

Twitter Thread by Billy Bostickson ■■■&■ ■



Billy Bostickson ■■■&■ ■

@BillyBostickson



1. Some useful, albeit not fully developed, critiques of:

"The Origins of SARS-CoV-2: A Critical Review"

<https://t.co/C9TyRyqHUr>

have just been published here:

<https://t.co/qCmzGCzRxn>

by members of DRASTIC & others

@angoffinet @BahulikarRahul @MonaRahalkar @gdemaneuf

2. A refreshing contrast to the so-called "expert reactions" found here, including from one of the authors of the review (Prof David Robertson)!

"expert reaction to a preprint reviewing the evidence on the origins of SARS-CoV-2"

<https://t.co/6kG6rstweP>



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Please note this is a comment from one of the authors, NOT a third party comment, but sending out in case useful as there wasn't a press release: **Prof David L Robertson, MRC Investigator, Head of CVR Bioinformatics MRC-University of Glasgow Centre for Virus Research (CVR), said:**

“In a review of the evidence as a group of experts in virus evolution and molecular virology we concluded the most parsimonious explanation for the origin of SARS-CoV-2 is a zoonotic spillover event. The contact tracing of early cases in Wuhan, obtained from the WHO report earlier this year, exhibits striking similarities to the early spread of the first SARS-virus, where humans infected early in the epidemic lived near or worked in animal markets. While the intermediate animal species has not been found, there is clear evidence of susceptible animals being present in the Wuhan market throughout 2019, and related viruses have been found circulating in horseshoe bats, again very similar to the first SARS-virus. Altogether the evidence points to a zoonotic event and not a leak from a laboratory in Wuhan. The “lab leak” scenario alternates between it was made in a lab and it was an accidental release of a natural virus, neither of which there’s any evidence for. It’s of critical importance to understand the origin of SARS-CoV-2 so we can assess the risk of future spillover events.”

3. Peter Gutierrez points out in his response that 4 of the authors of “The Origins of SARS-CoV-2: A Critical Review”, also wrote “Proximal Origin of SARS-COV-2”.

His critique focuses on:

1. RaTG13
2. Enhanced adaptation to the human host

<https://t.co/eW8b2iK5xe>

"This demonstrates beyond reasonable doubt that RaTG13 is not the progenitor of SARS-CoV-2, with or without laboratory manipulation or experimental mutagenesis."

This conclusion is spurious at best. They base their conclusion on their analysis of the 1AB gene, disregarding the rest of the genome. But, RaTG13 1AB gene is 96% identity similar to Covid-19 1AB gene, according to Zhou below. Slightly less than RmYN02, RpYN06 and PrC31's, but pretty close. More importantly, RaTG13 S gene is 96% identity amino acid similar with Covid-19. RmYN02, RpYN06 and PrC31 S genes are only 76% and 63% similar to Covid-19, and their RBDs even less. Making them less likely Covid-19 immediate progenitor. The better science is represented by the articles,

"A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein", Hong Zhou, Xing Chen, and others

"Evidence for SARS-CoV-2 related coronaviruses circulating in bats and pangolins in Southeast Asia", by Supaporn Wacharapluesadee, Chee Wah Tan, and others

"Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses", by Hong Zhou, Jingkai Ji, and others

4. As to be expected, Sydney University and its iconic virologist, Eddie Holmes, who is "not available for interview", are crowing over this biased review

<https://t.co/xrjpN1NxpO>

— **Focus on lab-leak distracting from work to prevent next pandemic**



Professor Edward Holmes.

This review contains elementary errors as exposed here:

1. <https://t.co/YJ50huifly>

one of the authors (Stuart Neil) then claimed

"Didn't N501Y come up in ACE2 TG mice too?

<https://t.co/HscNSEKdrZ>



All your natural origin friends in one place ;)

Origins of SARS-CoV-2: A Critical Review <https://t.co/j4A4rtmi8S>

via @Topo_Ligio

Fallacy of the "straw mouse", denying evolution in wild type mice, when the claim is actually that it may have "evolved" in hACE2 mice, NOT wild mice. pic.twitter.com/7LCnSAhw6g

— Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) July 7, 2021

Professor Neil failed to respond

<https://t.co/ldzuAMDIF9>

Human lung xenograft & adenovirus hACE2 mice need to be immunosuppressed/deficient e.g. SCID or Rag1-2 KO2 mice, so as not to reject the allograft cells & transgenic ACE2.

