Twitter Thread by Dr Emma Hodcroft

Dr Emma Hodcroft @firefoxx66



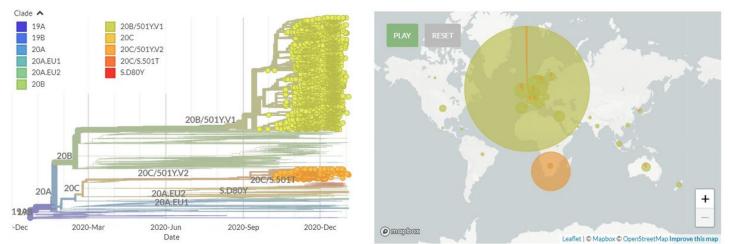
Happy Tuesday! The latest focal S:N501 build is now updated with sequences from 11 Jan.

There are 101 new sequences in the 501Y.V1 (B.1.1.7 #b117) & 501Y.V2 variants.

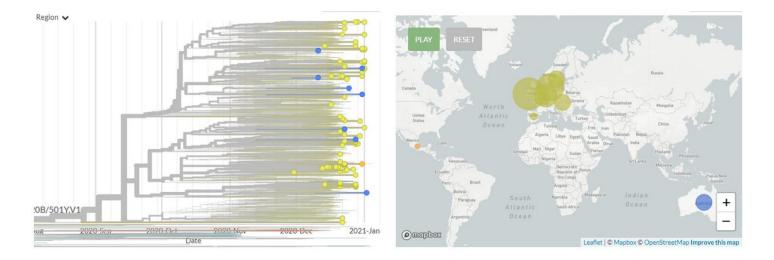
Additionally, I'll include some updates on S:E484K in this thread.

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https://t.co/dXx6nk6Llz

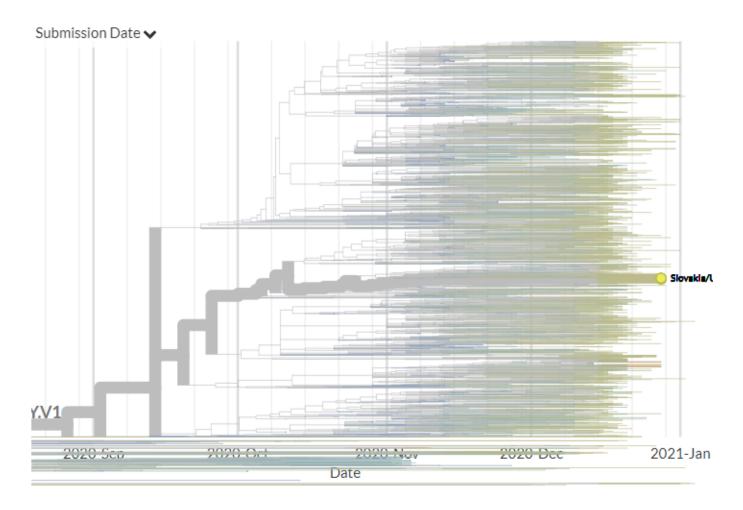


There are 97 new non-UK sequences in 501Y.V1, including the first sequences in the cluster from Slovakia, Mexico, & Belgium, plus additional sequences from the Netherlands, Denmark, Australia, Spain, Ireland, & Sweden.

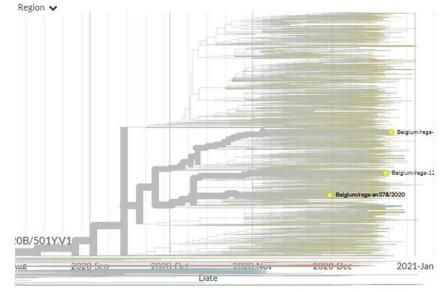


Slovakia has 10 sequences that fall in 501Y.V1 for the first time. These are closely linked, & likely indicate a single introduction and ongoing transmission (remember: vertical distance is not meaningful on the same branch - position of the 2 English samples is arbitrary).

