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Twitter Thread by Daoyu

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It seems that it is a deeply cultured, but in deed ancestrally derived, sequence of SARS-CoV-2, that have many of the VERO cell specific mutations and deletions already in.

@jbloom_lab but it is not likely a clinical specimen from China because of the USA/WA-1 base which is not in Wuhan.

@jbloom_lab It had T22657C, T3346C, A21562C and G487T. all of which is in RaTg13 but not in WuHu-1. also T1963C and T22963C in BANAL-52. not all of the reads were H655Y and del I68-T76.

@jbloom_lab And it is actually clustered closely to the A/North America lineage, which shouldn't have appeared in a Chinese lab. also not there in Wuhan either.

@jbloom_lab also only one of the SRRs harbored T18060C it seemed.

@jbloom_lab It seems that both Ancestral A, A/Wuhan and B are present in these.

@jbloom_lab but the key is that reads from these SRRs harbors at least minor sequences that are more ancestral than Wuhan or even USA/WA/1. in addition to sequences that have evolved separately. the date of which this is sequenced is important.

@jbloom_lab https://t.co/DtjyycKy1v
I68-T76 seems to be one of the specific deletions happening in CaCo-2 cells. It is recurrent but mainly a culture artifact. Only half of the genomes have this deletion. None of the “all datasets” mutations have 100% coverage (all ~70% alt coverage).

@jbloom_lab H655Y is https://t.co/dM1YecX8sd a signature of VERO E6 cell passage. https://t.co/vytn6YVRYQ

https://t.co/TVXC4QOjt0

https://t.co/v3j78QFBoc

@jbloom_lab These are consistent with the CaCo-2, VERO E6 and CHO in the reads. It is possible that CHO leads to stable SARS-CoV-2, but it have not been confirmed. The only cell lines where P681 remain stable and purified is CaLu-3.

https://t.co/kNmg87kB6v

https://t.co/FtjifSGItc