two strains as MERS-related viruses doing comparisons based primarily on sequence. Across genomic structure and sequence similarities across viral proteins, the authors characterize these 2 viruses as key relatives of the epidemic MERS-CoV strains and suggest similar progenitors. Coupled with recombination analysis, the authors convey binding and pseudotyping studies that indicate the ablility of these virus spike to use human and bat DPP4 receptor, making a crucial link to the emergent wild-type MERS-CoV.
Overall, the results indicate a wealth of MERS-related viruses that exist in bat populations. The sequences derived across a range of bat species in multiple locations suggest that viruses similar to MERS-CoV exist around the world and may harbor considerable diversity. Importantly, use of biologically relevant binding and pseudotyping assays suggest that DPP4 as a key receptor beyond just MERS-CoV infection. The data also adds to prior evidence that bats are the reservoir for MERS-like viruses. However, despite the wealth of sequence data and adequate biochemical analysis, the results provide only an incremental advance relative to other manuscripts. The absence of a data from coronavirus infection utilizing this spike diminishes the result. Similarly, exploration of cross reactivity and neutralization with MERS-CoV antibodies would be useful and informative. Despite that, the results provide significant information for further studies in this area and can seed future studies exploring both structure as well as infection with live virus.
Comments
1. The use of MERSr-CoV as the abbreviation for MERS-related CoV is not appropriate. In examining the text, distinguishing between MERS-CoV and MERSr-CoV is too difficult. The authors should use a different desigations (i.e. MERSlike, MERSrelated, etc). Otherwise, in reading and analysis, the text is confusing and difficult to analyze.
2. While the use of pseudotyping experiments is relevant, it is not equivalent to use of live coronavirus infection. However, these studies are well outside the scope of this manuscript. As such, the limitations of the pseudotyping studies should be addressed in the discussion.
3. The authors should consider examination of cross reactivity and neutralization with MERS-CoV antibodies using their pseudotyping systems. While not always equivalent to viral infection, the information would provide insight into relative similarities in antigenicity of these MERS-related

> Statistics are needed on fig 6. While the result is clear, the statistical comparison is necessary.

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