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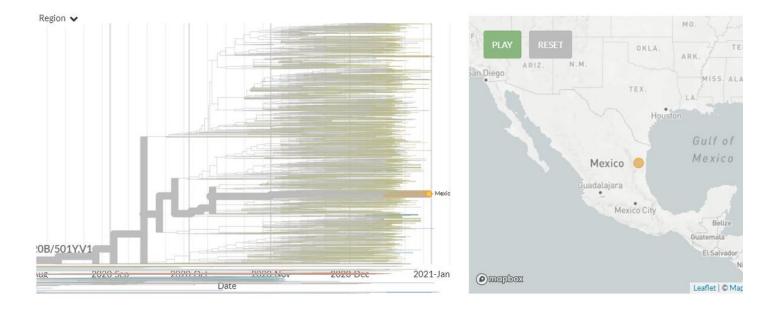
Belgium has 5 sequences in 501Y.V1 for the 1st time, indicating 3 separate intros. 3 seqs cluster together (zoomed, divergence), indicating a single introduction. The connection to Netherlands might indicate transmission, or 2 transmissions from same diversity in the UK.



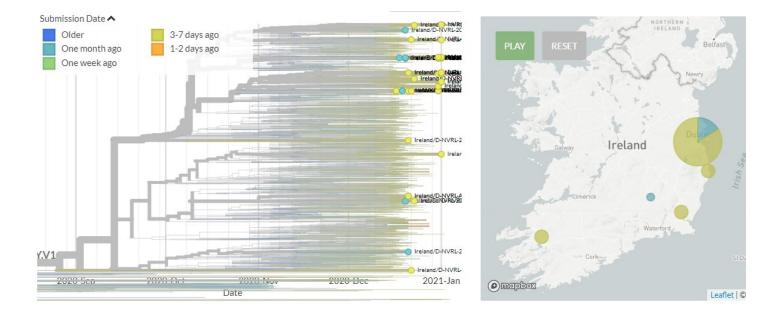


Mexico also has a sequence that falls into 501Y.V1 for the first time.



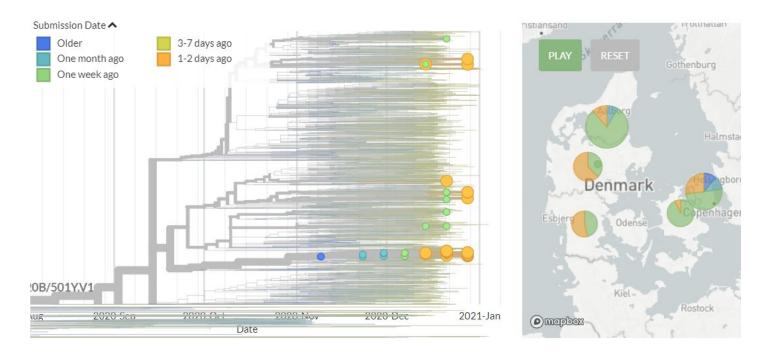


Ireland has 36 new sequences. Many represent separate introductions, but some do cluster with older sequences & may represent local transmission, or introductions from the same UK diversity.



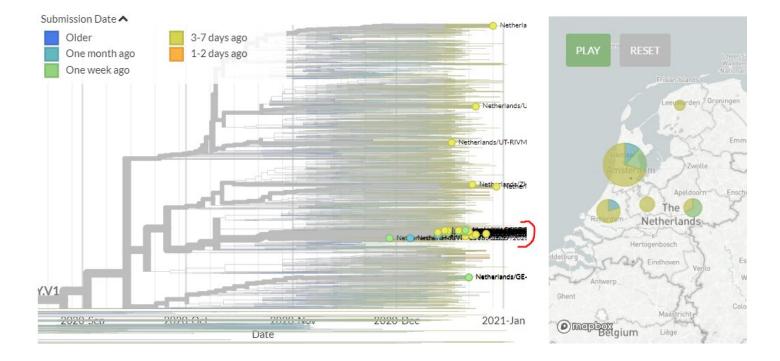
Denmark has 29 new sequences (orange). These represent both new introductions, and further expansion of the large cluster (zoomed view).

