Collection

New SARS-CoV-2 variant

Information on the new variant of the SARS-CoV-2 virus.

Published 21 December 2020
Last updated 29 December 2020 — see all updates
From: Public Health England

Contents

Data from Whole Genome Sequencing, epidemiology and modelling suggest the new variant 'VUI – 202012/01' (the first Variant Under Investigation in December 2020) transmits more easily than other strains.

We currently have no evidence that the variant is more likely to cause severe disease or mortality, but we are continuing investigations to understand this better.

The way to control this virus is the same, whatever the variant. It will not spread if we avoid close contact with others. Wash your hands, wear a mask, keep your distance from others, and reduce your social contacts.

Guidance and information

COVID-19 (SARS-CoV-2): information about the new virus variant

New SARS-COV-2 variant: information and risk assessment – slide set

Central Alerting System (CAS) alert

New variant clustering in households analysis (ONS)

Investigation of novel SARS-COV-2 variant: Variant of Concern 202012/01
28 December 2020 Guidance

SARS-CoV-2 lateral flow antigen tests: evaluation of VUI-202012/01
23 December 2020 Guidance

News and announcements

NERVTAG statements on COVID-19 (SARS-CoV-2) (updated regularly)

PHE investigating a novel variant of COVID-19
14 December 2020, News story

Rapid evaluation confirms lateral flow devices effective in detecting new COVID-19 variant
23 December, Press release

Confirmed cases of COVID-19 variant from South Africa identified in UK
23 December, News story

Statement from Chief Medical Officer, Professor Chris Whitty, about new strain of COVID-19
19 December 2020 Press release

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Investigation of novel SARS-COV-2 variant: Variant of Concern 202012/01
Chief Medical Officer's annual report 2020: health trends and variation in England
NERVTAG: Certifying COVID-19 immunity, 19 November 2020
The Exercise of Commissioning Functions by the NHS Commissioning Board (Coronavirus) Directions 2020
NERVTAG: Is there evidence for genetic change in SARS-CoV-2 and if so, do mutations affect virus phenotype? - 30 September 2020

NERVTAG meeting on SARS-CoV-2 variant under investigation VUI-202012/01

Date & Location of meeting: 11:00 – 13.00 18 December 2020 - Via telecon only
In attendance: Chair: Peter Horby (PH) NERVTAG Members: Peter Openshaw (PO), Andrew Hayward (AH), Wei Shen Lim (WSL) Julian Hiscox (J Hi), John Edmunds (JE), Neil Ferguson (NF), Robert Dingwall (RD), Muge Cevik (MC), Wendy Barclay (WB), James Rubin (JR), David Connell (DK), Jim McMenamin (JMM), Calum Semple (CSm), Cariad Evans (CE), NERVTAG Secretariat: Ruth Parry PHE Observers: Meera Chand (MCh), Maria Zambon (MZ) DHSC Observers: Sadia Dorsani (SD), Ursula Wells (UW), Jonathan Van Tam (JVT)
Apologies: Chloe Sellwood (CSe), Ben Killingley (BK)

Brief summary of NERVTAG opinion - signed off by Chair.

- The committee received and considered three documents:
    - The PHE document 'New evidence on VUI-202012/01 dated 18 December
    - Ct monitoring data from ONS/Oxford University COVID-19 Infection Survey
    - Bonsall paper: Early analysis of a potential link between viral load and the N501Y mutation in the SARS-CoV-2 spike protein
- Four analytic approaches were reviewed regarding the transmissibility of VUI-202012/01
    - Growth rate from genomic data: which suggest a growth rate of VUI-202012/01 that that is 71% (95%CI: 67%-75%) higher than other variants.
    - Studies of correlation between R-values and detection of the variant: which suggest an absolute increase in the R-value of between 0.39 to 0.93.
    - PCR ct values: which suggest a decrease of ct value of around 2 associated with the new variant.
    - Viral load inferred from number of unique genome reads: which suggests 0.5 increase in median log10 inferred viral load in Y501 versus N501.
- It was noted that variations in observed ct values can change with epidemiology since the stage of illness at which infection is detected can vary with incidence of cases, awareness of transmission, and the availability of tests.
- It was noted that VUI-202012/01 can be challenging to sequence so estimates of frequency of this variant may be underestimates.
- It was noted that whilst previous variants have successfully emerged in periods of low prevalence without clear evidence of having a selective advantage, the emergence and subsequent dominance of VUI-202012/01 in a period of relatively high prevalence suggests VUI-202012/01 does have a selective advantage over other variants.
- It was noted that VUI-202012/01 has demonstrated exponential growth during a period when national lockdown measures were in place.
- **In summary, NERVTAG has moderate confidence that VUI-202012/01 demonstrates a substantial increase in transmissibility compared to other variants.**
- NERVTAG concluded that there are currently insufficient data to draw any conclusion on:
    - Underlying mechanism of increased transmissibility (e.g. increased viral load, tissue distribution of virus replication, serial interval etc)
    - The age distribution of cases
    - Disease severity: 4 deaths in around 1000 cases have been identified but further

work is needed to compare this fatality rate with comparable data sets.

    - Antigenic escape. The location of the mutations in the receptor binding domain of the spike glycoprotein raises the possibility that this variant is antigenically distinct from prior variants. Four probable reinfections have been identified amongst 915 subjects with this variant but further work is needed to compare this reinfection rate with comparable data sets.

