

# Twitter Thread by Dr Emma Hodcroft



**Dr Emma Hodcroft**

@firefox66



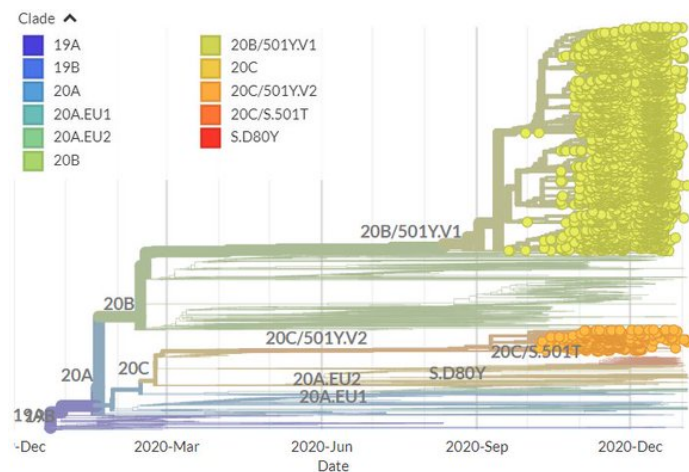
**Happy Tuesday! The latest focal S:N501 build is now updated with sequences from 11 Jan.**

**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.**

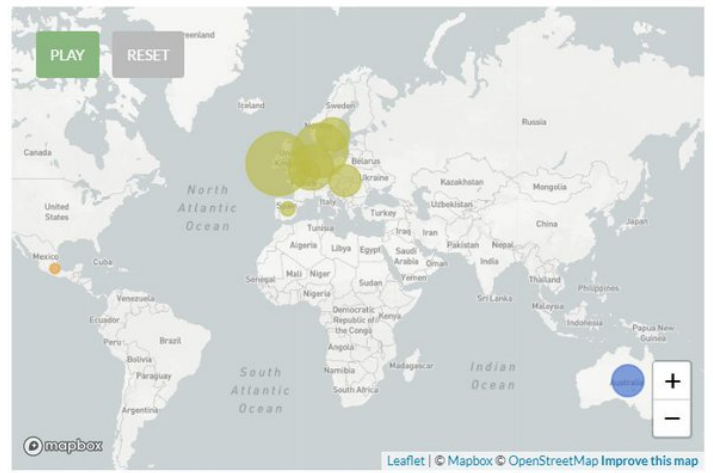
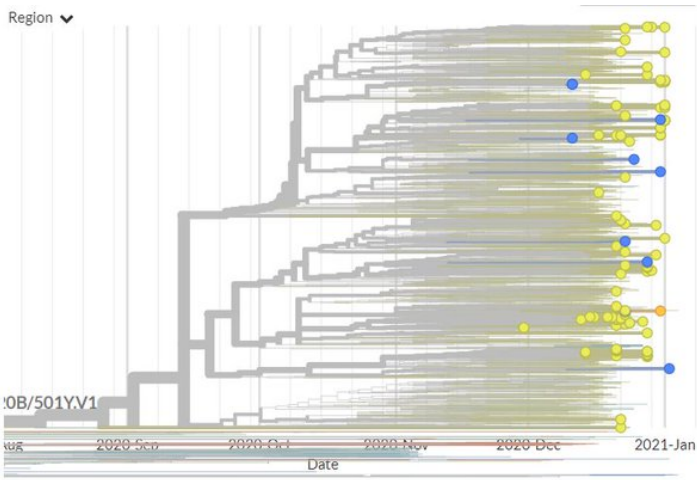
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<https://t.co/dXx6nk6Llz>



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.

