

Twitter Thread by Daoyu



Daoyu

@Daoyu15



@WisdomRebel <https://t.co/iHKwUoNLJ5>

<https://t.co/sxm17Eu9hV>

<https://t.co/FtjifSGltc>

PRRA is highly purified in the CaLu-3 cell line when FBS is added to inhibit trypsin. Stu lied about that in his defense on the FCS identity. <https://t.co/GzM7uA6vup> the Gallaher article contain glaring

@AngloScot2 @WisdomRebel Mistakes and is completely impossible as HKU9 + RaTG13 only lead to a frameshift inactivated S and not a furin cleaved S.

<https://t.co/gmDXK9OluN>

The serological test the WIV claimed to be negative in Shi's addendum is the exact same test they claimed positive in 2012 in the PhD

@AngloScot2 @WisdomRebel thesis, and Stu once again lied about it. <https://t.co/Uiy8U9BTYp> significant evidence in the form of contaminated SRA datasets suggest that the DEFUSE grant have been funded in China, as the full-length HKU4 is not a part of the 2016-2019 grant, but is found before the start

@AngloScot2 @WisdomRebel Date of the 2020-2024 grant of June 2020. The WIV also contained several HKU3-like Coronaviruses, particularly in mice in an 2017 GEO experiment, which is consistent with the published HKU3 and batified mice experiment in the DEFUSE document (evidence from an already conducted

@AngloScot2 @WisdomRebel Experiment). Either DEFUSE or fast-tracked form of the 2020-2024 grant in 2019 would have lead to full-length Sarbecovirus clones being used, leading to SARS-CoV-2 in the lab—they used HKU4 in stead of HKU5 for the MERS spike experiment indicating that backbone sequence distance

@AngloScot2 @WisdomRebel Can not be too high for CoV chimeras, requiring the 4991 backbone or full-length 4991 to be used. In addition, <https://t.co/sxm17Eu9hV> the 201801-202102 grant of the WIV fits perfectly to DEFUSE since this is consistent with neither the Understanding risk of bat coronavirus

@AngloScot2 @WisdomRebel Emergence grant nor the EID hotspots in southeast asia grant.

<https://t.co/YwSTyD3N8B>

<https://t.co/ySjXCH0k2V>

In addition, the claim that the first infection was connected to the wet market is incorrect since the WHO report and the Zenodo-cell article used a resolution

@AngloScot2 @WisdomRebel Of cases that were far too low (which resulted in assigning cases to the wrong side of the yangtze river) and have intentionally omitted the headquarters of the WIV <https://t.co/w7d6bwbAn9> in Wuchang. In addition, the first patient on the WHO report went only to a supermarket in

@AngloScot2 @WisdomRebel Jiangxia, not any wet markets, and it just happened that the RT-mart he visited <https://t.co/khQsq8ULAp> is in Jiangxia, right next to the BSL-4 building of the WIV.

@AngloScot2 @WisdomRebel In addition, in contradiction to the Stu's another claim that 4991 is "sequenced only after 2020", the full-length sequence of 4991 was already discussed in 2018, and the S protein show significant divergence from RaTG13 when compared against SARS-CoV Urbani. <https://t.co/VI7I3PwJoK>

5/6

Finally, are you really the same as 4991 or are you a hair different in your spike protein? About 1.1% different so that the difference between your S gene and that of SARS1 would be 1.1% different than the diff reported for 4991 and SARS1 in 2019?<https://t.co/K84RLuj55Y> pic.twitter.com/IsSfMjenLI

— Yuri Deigin (@ydeigin) [June 1, 2021](#)

@AngloScot2 @WisdomRebel <https://t.co/ejV0sllzj5>

@AngloScot2 @WisdomRebel <https://t.co/ELNPYGVn00>

In addition, other anomalies are found in the RBD, especially that of T403 and D501.

@AngloScot2 @WisdomRebel <https://t.co/sxsPdd3kBd>

@AngloScot2 @WisdomRebel <https://t.co/bJma8XExej>

In addition, evidence in the form of out-of-whack substitution ratios was found in the RBD of RaTg13, indicating that accelerated evolution in the form of 5-Fluorouracil usage was present in the S protein—which they then go on to compensate in a completely

@AngloScot2 @WisdomRebel Unnatural way in the S2 and the ORF1b using loads and loads of dS changes, throwing the ratios of dS/dN out of whack in both locations. <https://t.co/J2YFuLKOqY>

@AngloScot2 @WisdomRebel <https://t.co/KmOFPkqo1H>

@AngloScot2 @WisdomRebel The CGG-CGG pair is at the end point of RNA editing and can not be mutated in the CoV system except for very rare circumstances of RdRp error—it mutates at a rate that is less than 1/10 the rate others can, and no immediately ZAP-beneficial mutation lead to a dS on the CGG pair.

