Twitter Thread by Daoyu

Daoyu
@Daoyu15

https://t.co/OuQaBRFPu7

Unfortunately the "This work includes the identification of viral sequences in bat samples, and has resulted in the isolation of three bat SARS-related coronaviruses that are now used as reagents to test therapeutics and vaccines." were BEFORE the

@franciscodeasis chimeric infectious clone grants were there.https://t.co/DAArwFkz6v is in 2017, Rs4231. https://t.co/UgXygDjYbW is in 2016, RsSHC014 and RsWIV16. https://t.co/krO69CsJ94 is in 2013, RsWIV1. notice that this is before the beginning of the project https://t.co/HPJhwq7NgH

@franciscodeasis starting in 2016. Also remember that they told about only 3 isolates/live viruses. RsSHC014 is a live infectious clone that is just as alive as those other "Isolates".

@franciscodeasis P.D. somehow is able to use funds that he have yet recieved yet, and send results and sequences from late 2019 back in time into 2015,2013 and 2016!

@franciscodeasis https://t.co/4wC7k1Lh54 Ref 3: Why ALL your pangolin samples were PCR negative? to avoid deep sequencing and accidentally reveal Paguma Larvata and Oryctolagus Cuniculus?

@franciscodeasis Ref.5: "However, inspection of Figure 4 shows that clade B is connected to viruses lacking T8782C and C28144T by single mutational steps via other human isolates, so this explanation requires not only positing two markets with two progenitors differing by just two mutations,

@franciscodeasis but also the exceedingly improbable evolution of one of these progenitors towards the other after it had jumped to humans."

@franciscodeasis in fact, both T8782C without C28144T and C28111T without T8782C have been found in humans. clearly these are impossible to be "two separate markets" as A and B have been found to be connected by single mutations in humans--requiring the exceedingly improbable event of one

@franciscodeasis progenitor evolving toward the other in humans.

@franciscodeasis https://t.co/4gQ4cwKyGk

@franciscodeasis As for ref 4? Why ALL the closest bat-borne backbones for SARS-CoV-2 LACKED the Spike that is necessary for infection of anything that isn't it's own species? RpYN06 had ZC45 S, which infect only R. Pusillus and R. Blythi. RpACE2 have been experimentally confirmed to be not

@franciscodeasis Usable by any RBD/RBM from the clade SARS-CoV or SARS-CoV-2, and could not have been able to recombine with any of these because of physical isolation between R. Pusillus and SARS-CoV-2-like Spike and RBD.

@franciscodeasis https://t.co/3vdIBEBA1k

@franciscodeasis Ref 6? Why the “full-length genomes” claimed by the RaTG15 paper were DISCONTIGUOUS with the RdRp sequences deposited under the title “Origin and cross-species transmission of bat coronaviruses in China” in 13-Aug-2019? https://t.co/gBfRmGcTf4 https://t.co/2E63NmRjTE

@franciscodeasis No other Betacoronaviruses have been isolated from R.blythi.

@franciscodeasis @garyruskin