Twitter Thread by Ewan Birney



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Now, a more technical tweet thread to give updates on the science - which is moving fast. Again, I recommend following @arambaut, @firefoxx66, @EBIgoldman, @The_Soup_Dragon, @pathogenomenick and @jcbarret along with others to stay on the cutting edge of this

Most important has been the paper by the @CovidGenomicsUK consortium on the new variant, here: https://t.co/b7yFFPXmsE

(This is super-rapid pre-print on https://t.co/PHmxAcVUoB - other people will pick over this no doubt - but the openness of the data and quality of analysis from this group means this is super solid, and any updates on discussion likely to happen fast)

Two key take aways from this paper for me:

1. There is a big jump in number of changes - too big to be explainable with the natural progression over time. @arambaut and colleagues point out that similar big jumps have happened in immunocompromised patients treated via convalescent plasma + drugs

2. This means there are both a number of potential things that could have changed and that it might be that there is synergistic effects - one now needs to test out what things are different in the lab and then work through each one in turn if there is a difference.

The other complication to this is that the 69/70 deletion is present on this branch. This deletion is complex for a variety of reasons

1. Firstly it is recurrent. We have seen this globally in Lyon (but to stress - *just* this event not the whole strain) and in the Danish outbreak that ended up in Mink farms (again, *just* this change not the whole set).

It is unusual to have sequenced so many individuals where one has a slow(ish) moving mutation rate and recurrent mutation. This is what gives @EBIgoldman and colleagues some new headaches (should one collapse multiple observations of the same sequence in likelihood calcs?)

2. This site overlaps with primer sites for some widely used RT-PCR tests. To stress, nearly all RT-PCR tests use 3 (sometimes more!) sites to assess, so having one "drop out" as it is called is ok.

This sounds concerning at first glance but shouldn't be (this is why they do 3 sites!) and for sure the test site will be moved. However, it does mean we can see this in the RT-PCR testing itself.

Here is Tony Cox, @The_Soup_Dragon showing how this variant rose over time. Please note that early on the red line here is likely to be a mixture of viral versions which have this change, but then you can see it take off. https://t.co/BWCHYFR1qy

> MK LHL testing data showing increasing prevalence of H69/V70 variant in positive test data - which is detected incidentally by the commonly used 3-gene PCR test. pic.twitter.com/1U0pVR9Bhs
>
> — Tony Cox (@The_Soup_Dragon) December 19, 2020

This means we've got the numbers for lineage displacement (not just growth), meaning scientists can be pretty confident that this version of the virus is growing.

The recurrent mutation of this virus is interesting, and this variant also shares a mutation with a South African strain that also came into the news for potential faster transmission - to stress, these are certainly different lineages.