So, why do you think N501Y would emerge in TG hACE2 mice without a functional immune system or mouse ACE2?

— Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) July 8, 2021

You will have to dig into the answers here

<https://t.co/OaLzUfIPuA>

A thread with papers to educate Stuart here:

<https://t.co/BFVxXIVKj4>



Stuart Neil @stuartjdneil · Jul 8

So maybe you can tell me why you get adaptive mutations in mouse passage outside spike? Those should happen in Tg mice too. Where are they?



3



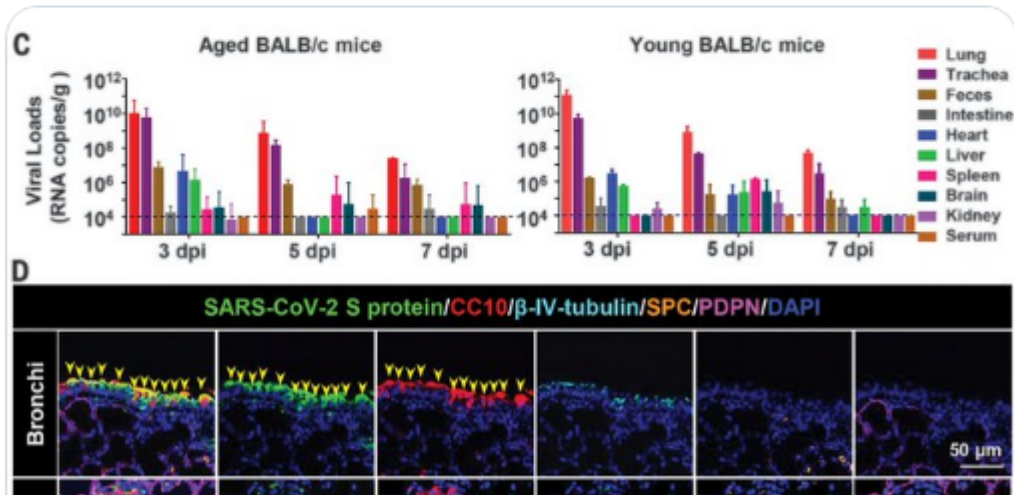
1



Billy Bostickson @BillyBostickson · Jul 9

science.sciencemag.org/content/369/65...

I suspect that the reason for the emergence of N501Y in this specific experiment is that the balb/c mice used in the experiment were non hACE2 mice and immunocompetent mice.



Didnlu2019t N501Y come up in ACE2 TG mice too? <https://t.co/cRR1qITUtB>

— Stuart Neil (@stuartjdneil) July 7, 2021

Which he didn't take kindly to

<https://t.co/k93d6gVR8s>

I guess it was his way of admitting he was wrong about N501Y?



Stuart Neil @stuartjdneil · Jul 8

...

Are you just going to quote the entire history of TG mice for CoV research?

We know they had Th mice for recombinant CoV infection.

But it's all irrelevant

They needed to have the right virus. And thus far is there is zero evidence that they did.



3



1



4



Billy Bostickson 🇬🇧👁️&👁️🆓 @BillyBostickson · Jul 8

...

Just trying to jog your memory, sorry for speaking out of turn, Prof.
"I'd heard it did. Can't remember where now"



1



Stuart Neil @stuartjdneil · Jul 8

...

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1



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— Stuart Neil (@stuartjdneil) July 7, 2021

Again Prof Neil, one of the authors of the review continues to embarrass himself. I am starting to think that the flawed N501 claim was actually written by him.

<https://t.co/Syn3CNd5ne>



So maybe you can tell me why you get adaptive mutations in mouse passage outside spike? Those should happen in Tg mice too. Where are they?

