# NERVTAG/SPI-M Extraordinary meeting on

# SARS-CoV-2 variant of concern 202012/01 (variant B.1.1.7)

## Note of meeting

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| **Date & Location:** 12:00 – 13.30 21 December 2020 - Via telecon only |
| **In attendance:**<br>Chair: Peter Horby (PH)<br><br>NERVTAG Members: Andrew Hayward (AH), Julian Hiscox (JHi), John Edmunds (JE), Neil Ferguson (NF), Wendy Barclay (WB), Wei Shen Lim (WSL), Cariad Evans (CE)<br><br>SPI-M: Angela McLean (AM), Graham Medley (GM), Julia Gog (JG), Tom Irving (TI), Daniela DeAngelis (DD), Mark Woodhouse (MW), Matt Keeling (MK)<br><br>Secretariat: Ruth Parry, Elaine Stanford, Stephen Barnard<br><br>PHE: Gavin Dabrera (GD), Meera Chand (MCh), Susan Hopkins (SH)<br><br>DHSC Observers: Sadia Dorsani (SD), Jonathan Van Tam (JVT), Luke Collet-Fenson (LC-F), Jenny Harries (JHa), Emma Stapley (ES), Paul Allen (PA)<br><br>Invited experts/ presenters: COG UK: Andrew Rambaut (AR), LSHTM: Nicholas Davies (ND), University of Cambridge: Ravi Gupta (RG)<br><br>SAGE/SAGE Secretariat: Patrick Vallance (PV), Stuart Wainwright (SWa), Simon Whitfield (SWh), Carl Mayers (CM)<br><br>C-19 Task force: Nick Allan (NA), Ben Cropper (BC)<br><br>Cabinet Office: Emma Payne (EP), Rob Harrison (RH)<br><br>DAs: Wales, Fliss Bennee (FB), Rob Orford (RO), Svcotland: David Crossman (DC), Northern Ireland: Ian Young (IY)<br><br>No 10 Advisors: Imran Shafi (IS), Ben Warner (BW) |
| **Apologies:** none |

**Brief meeting summary - signed off by NERVTAG Chair**

- The committee reviewed current data on SARS-CoV-2 virus variant B.1.1.7 also termed variant of concern 202012/01 and previously known as variant under investigation 202012/01.

- Public Health England (PHE) presented data on the frequency and geographic distribution of samples that were PCR positive for SARS-CoV-2 on the N and OR targets but negative on the S-gene target. At the Milton Keynes laboratory, 97% of S-gene failures that have been sequenced are variant B.1.1.7. Therefore, S-gene failure is used as proxy for variant B.1.1.7.

- The PHE data show that S-gene failures are comprising an increasing proportion of positives over the last 3 weeks and is now dominant in London and the East of England. It is also spreading to the South East and South West.

- Three independent analyses were presented of the growth rate of B.1.1.7 and S-gene drop-out viruses.

- University of Edinburgh (Andrew Rambaut) used a phylogenetic method to estimate exponential growth rates from SARS-CoV-2 genomes sequences from Kent and London and estimated the R-value for B.1.1.7 to be 1.57 [1.45, 1.69] or 1.72 [1.55, 1.95] depending on the time window used for analysis.

- Imperial College London (Neil Ferguson) used several methods:

    - Logistic growth model for the frequency of the variant among all sequences indicates B.1.1.7 grows +71% (95%CI: 67%-75%) faster per generation (6.5 days) than other variants

    - A regression model predicting the reproduction number of the virus by week and NHS STP region estimated that lineage B.1.1.7 had a reproduction number 0.39 (95% CI:0.24:0.55) higher than non-variant lineages during the period of the second lockdown in England

    - Using s-gene failure as a proxy for membership in lineage B.1.1.7, the mean ratio of weekly growth factors at NHS STP region level for variant vs non-variant viruses was 1.47 (95% CI: 1.34-1.59) during a 5 week period spanning the second English lockdown – indicating the virus had a 47% {95% CI: 34%-59%) higher transmissibility.

    - Using s-gene failure as a proxy for membership in lineage B.1.1.7, the mean difference in weekly growth factors (which approximate reproduction numbers) at NHS STP region level for variant vs non-variant viruses was 0.45 (95% CI: 0.28-0.60) during a 5 week period spanning the second English lockdown – indicating the virus had a 47% {95% CI: 34%-59%) transmission fitness advantage

- London School of Hygiene and Tropical Medicine (Nicholas Davies & John Edmunds) fitted a two-strain model of SARS-CoV-2 transmission to observed hospital admissions, hospital bed occupancy, deaths, PCR prevalence, seroprevalence, and frequency of the novel SARS-CoV-2 variant B.1.1.7-N501Y in the South East, East of England, and London regions of England. It was estimated that the novel variant is 56% (95% credible interval across three NHS England regions 50-74%) more transmissible than other circulating strains of SARS-CoV-2.

- All three analyses were consistent in estimating a faster growth rate of B.1.1.7 compared to other SARS-CoV-2 virus variants circulating in England.

- There is some uncertainty about the magnitude of the additional growth rate of B.1.1.7 compared to other SARS-CoV-2 virus variants, but all estimates are compatible with a meaningful increase.

- **The committee therefore has high confidence that B.1.1.7 can spread faster than other SARS-CoV-2 virus variants currently circulating in the UK.**

- The underlying cause of that faster spread is, as yet unclear. A range of factors including the time it takes for infected people to become infectious, the amount of virus they then shed and the ability of that virus to bind to host cells are all possible contributors to the underlying observation that the new variant spreads faster.

- The is considerable uncertainty around other aspects of variant B.1.1.7 including the age distribution of cases and the severity of illness. Greater clarity on these issues should be available in the next few days. The lag from infections to hospitalisations and deaths means that it will take some time before there can be confidence around disease severity associated with infection with B.1.1.7.

- Preliminary analysis by Imperial College suggests that in children aged <15 years there may be an increase in transmission of variant B.1.1.7 compared to other variants. Modelling by LSHTM suggests that with this variant, school closure may be needed to maintain R below 1. **However, these data are preliminary, and more work is required before any firm conclusions can be reached.**

- There are currently no data on the ability of serum from patients who have recovered from COVID-19 or have been vaccinated against SARS-CoV-2 to neutralise variant B.1.1.7. This work is ongoing but will not be available for around two weeks.

- The committee supported ongoing urgent efforts to establish the geographic extent of B1.1.7 variant in other parts of the UK. There was particular need to establish if the increase in transmission in parts of Wales is related to variant B.1.1.7.