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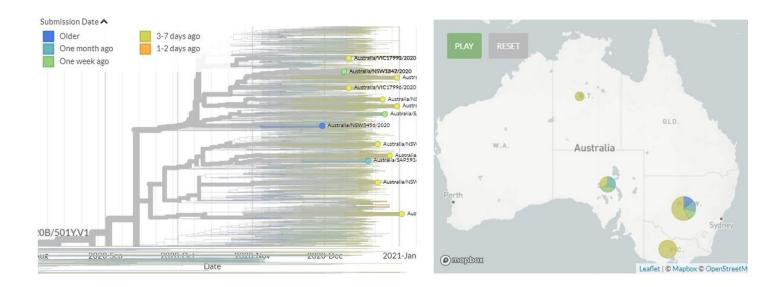
The Netherlands have 6 new sequences. All fall within the section of the tree marked in red.

Zooming in, the new sequences are marked in red: 2 are separate introductions. Zooming in further (divergence view), cluster at the top are identical to an older sequence.

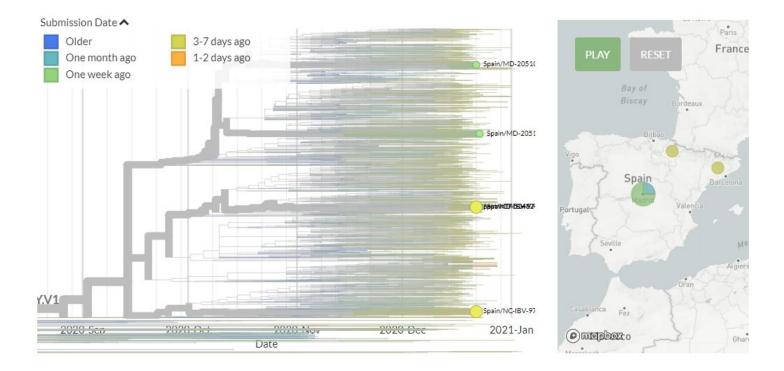


Australia has 6 new sequences, including the first from Northern Territory and Victoria. 1 pair of sequences from Victoria are identical to each other, representing one introduction.

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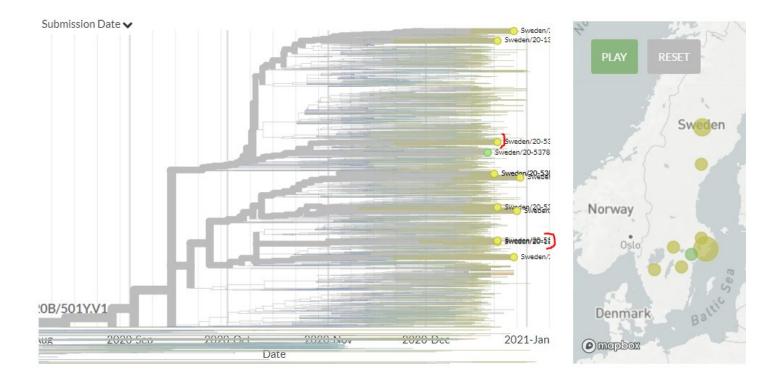


Spain has 2 new sequences (yellow). One represents a separate introduction. The other links to older Spanish sequences, but it's unclear from sequences alone if this is local transmission or transmissions from a common source.



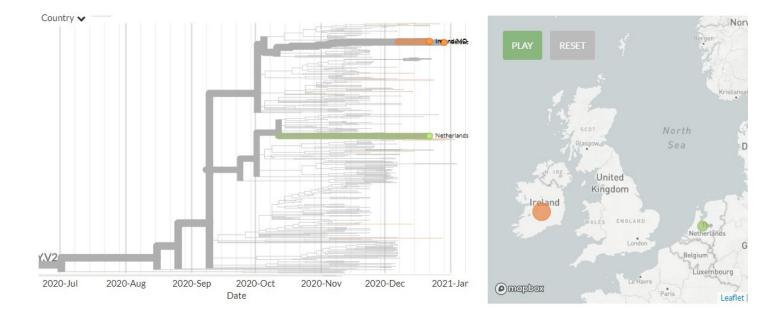
Sweden has 2 new sequences, marked in red. Both represent independent introductions. The second one is hard to see, but zooming in shows this more clearly.