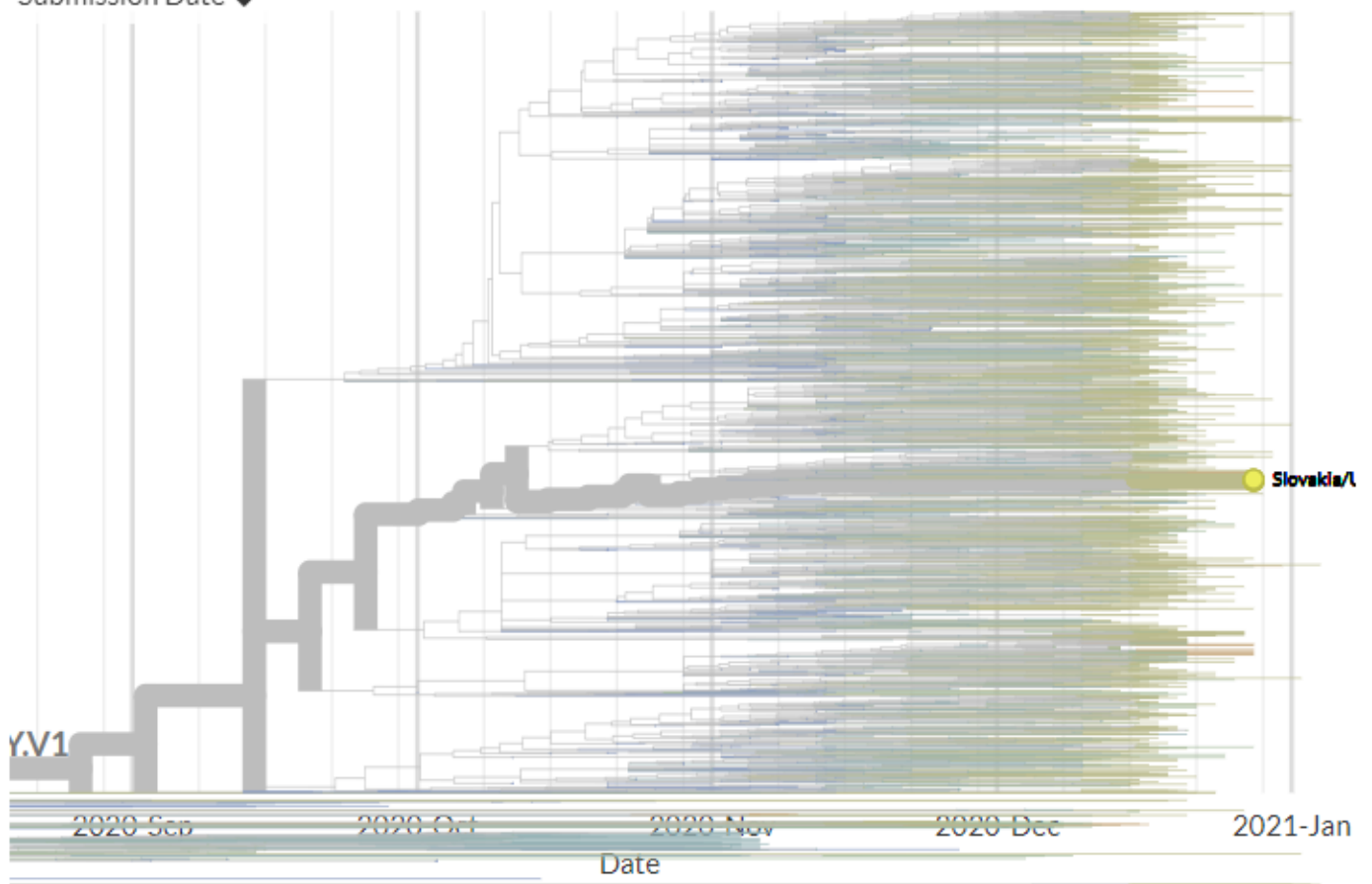
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Slovakia has 10 sequences that fall in 501Y.V1 for the first time. These are closely linked, & likely indicate a single introduction and ongoing transmission (remember: vertical distance is not meaningful on the same branch - position of the 2 English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

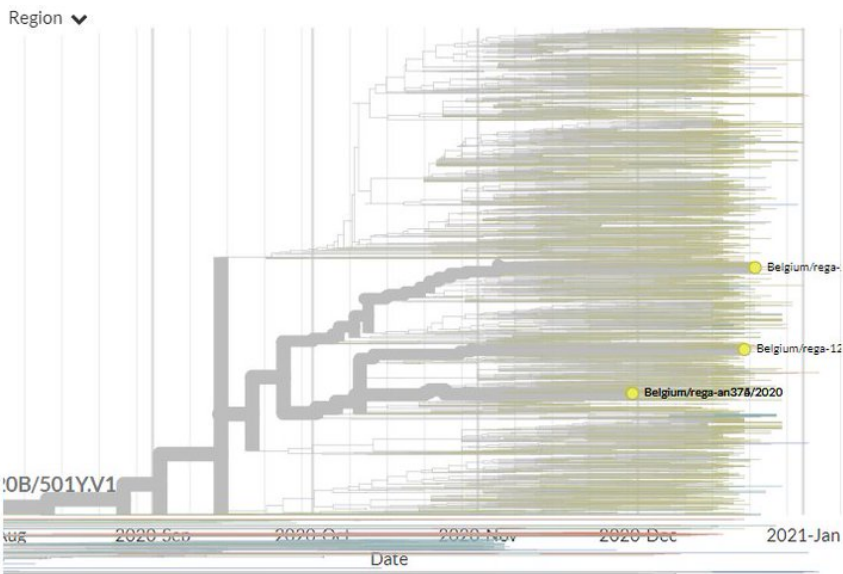
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Submission Date ▾



