Twitter Thread by Dr Emma Hodcroft



Dr Emma Hodcroft
@firefoxx66

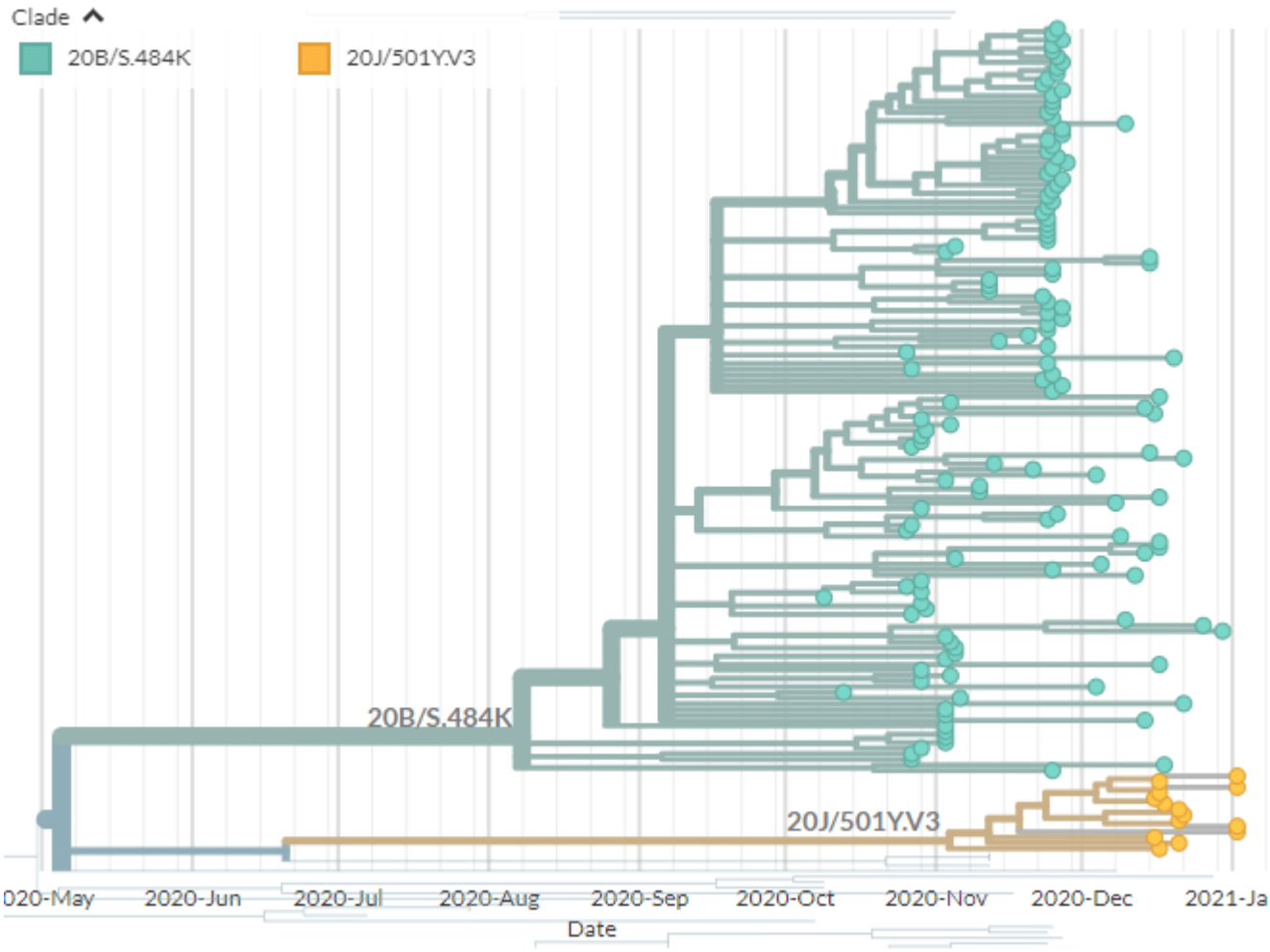
Lots of tweets about this today!
Let's see what we can see in the focal S:E484 build!