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Now turning to 501Y.V2:

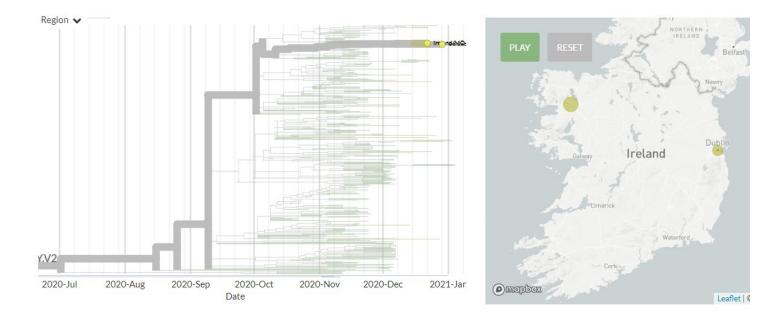
There are 4 new non-South African sequences in 501Y.V2, including the first from Ireland (3) and the Netherlands (1).



Ireland has 3 sequences in 501Y.V2 for the first time. They cluster together, and may indicate either local transmission, or a common exposure (pictures 1 & 2).

The Netherlands has its first sequence in 501Y.V2 (picture 3).

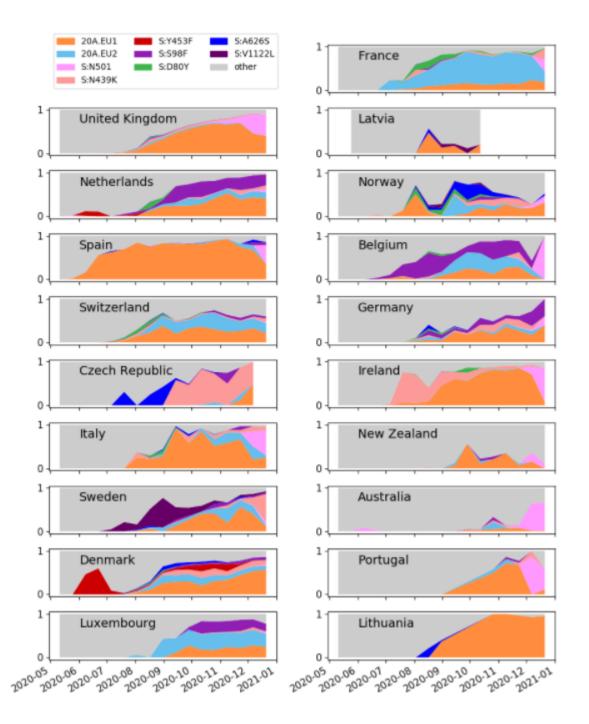
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As usual, the updated country graphs are also available. As always, interpret with care: countries are selectively sequencing to track 501Y.V1, so proportions of sequences are not representative for many countries.

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https://t.co/c7wlQOLRiq

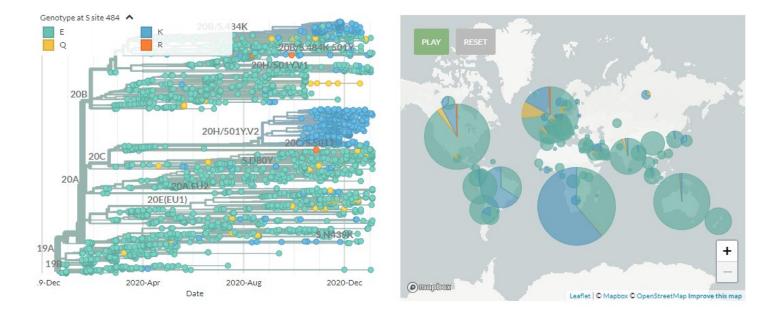


Finally, an updated focal S:E484 build is also up.

S:E484K is found predominantly in the 501Y.V2 variant, & in a cluster of sequences primarily in Brazil, though it has appeared numerous times in the past.

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https://t.co/Od95D6DL74



S:E484K has been discussed recently as there are suggestions it may impact how well the immune system can recognise the virus, particularly if you've been infected with SARS-CoV-2 before.