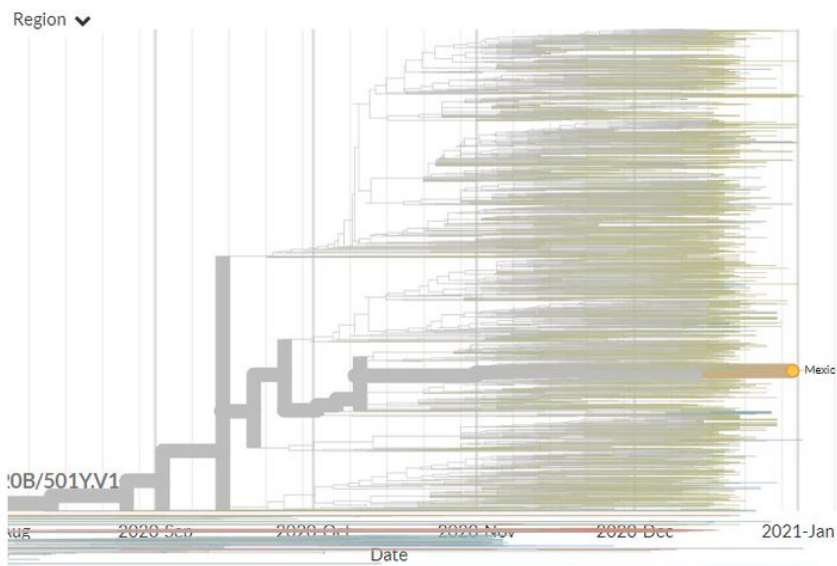
Belgium has 5 sequences in 501Y.V1 for the 1st time, indicating 3 separate intros. 3 seqs cluster together (zoomed, divergence), indicating a single introduction. The connection to Netherlands might indicate transmission, or 2 transmissions from same diversity in the UK.

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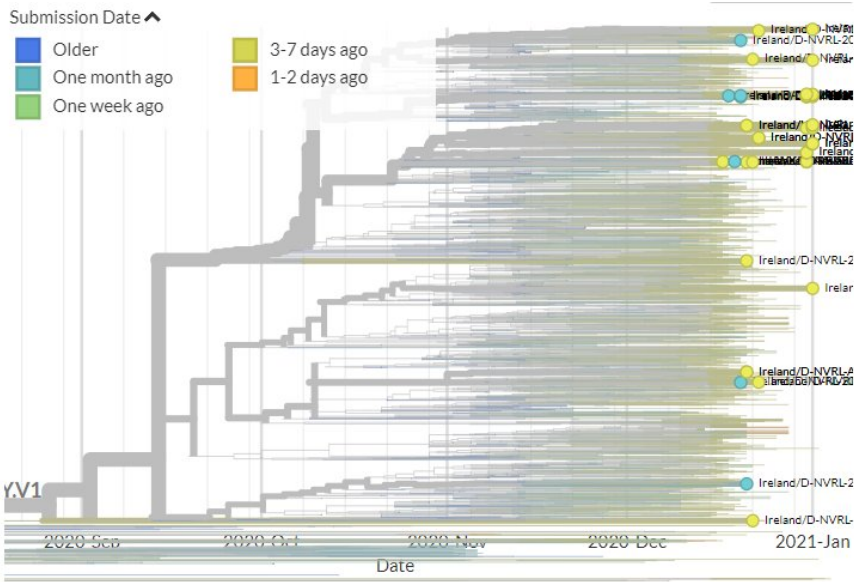
Mexico also has a sequence that falls into 501Y.V1 for the first time.

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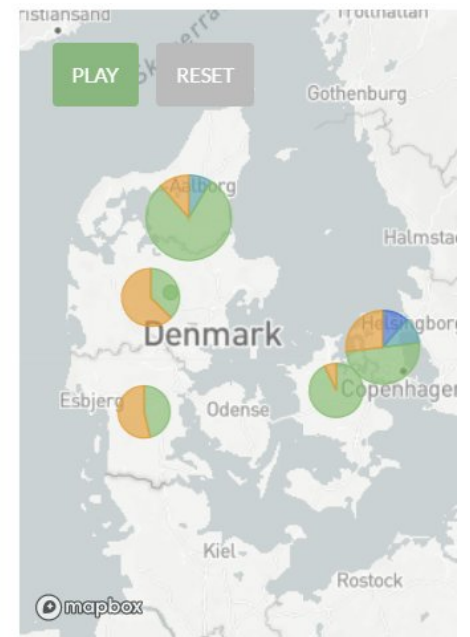
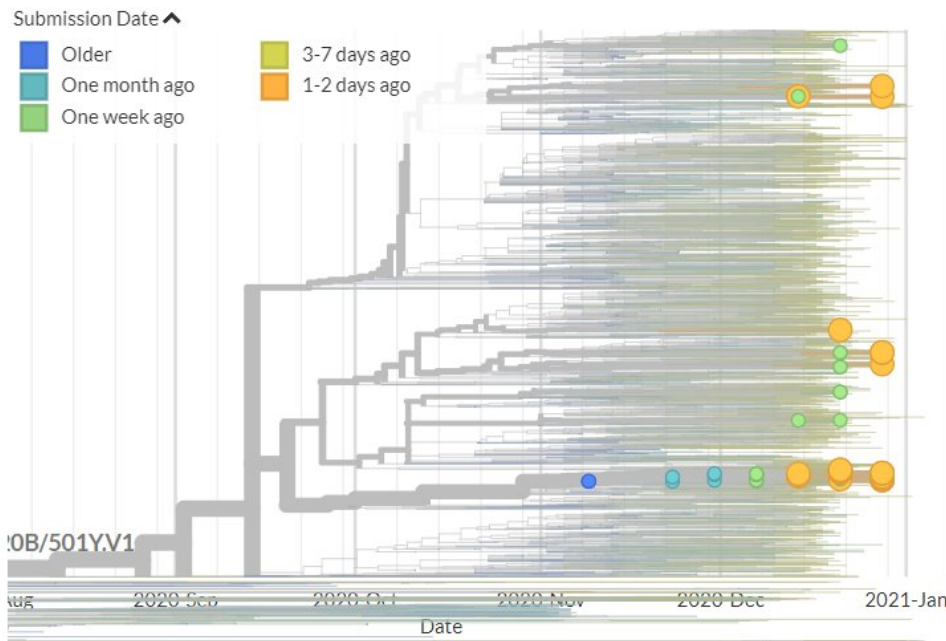
Ireland has 36 new sequences. Many represent separate introductions, but some do cluster with older sequences & may represent local transmission, or introductions from the same UK diversity.