Phylogenetics (what I do - making 'family trees' from virus genetics) can be very informative to see how different variants are spreading, and how cases

There are two variants circulating predominantly in Brazil:
- 20B/S.484K seems to be older & more widespread. It has (among others) a mutation at position 484
- 20J/501Y.V3 is smaller & detected recently. It has mutations at 501 *and* 484.

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https://t.co/Cw5u2kuATa



The variant predominantly in the UK (501Y.V1 / B.1.1.7) and the variant predominantly in South Africa (501Y.V2) also both have 501. 501Y.V2 *also* has the 484K mutation.

Why are there concerns about these mutations? You can read more at https://t.co/wVE7ubYBoy!

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S:N501

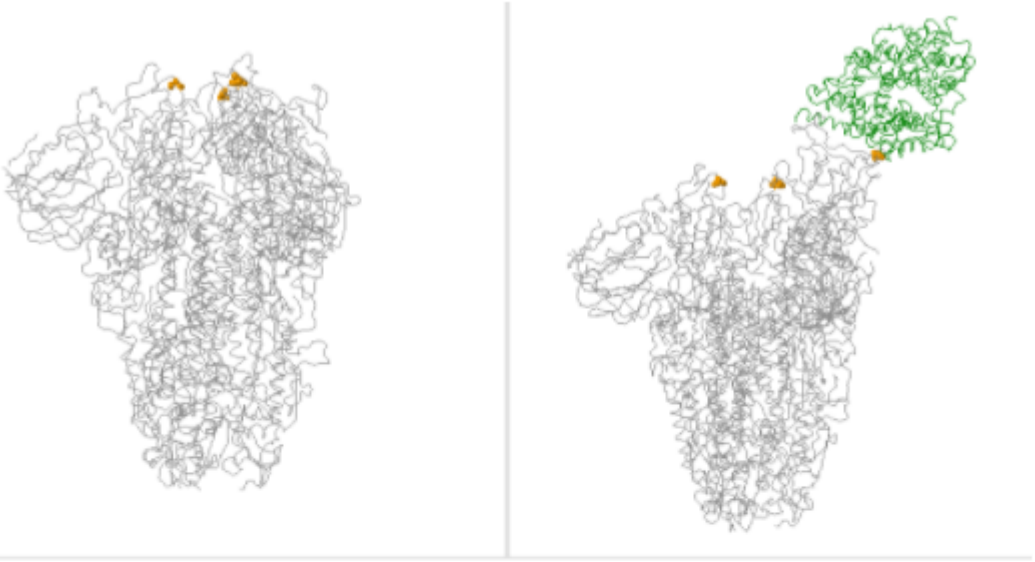


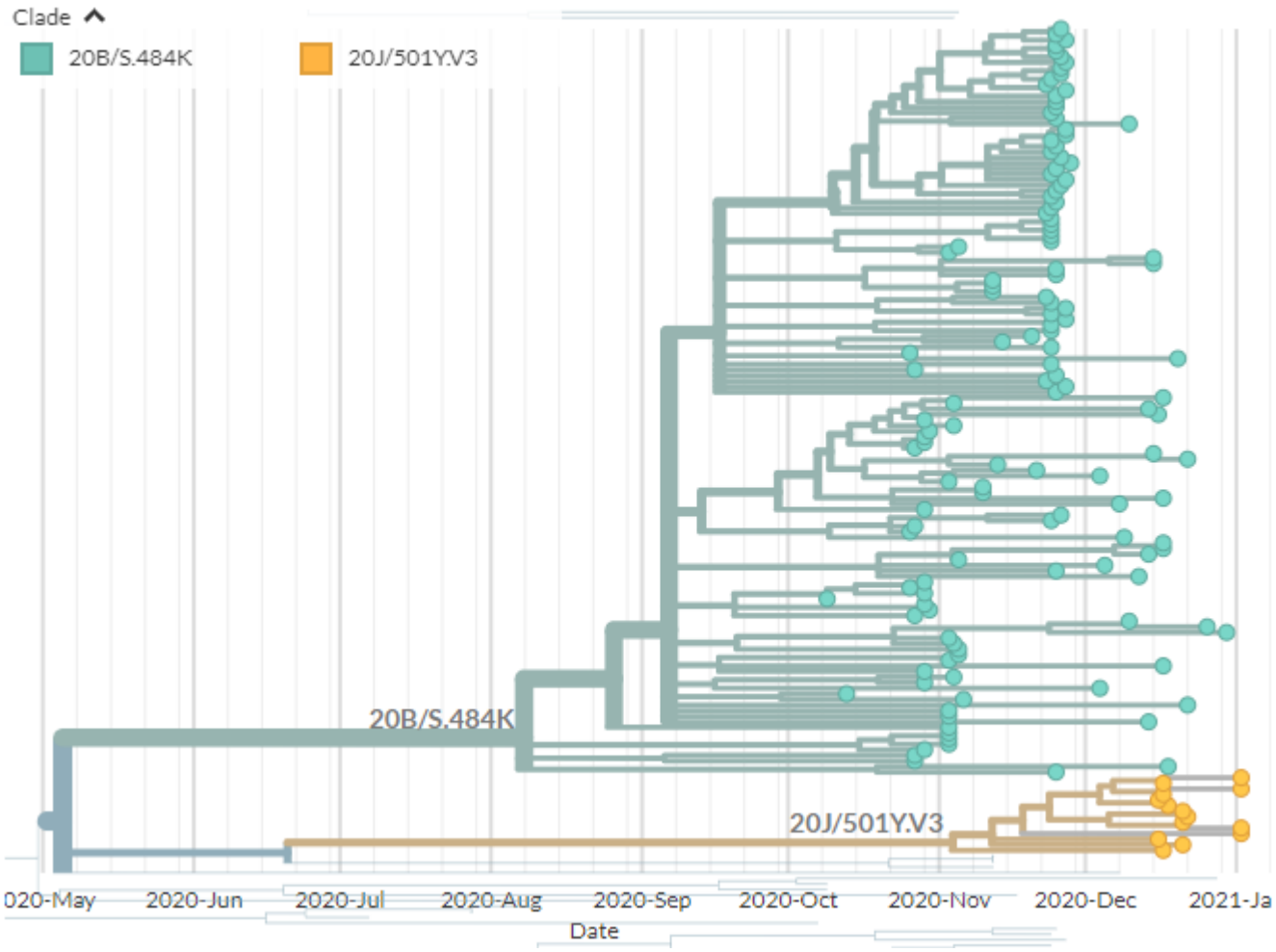
Figure made via GISAID

Dedicated S:N501 Nextstrain build

Table and charts of mutation distribution

- Defining mutations:
  - Has appeared multiple times independently: each can be associated with different accompanying mutations
  - Amino-acid changes are `N501Y` (nucleotide mutation `A23063T`), `N501T` (nucleotide mutation `A23064C`), and `N501S` (nucleotide mutation `A23064G`)
- `S:N501`
  - Mutation is in the receptor binding domain (RDB), important to ACE2 binding and antibody recognition
  - N501Y is associated with recently reported 'new variants' in the UK and South Africa:
    - '20B/501Y.V1' (B.1.1.7) was announced in the South East of England on 14 Dec 2020 (COG-UK Report, Rambaut et al., PHE report, PHE Technical Report 2, PHE Technical Report 3)
      - This particular variant is associated with multiple mutations in Spike, including: `N501Y`, a deletion at 69/70 (as seen in `S:N439K` & `S:Y453F`) (Kemp et al. bioRxiv (21 Dec)), `Y144` deletion, and `P681H` (adjacent to the furin cleavage site).
      - There is also a notable truncation of `ORF8`, with `Q27*` (becomes a stop codon) (deletion of `ORF8` was previously associated with reduced clinical severity (Young et al. Lancet)), and mutations in `N`: `N:D3L` and `S235F`.
    - '20C/501Y.V2' (B.1.351) is found in South Africa and was also announced in December 2020 (Tegally et

