

From: [Weiss, Susan](#)
To: [Liu, Shan-Lu](#)
Subject: Re: [External] FW: Your article proofs for review (ID# TEMI 1733440)
Date: Friday, February 21, 2020 10:13:18 AM

Henry and I have been speculating- how can that site have appeared at S1/S2 border- I hate to think to was engineered- among the MHV strains, the cleavage site does not increase pathogenicity while it does effect entry route (surface vs endosome) . so for me the only significance of this furin site is as a marker for where the virus came from- frightening to think it may have been engineered

From: "Liu, Shan-Lu" <liu.6244@osu.edu>
Date: Friday, February 21, 2020 at 9:50 AM
To: "Weiss, Susan" <weissr@pennmedicine.upenn.edu>
Cc: Lishan Su <lishan_su@med.unc.edu>
Subject: Re: [External] FW: Your article proofs for review (ID# TEMI 1733440)

Susan, I completely agree with you, but rumor says that furin site may be engineered. Importantly, the virus RNA sequence around the furin site (288 nt), before and after, has 6.6 % differences, but with no amino acid changes at all.

Shan-Lu Liu sent from iPhone

On Feb 21, 2020, at 5:42 AM, Weiss, Susan <weissr@pennmedicine.upenn.edu> wrote:

Shan-Lu

Maybe too late to add to the paper, but I think the fact that the RaTG13 spike does not include a furin sequence makes it unlikely that it is the precursor to SARS-CoV-2.

I find it hard to imagine how that sequence got into the spike of a lineage b betacoronavirus- not seen in SARS or any of the bat viruses.

The BioRx preprint on Pangolin sequence is very weak- says the RBD from the pangolin virus is closer to SARS-CoV-2 than RaTG13 is. But again pangolin sequence lacks the furin site.

The furin site to me is a good marker for ancestral virus

Any thoughts on this?