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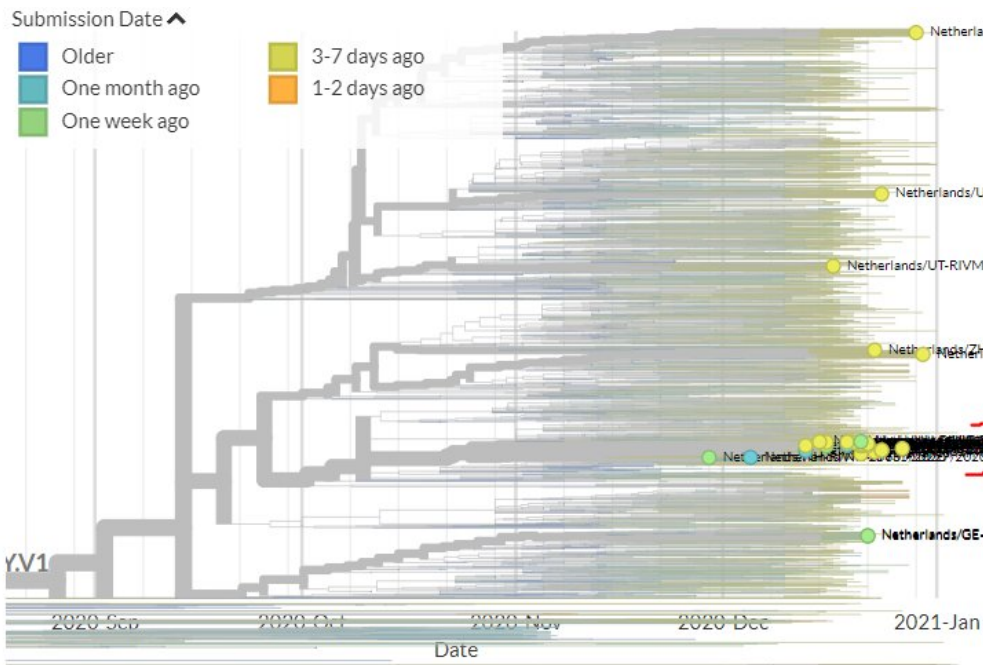
Denmark has 29 new sequences (orange). These represent both new introductions, and further expansion of the large cluster (zoomed view).

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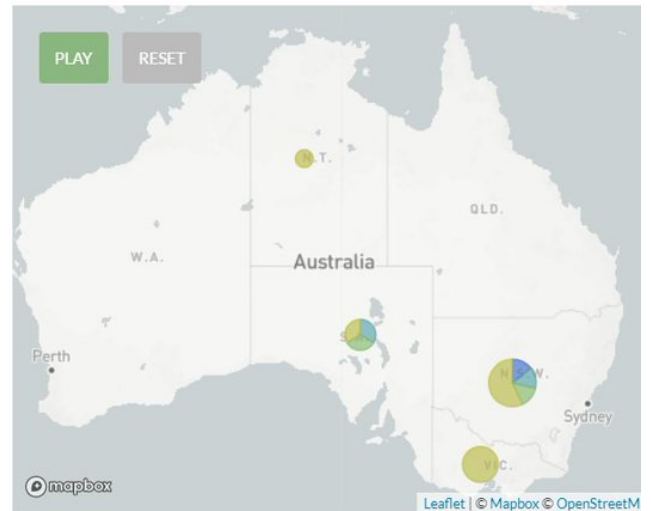
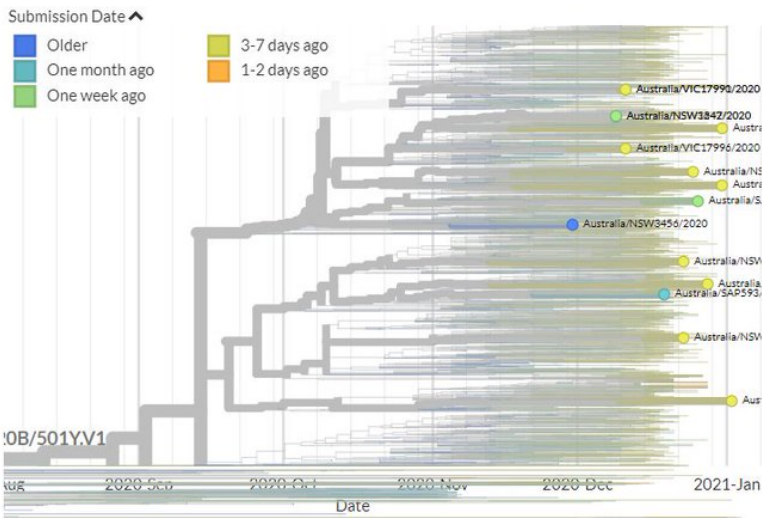
The Netherlands have 6 new sequences. All fall within the section of the tree marked in red. Zooming in, the new sequences are marked in red: 2 are separate introductions. Zooming in further (divergence view), cluster at the top are identical to an older sequence.