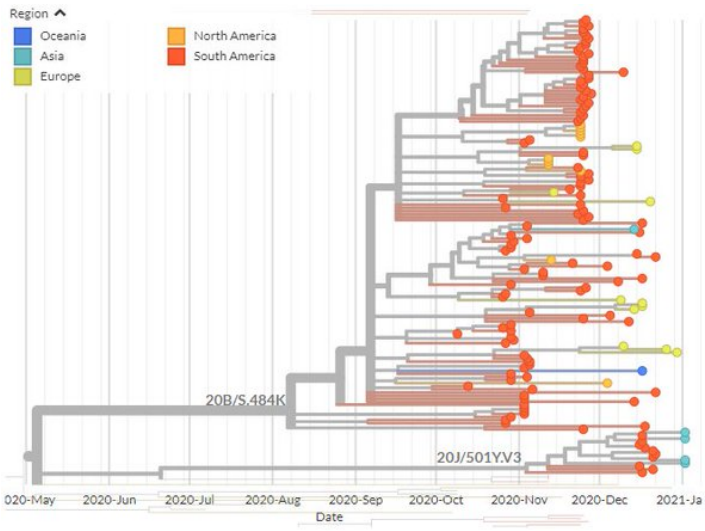
The view below is from an analysis focusing on sequences with a mutation at 484. It shows all the samples in the 2 variants (20B/S.484K & 20J/501Y.V3) & how they're related. More closely related = closer together (very, very roughly).

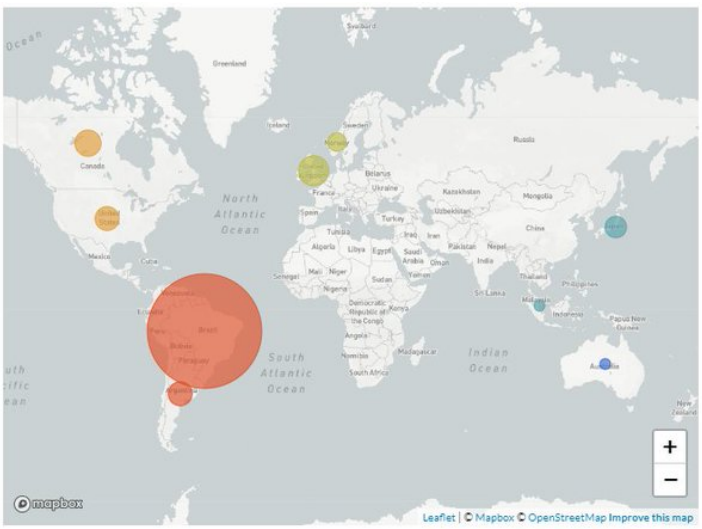


We can colour these samples by region to see where they're from. As we expect - most are in Brazil! A few are in Argentina (also red).