@AngloScot2 @WisdomRebel If you count this low rate of mutation that is possible in the CGG-CGG pair, it is under neutral to slightly positive selection, and not negative or purifying selection. <https://t.co/jDy6RoYdSM> as for the multi-market hypothesis? Sichuan had loads and loads (1/4 of all sequences)

@AngloScot2 @WisdomRebel That had only T8782C but not C28144T, four of such genomes were found in early Wuhan as well. The 8782/28144 distinction in Wuhan appears in-host before other changes begin to show, so there is no need of two separate introductions for A and B lineage. It happened in humans.

@AngloScot2 @WisdomRebel The FCS PRRARS is highly purified in CaLu-3 cell cultures. Any change to the AA gives significantly reduced infectivity. Therefore, a canonical FCS of RRARR will simply mutate and revert into PRRAR within just 3 passages in the CaLu-3 cell line.

@AngloScot2 @WisdomRebel <https://t.co/53dG1S7LnL>

Neil says: scientists would use established viral backbones to test new RBDs or a FCS

Wrong

P11 PREEMPT states that they wanted to generate full length backbones of 3-5 new bat-CoVs per year.

The aim was to investigate novel viruses out there that could become pandemic.

— valentin bruttel (@VBruttel) [November 11, 2021](#)

@AngloScot2 @WisdomRebel <https://t.co/pNwWQ8a7jy>

Neil says: new backbones too much work

Wrong.

new viral backbones can be made in 1 week: <https://t.co/FkQg7SVcXE>

— valentin bruttel (@VBruttel) [November 11, 2021](#)

@AngloScot2 @WisdomRebel And “when clear mismatches occur, we will introduce appropriate human-specific cleavage sites and evaluate growth potential in VERO and HAE cultures”. The PRRA is most conserved upon conjugate gradient selection with CaLu-3 as main passage cells and VERO E6 for stock preparation <https://t.co/c7UNQR1cnY>

Neil says: They didn't plan to introduce new FCS sites, would use a classical FCS to be sure it works

Wrong

P11 PREEMPT states they would review deep sequence data for SARSr-CoV that encode functional proteolytic cleavage sites, and introduce these into low risk parental strain

— valentin bruttel (@VBruttel) [November 11, 2021](#)

@AngloScot2 @WisdomRebel between passages. <https://t.co/nRTIU93WGP>

@AngloScot2 @WisdomRebel <https://t.co/Ff9XAc4ao3>

In deed, CaLu-3 have 1/4 O-linked glycosylation that inhibits cleavage upon P681, saving the heparan sulfate binding peptide without compromising TMPRSS2 usage or immunogenicity. VERO E6 had even more O-linked glycosylation and HS binding as it have even

@AngloScot2 @WisdomRebel More uncleaved fractions with the PRRA compared to CaLu-3, and show a more pronounced advantage with PRRARS compared to RRRARS.

@AngloScot2 @WisdomRebel <https://t.co/UpOM1kGzTK>

@AngloScot2 @WisdomRebel In addition to the extremely high stability of PRRA in CaLu-3 and it's lack of stability in-vivo, some of the earliest patients in Wuhan harbored, by digital PCR and nanopore sequencing, large deletions across the QTQTN and SPRRARS <https://t.co/YPHooePHko> that are specific to

@AngloScot2 @WisdomRebel VERO E6 cell cultured SARS-CoV-2 strains--indicating that some of the quasispecies from the original cell culture were held over into the very first patients of SARS-CoV-2, strongly supporting the hypothesis that the PRRARS sequence being the result of composite selection

@AngloScot2 @WisdomRebel pressure generated from serial passage in CaLu-3 with stock preparation and storage in VERO E6 between passages, standard laboratory practices when it comes to the serial cell passage of viruses, which may also be employed if a transmissible vaccine (respiratory transmission with

@AngloScot2 @WisdomRebel no pathogenesis in aged WT BalB/C mice).