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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.

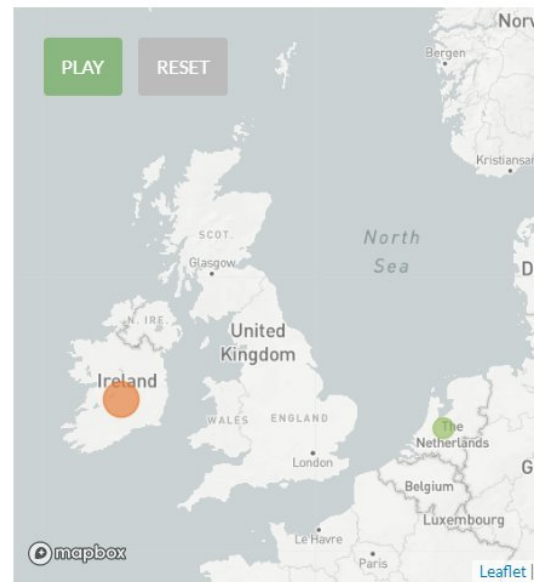
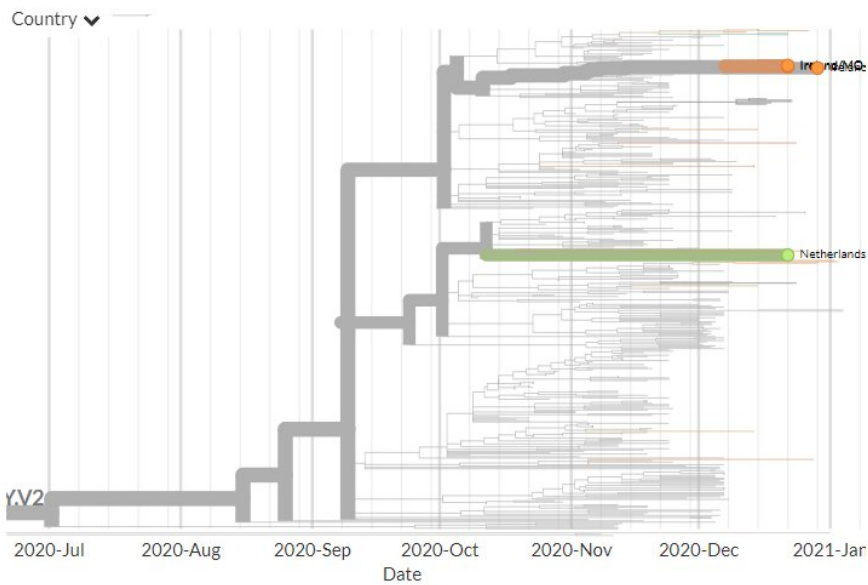
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Spain has 2 new sequences (yellow). One represents a separate introduction. The other links to older Spanish sequences, but it's unclear from sequences alone if this is local transmission or transmissions from a common source.

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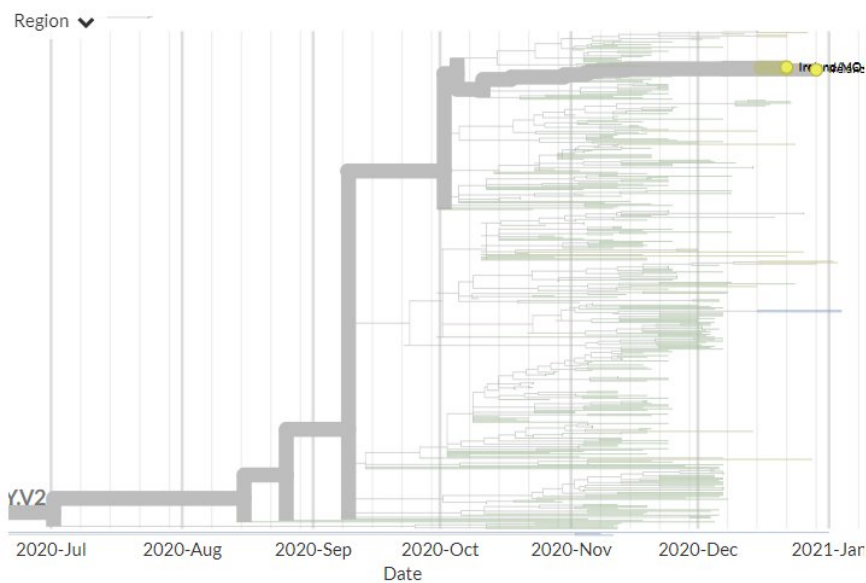




Ireland has 3 sequences in 501Y.V2 for the first time. They cluster together, and may indicate either local transmission, or a common exposure (pictures 1 & 2).