— Stuart Neil (@stuartjdneil) July 7, 2021

Wrong again, "Prof"

<https://t.co/CH4jY6HOfe>



Billy Bostickson

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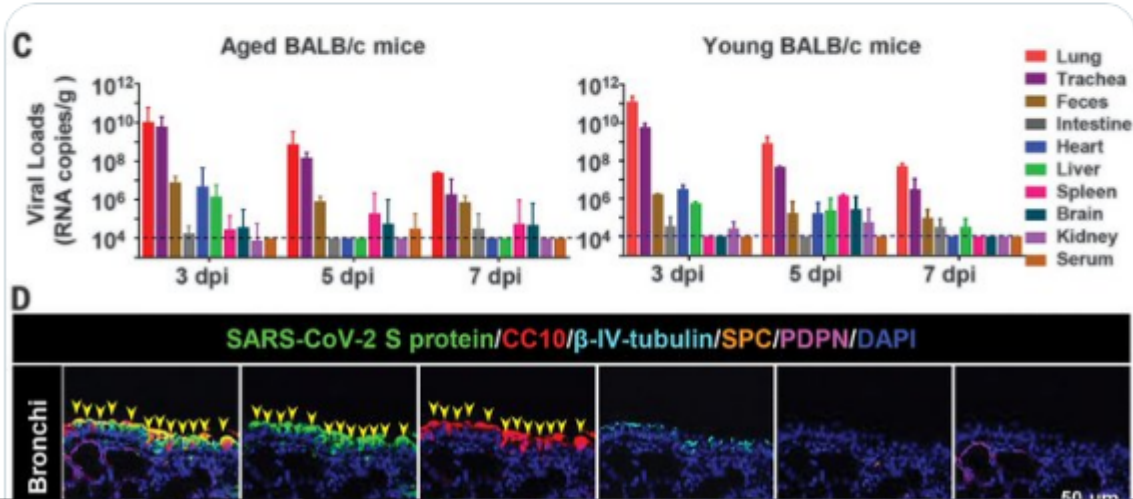


...

Replying to @stuartjneil and @babarlephant

science.sciencemag.org/content/369/65...

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<https://t.co/I90OOCJg7o>

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— Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) July 8, 2021

He just can't admit his error, so I have to remind him

<https://t.co/ZIPRFOHDGE>



Stuart Neil @stuartjneil · Jul 10

...

Yes. We know this. Immune escape potentially one explanation. Selection for better human ACE2 use is another. Not mutually exclusive either.

Are you trying to make a point Billy because it appears pretty obscure if you are?

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Billy Bostickson 🇬🇧 👁️ & 👁️ 🆓
@BillyBostickson

...

Replying to @stuartjneil

It's a simple point, that you are wrong about N501Y

"Taken together, these patterns of detectable selection suggest that the adaptive value of signature 501Y lineage RBD mutations may have only manifested after a selective shift that occurred shortly before November 2020"

It's a simple point, that you are wrong about N501Y

"Taken together, these patterns of detectable selection suggest that the adaptive value of signature 501Y lineage RBD mutations may have only manifested after a selective shift that occurred shortly before November 2020"

— Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) July 10, 2021

A further elementary error in the review paper

The Straw Lab Fallacy

<https://t.co/kS9wCBkgvr>

They haven't even done the basic research.

They conjured up a straw lab, the bsl4 lab

Most bat coronavirus work was done at the older complex in xiaohongshan. The labs (plural) and their locations are listed here along with documented biosafety issues: <https://t.co/ewo9oZUuqU>

— Billy Bostickson \U0001f3f4\U0001f441&\U0001f441 \U0001f193 (@BillyBostickson) July 11, 2021

To be continued....

Another critique (July 8th) - 30 Tweets

A long thread by [@Rossana38510044](#) debunking the claims in "Origins of SARS-CoV-2: A Pathetic Review"

<https://t.co/Un0h4cm3vi>

Saved:

<https://t.co/8eDdbKWdqf>

Archived:

<https://t.co/8bfaU4nWXo>

That was a surprise. So many well-known supporters of SARS2\u2019s natural origin join forces to publish an opinion piece in\u2026Zenodo \U0001f602<https://t.co/led9Zclop>

— Rossana Segreto (@Rossana38510044) [July 8, 2021](#)

An excellent and thorough critique by [@aychan](#) here (12th July)

A response to "The Origins of SARS-CoV-2: A Critical Review"

<https://t.co/QrqL9DIBGh>

Archived:

<https://t.co/UA29u7D3v0>