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https://t.co/Cw5u2kuATa

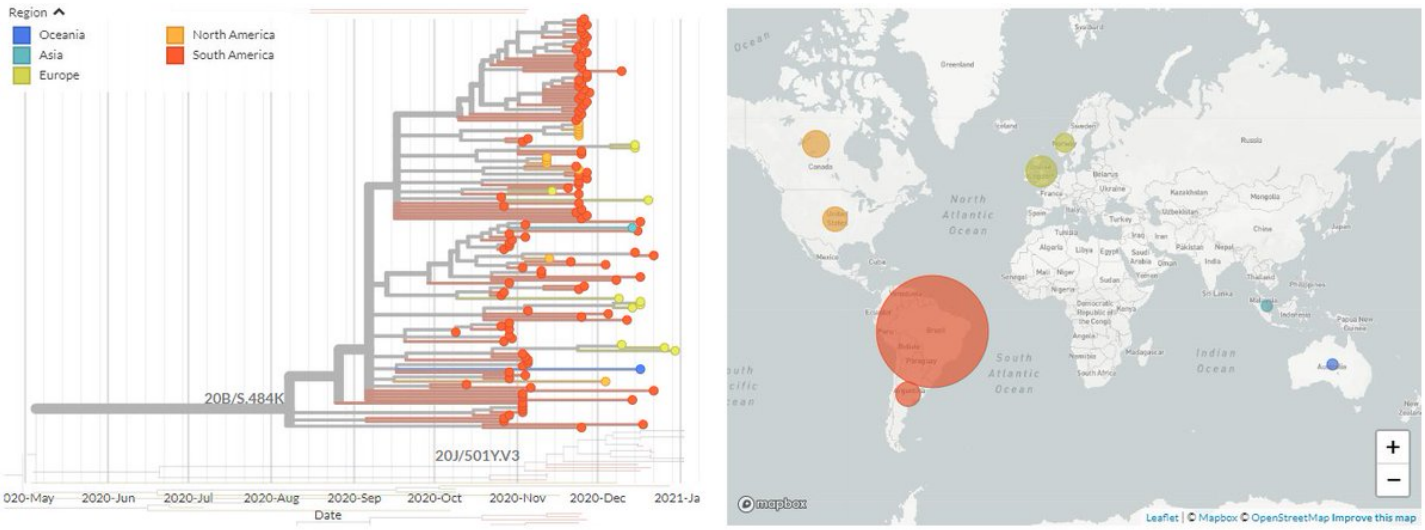




If we look just at 20B/S.484K (top cluster), we can see there are clusters of sequences in the UK, Canada & the USA, and exports to Norway, Malaysia, & Australia.

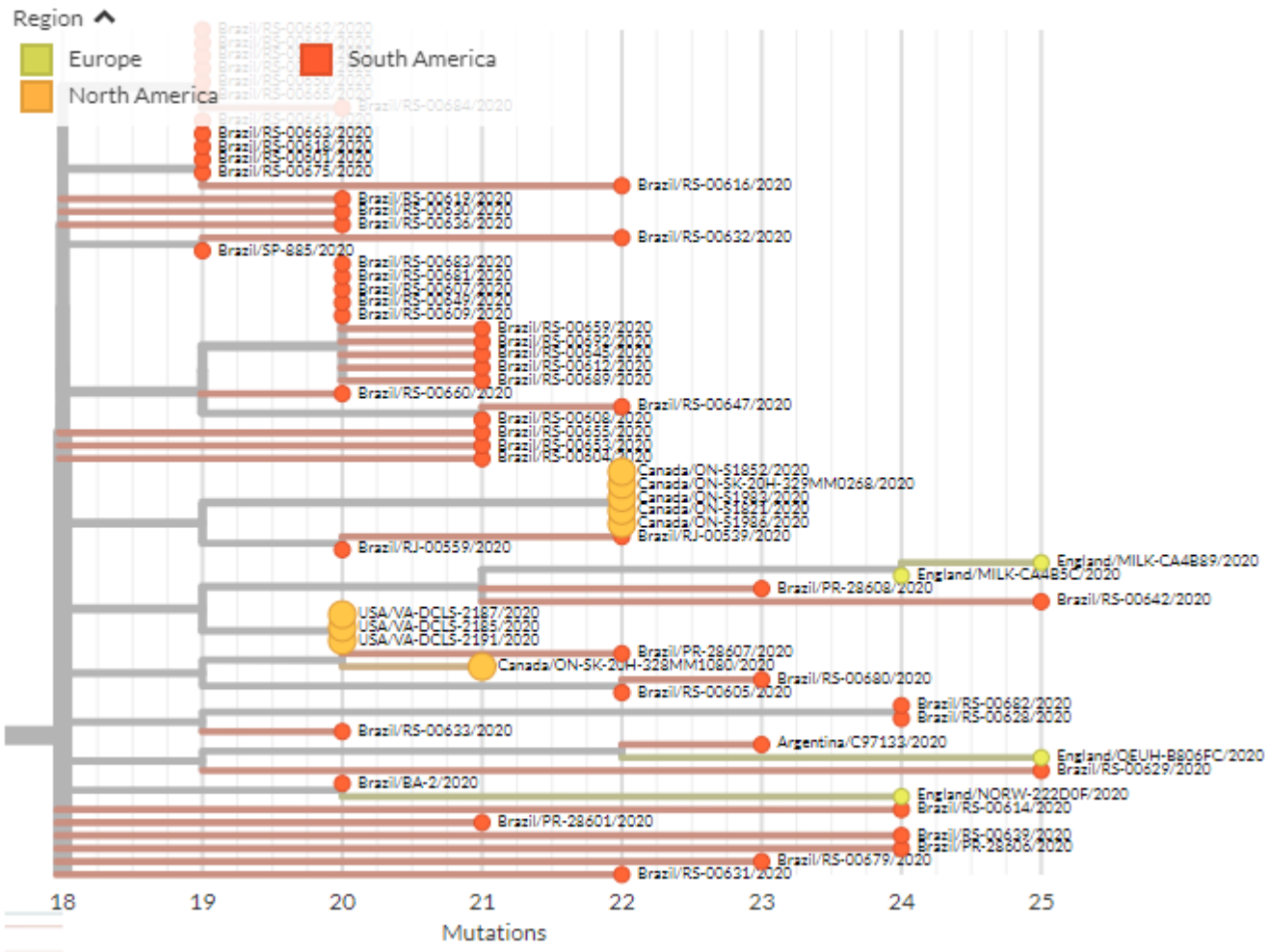
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https://t.co/D3AE3V9GOw