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

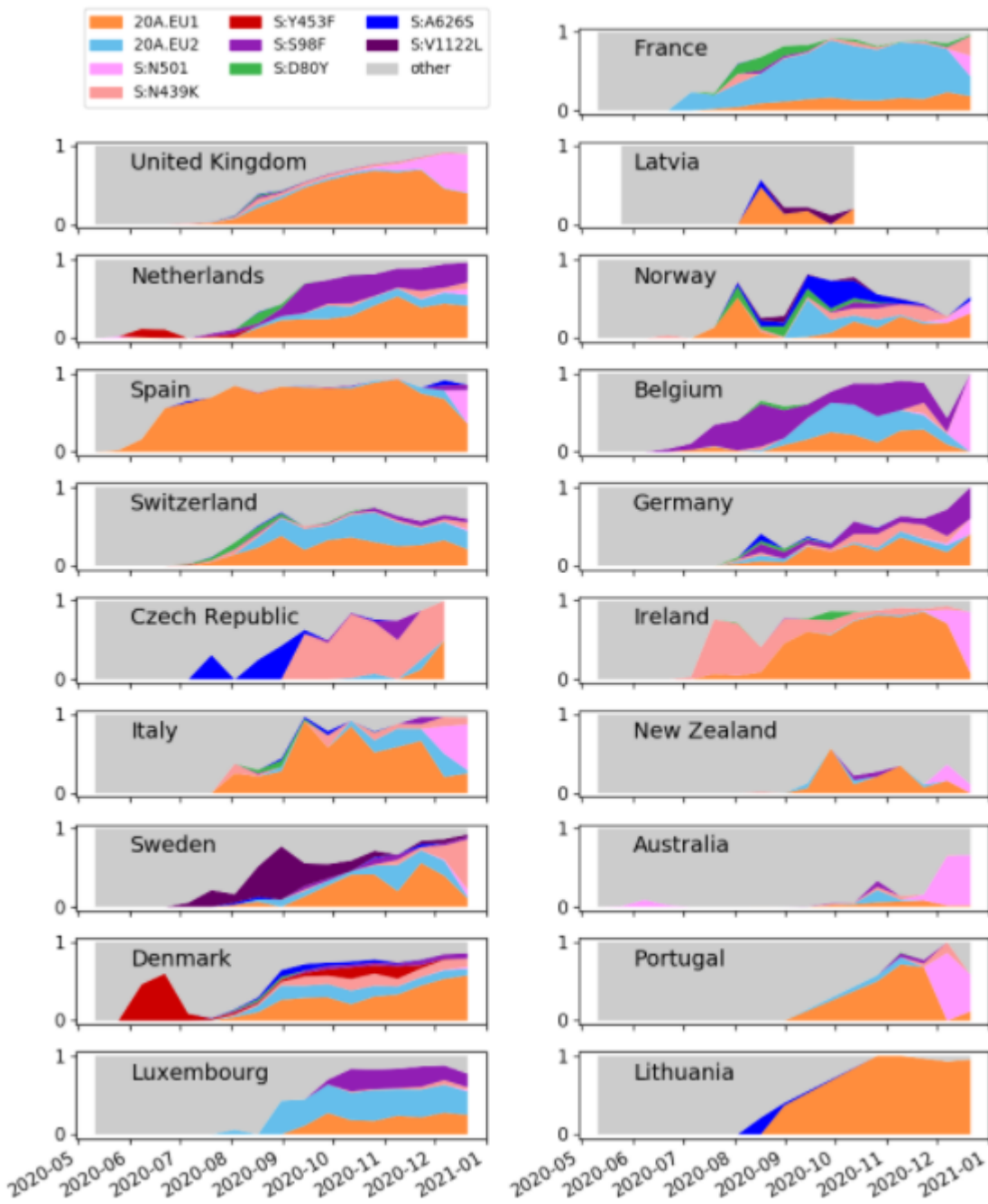
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As usual, the updated country graphs are also available. As always, interpret with care: countries are selectively sequencing to track 501Y.V1, so proportions of sequences are not representative for many countries.

