Twitter Thread by Rossana Segreto

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1. The same “gang” of the Proximal Origin paper
https://t.co/Xmp20I58AQ
in action again (only Lipkin is missing, who knows why) to push once more faulty arguments in support of SARS2’s natural

2. The newly identified Cambodian, Thai and Japan sequences are presented as evidence that some odd features of the SARS2’s genome are natural because present in other natural viruses, as RaTG13 and pangolin CoV were used in The Proximal paper.

3. First the FCS. @ydeigin and I wrote a preprint where we show that the claimed partial FCS insertion in RmYN02 is highly doubtful and the same applies to the new bat CoV sequences
https://t.co/0Goapx6cXj
https://t.co/5Z4Ndca98t

4. They present again only an amino acid biased alignment as in the Zhou paper
https://t.co/i9OZchD4LT
“adjusted by visual inspection” to push their false conclusion that all these CoVs have a partial FCS insertion at the S1/S2 junction and the FCS of SARS2 is therefore natural

5. SARS2 remains the only Sarbecovirus with a functioning FCS, as we describe here:
https://t.co/viqvfzv1Xa
and that can be easily inserted with the Seamless technology.

6. The special RBD of SARS2 was claimed to be natural in The Proximal paper because present in 2 pangolin CoV samples. Now we know we can’t trust those samples
https://t.co/U2qvG3tXBG

7. The new Cambodian CoV shows now a similar RBD claimed to possibly be able to bind to human ACE2, but not yet verified. It should be also demonstrated that this RBD is not the product of cell passage, as supposed to be for pangolin CoV.
https://t.co/cNEwlgtnBb

8. Important to notice that the presence of the QTQTNS motif might be the result of cell passage in presence of TMPRSS2 and Cathepsin
https://t.co/1D7iVZc8Md

> 9/ Moreover, the QTQTN motive proximal to the FCS is beneficial for virus entry in presence of Cathepsin, which is naturally produced by kidney cells. https://t.co/xPOK6w931P
>
> — Rossana Segreto (@Rossana38510044) October 3, 2020

9. This motif is often deleted together with the FCS or alone in cell cultures without selection pressure:
https://t.co/GFrrxzCvbq

10. “Notably, the QTQTNS motif near the S1/S2 cleavage site is present in Cambodian bat coronavirus, RaTG13, GD Pangolin coronavirus and SARS-CoV-2. None of these sequences were determined until after the COVID-19 pandemic began.” Exactly, this is very weird.

11. I find alarming that “experts” are retweeting false information from another “expert” to support their conclusions, for example that the QTQTNS motif arose multiple times as proof that SARS2 is natural:
https://t.co/pBF4ZDqNat

> You know virology is broken when one top virologist approvingly retweets another top virologist's complete nonsense.
>
> Look at the QTQTNS fragment's underlying nucleotides - they are identical. No way this has "arisen independently in multiple bat sarbecoviruses". EvoBio 101 FAIL! pic.twitter.com/SNxesiwYPg
>
> — Yuri Deigin (@ydeigin) February 23, 2021

12. And even if the Cambodian and the pangolin CoV are natural, what do they show? RaTG13 is still much closer to SARS2. But the cave where it has been collected is not accessible to independently collect and analyse the samples there.
https://t.co/DjbJm40hni

13. Another faulty observation: “On the contrary, SARS-CoV-2 binds efficiently to ACE2 of several animal species thereby invalidating claims that the SARS-CoV-2 RBD was either selected or specifically optimized for human ACE2 binding”.

14. But the binding of SARS2 is still best for human ACE2!
https://t.co/lp9C8vtBWg
https://t.co/viqvfzv1Xa
And of course, after millions of passages in humans the virus can mutate to bind even better than possibly obtained in cell culture or humanized mouse.

15. The best is their conclusion:” Newly sequenced sarbecoviruses from bats captured in Cambodia, Thailand and Japan possess different combinations of spike motifs in the RBD and the S1/S2 junction that were first described in SARS-CoV-2...

16. ..These observations are consistent with the natural origin of SARS-CoV-2 and strongly inconsistent with a laboratory origin.” Not at all, it is still very possible that the FCS of SARS2 has been artificially inserted and the RBD optimized by passage to strongly bind to hACE2

17. I hope to be proven wrong, but I fear to see this shameful preprint published in Nature again. Honestly, these authors should be interrogated. Why are they trying to push so hard a natural origin of SARS2 using faulty arguments?

18. Is this because of the fear of losing grants for their research?:” In this regard there have been suggestions that scientists should stop investigating the diversity of coronaviruses in bats and other animals (Baker, 2021)...

19. ...We contend that the world should do the opposite if we are to be better prepared to prevent the next pandemic of an emergent coronavirus.” Or do they have other reasons?