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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 its own species? RpYN06 had ZC45 S, which infect only R. Pustillus 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. Pustillus 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](#)