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<https://t.co/c7wIQLRiq>

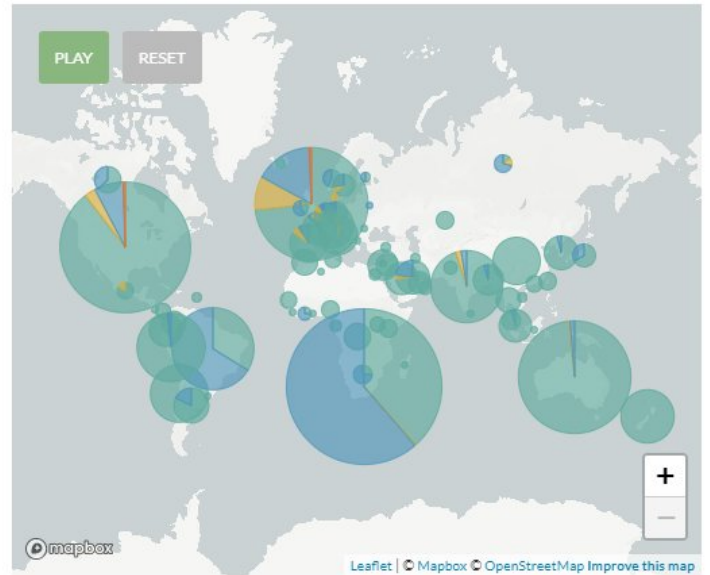
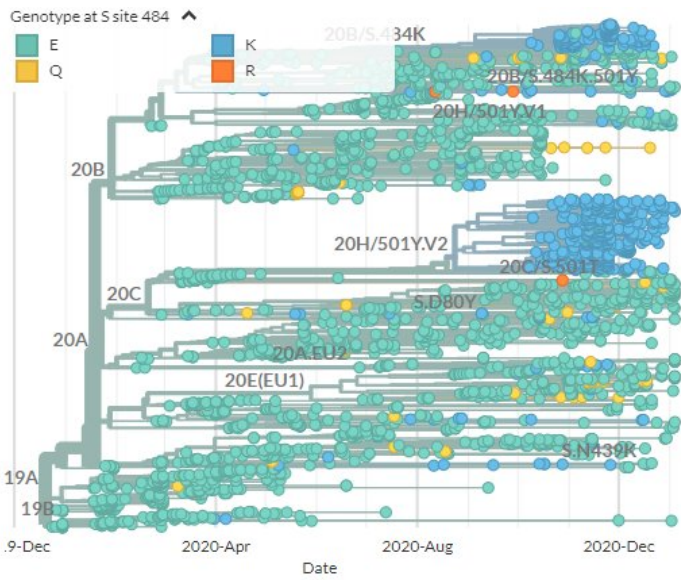


Finally, an updated focal S:E484 build is also up.

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/SmanZBHpsc>

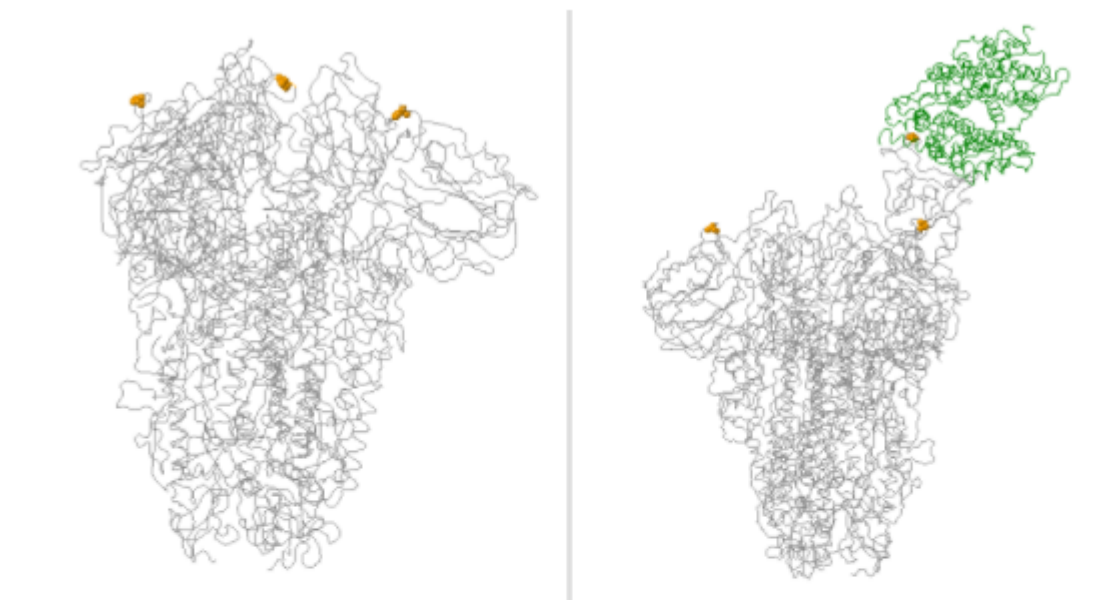


Figure made via GISAID

[Dedicated S:E484 Nextstrain build](#)

[Table and charts of mutation distribution](#)

- Defining mutations:
  - 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.
  - 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.