Importantly, the clusters in the USA & Canada are identical (though each country also has an additional imports), so they may be from a group of travellers returning, rather than local transmission (left pic). They also date from Nov - so not recent (right pic).

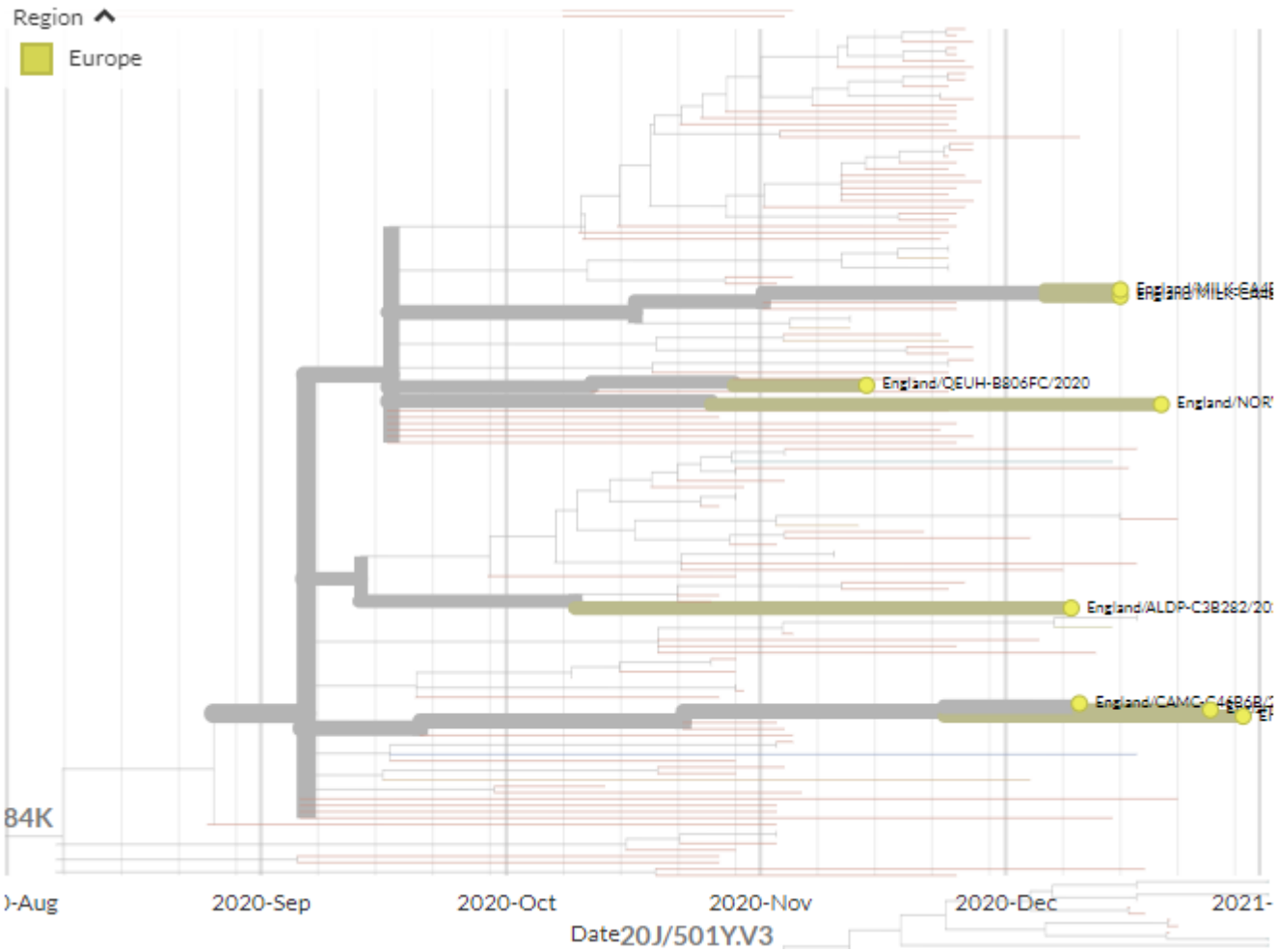
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We can see 8 UK sequences in the 20B/S.484K cluster. There are 2 clusters, but neither are identical. They could be from a common exposure (same part of Brazil, same travel group), or possibly be local transmission. These samples are from Nov & Dec.