Links to the studies are on https://t.co/SmanZBHpse

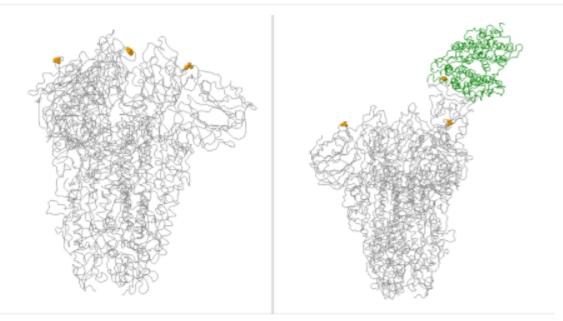


Figure made via GISAID

Dedicated S:E484 Nextstrain build

Table and charts of mutation distribution

- Defining mutations:
 - o Has appeared multiple times independently: each can be associated with different accompanying mutations
- S:E484
 - Primarily associated with the 501Y.V2 variant that arose in South Africa in the winter of 2020(Tegally et al., medRxiv), and a variant
 predominantly found in Brazil (de Vasconcelos et al., medRxiv), but has appeared independently numerous times around the world.
 - o Mutations at S:E484 may significantly reduce convalescent serum neutralization (Greaney et al., medRxiv)
 - There has been a case of reinfection associated with S:E484K : a woman previously infected with a non- S:E484K variant of SARS-CoV-2 was later reinfected with a virus carrying the S:E484K mutation (Nonaka et al., PrePrints)
 - In one study co-incubating SARS-CoV-2 with convalescent plasma, neutralization was completely escaped at day 73 due to an S:E484K mutation (Andreano et al., bioRxiv)

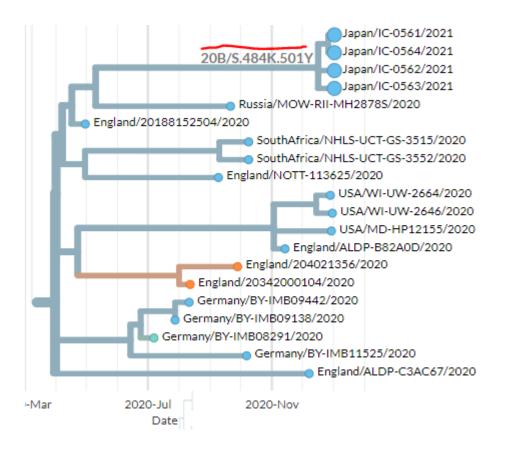
Additionally, over the weekend, travellers from Brazil to Japan were found to be infected with a novel variant with many mutations, including S:E484K & S:N501Y. Translated report linked below.

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https://t.co/G1ITeT3MoV

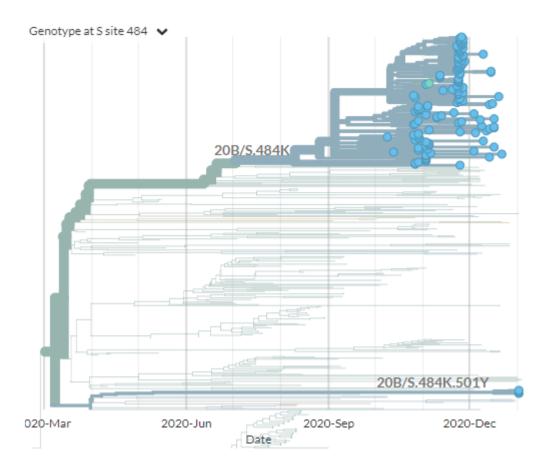
To help viewers identify these new samples from Japan, I've added a *temporarily* label to the S:E484K build: 20B/S.484K.501Y.

Additionally, I've added a *temporary* label to the Brazilian cluster with S:E484K: 20B/S.484K.



Interestingly, though the recent Japanese sequences carry S:E484K & seem to originate from Brazil, they do *not* branch from the larger 484K cluster in Brazil, but instead sit on a long branch separately within the 20B Clade.





Getting case numbers down saves #LivesAndLivelihoods, and reduces #SARSCoV2's opportunities to explore situations with unique selection pressures, potentially resulting in mutations expanding that we'd rather not see.

Help make my updates more boring: bring cases down!

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PS - For related but slightly-different-angle updates on 501Y.V1 (B.1.1.7) & 501Y.V2 (B.1.351), you should follow @AineToole & keep an eye on her tweets about updated reports!

https://t.co/fZDQqwvJmr

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Updated SARS-CoV-2 new variant report now available for 2021-01-11 at <u>https://t.co/e3J9becNTz</u>. @arambaut @viralverity @MOUGK pic.twitter.com/x4UabXv5Yt

- \xc1ine O'Toole (@AineToole) January 11, 2021