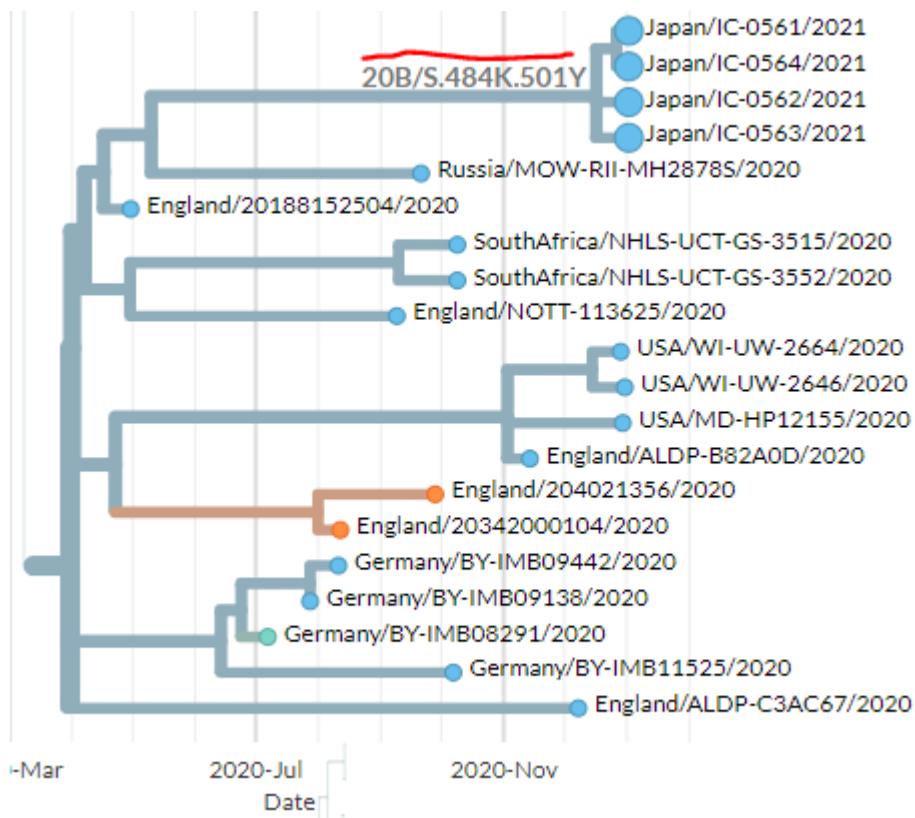
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<https://t.co/G1ITeT3MoV>

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.

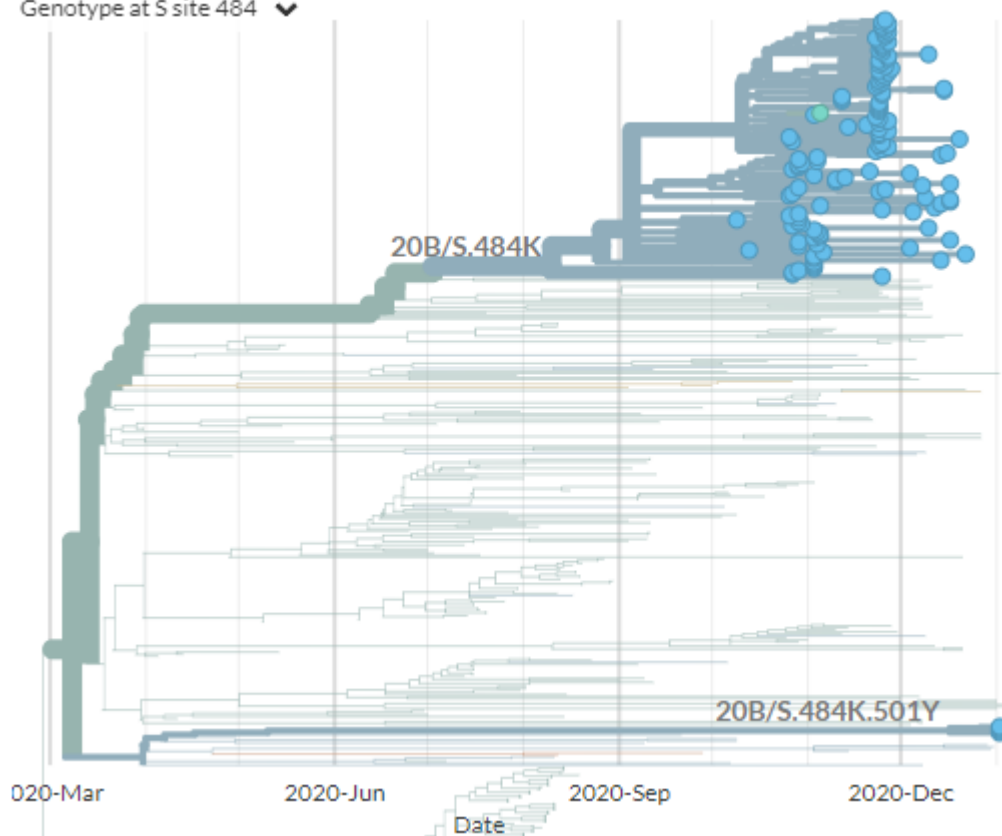
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Interestingly, though the recent Japanese sequences carry S:E484K & seem to originate from Brazil, they do \*not\* branch from the larger 484K cluster in Brazil, but instead sit on a long branch separately within the 20B Clade.

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Genotype at S site 484 ▼



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/fZDQgwvJmr>

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

— Aine O'Toole (@AineToole) [January 11, 2021](#)