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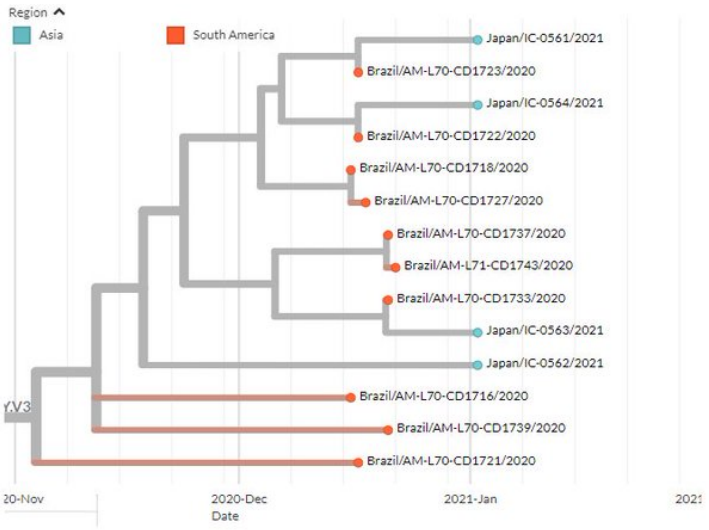
https://t.co/w5oISsCFYb



If we look at 20J/501Y.V3, we can see that sequences only are found in Brazil and Japan (known travel to Brazil), but no other countries.

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https://t.co/4IzibcXzmW





Hopefully, this thread helps distinguish what the '2 variants' are that are circulating in Brazil, and from which there have been samples detected in the UK.

And, I hope it shows how phylogenetics can help us 'tell viruses apart' & follow them as they move & change!

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To add: why are scientists concerned about these variants circulating primarily in Brazil?

@BillHanage write a fantastic thread here:

11/10

https://t.co/qvF92BV7CZ

> I\u2019ve thought long and hard about this. There is a constellation of circumstantial evidence around the most recently identified variant P.1, and what has been happening in Manaus, Brazil which makes me very seriously concerned. A thread \U0001f9f5
>
> — Bill Hanage (@BillHanage) January 15, 2021