Twitter Thread by Theo Sanderson

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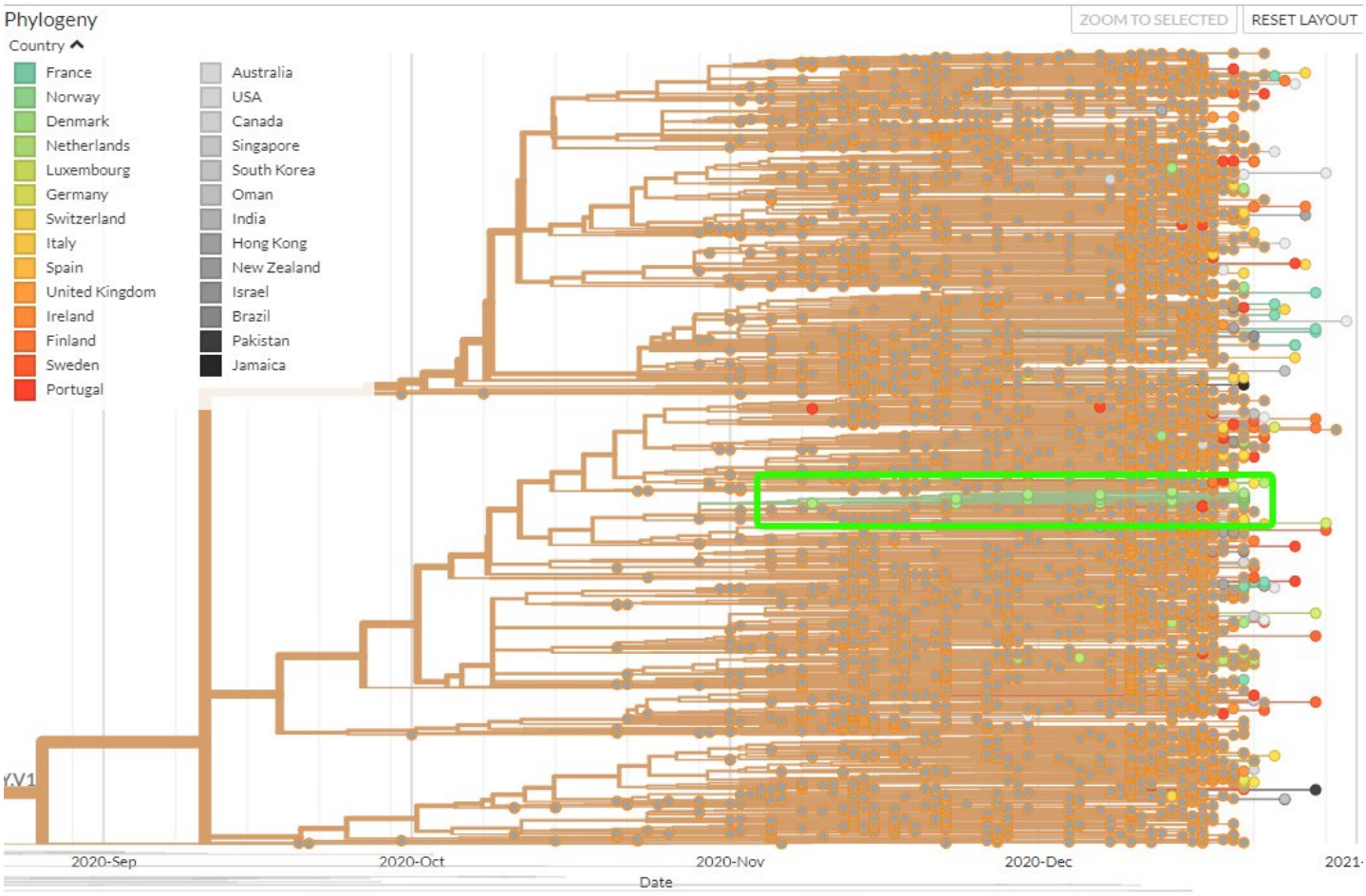
1/ Some people are looking at this map and saying: "it must have come from Europe". Here are a few reasons why that is unlikely.

> The spread of B.1.1.7 through England over November and December, with London inset at top-right. pic.twitter.com/fVfL0xijcx
>
> — Theo Sanderson (@theosanderson) January 8, 2021

2/ Though B.1.1.7 was especially prominent in Kent, the 2nd sequence ever sequenced was found in London, a day after the 1st. Due to superspreading it isn't possible to pinpoint for sure whether it originated in Kent or London. (If London, there's no argument for the continent).

3/ And suppose we did believe the new variant was introduced from abroad. Would we expect it to be introduced by sea or air? Far more arrivals to the UK in August/September occurred by air compared to sea.

4/ Genetic evidence. Suppose this highly transmissible variant had arisen in some other country, and made its way through France to the UK. It would also have left lots of descendants in Europe. We can look at a genetic tree of sequences and see that that is not the case.



5/ The grey/orange sequences here are UK sequences and the others are from an array of other countries. Specifically I've highlighted a lineage in Denmark which represents spread from a single introduction to Denmark, ultimately from the UK.

6/ Given there is evidence of spread from a single point in the UK, if the UK was not the source of the outbreak we'd expect all these UK grey sequences to group together, like these Danish sequences do.

7/ We'd expect to see at least some European "outgroups", looking like more distant relations on the family tree. But we don't.

8/ You can explore the tree more at https://t.co/XpB0fPkgo1

9/ One doesn't even necessarily need to invoke these phylogenetic arguments. We've seen how quickly this strain has taken over in the UK. We know it has not yet taken over in France. If it had existed in France before the UK, it would be the dominant strain there already.