- The committee discussed the geographic extent of spread of the variant:
    - Within the UK, the variant is concentrated in the London, South East and East of England but has been detected in various parts of the UK.
    - Few cases of this variant have been reported internationally but one confirmed export from the UK to Australia has been reported. It was noted that other countries have lower sequencing capability than the UK.
- NERVTAG endorsed the actions proposed by PHE and in addition noted that:
    - Better comparative data on reinfection, readmission and case fatality rates will be available next week.
    - Better data on the age distribution of infections with this variant will be available next week.
    - In vitro data on the ability of convalescent and post-immunisation sera to neutralise this variant will take at least a further week.
- Work is ongoing to evaluate the ability of Lateral Flow Devices to detect VUI-202012/01.
- **NERVTAG recommends that a joint NERVTAG-SPI-M subgroup of SAGE is convened to provide further advice on risk and risk mitigation measures for VUI-202012/01.**

New evidence on VUI-202012/01 and review of the public health risk assessment

NOVEL VARIANT INCIDENT MANAGEMENT TEAM

PUBLIC HEALTH ENGLAND WITH IMPERIAL COLLEGE, THE UNIVERSITY OF EDINBURGH, THE UNIVERSITY OF BIRMINGHAM AND THE WELLCOME SANGER INSTITUTE

Update on the submission of 11/12/20

New information:

1. Investigation of S gene target failure cases and new epidemiology data
2. Modelling on transmissibility
3. Proposed risk assessment

NERVTAG is asked to

- Note the new surveillance information using diagnostic PCR results
- Review the modelling findings
- Review and agree the risk assessment, specifically considering
  - Can the variant now be said to have increased transmissibility with moderate confidence?
  - Should impact on diagnostics be included in the risk assessment framework?

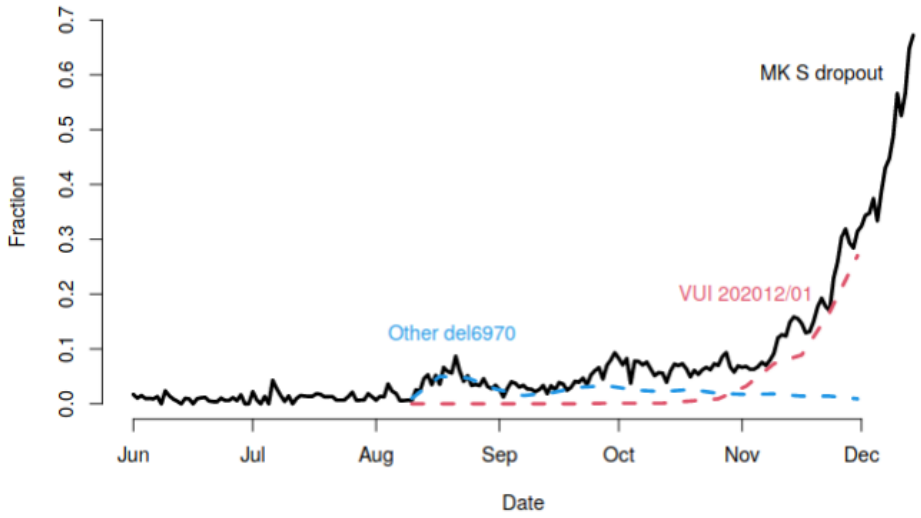
Data correct as of 15/12/2020

Analysis of cases with S gene target failure (SGTF) in diagnostic assays

- S-gene target failure (SGTF) in an assay commonly used in the LL has been shown through sequencing to be associated with deletions at position 69 and 70 (University of Birmingham)
- Deletion at 69/70 is found at the VUI but also in other lineages
- As of 16 Nov, of those SGTFs sequenced from the lighthouse laboratories, 87% were the VUI, rising to 97% in the latest genomic data in early December.
- These proportions will continue to be monitored

SGTF will be used as a proxy indicator for surveillance and trend analysis of the VUI from Monday 21 December (and retrospectively from 16 November onwards)

S gene target failure (provided by the Wellcome Sanger Institute)

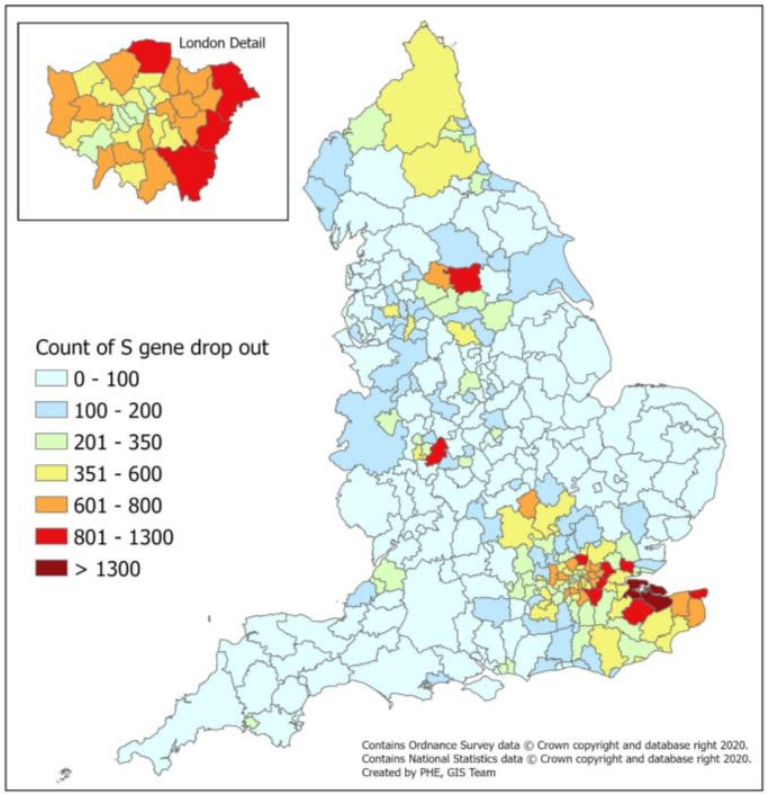


Fraction of all Milton Keynes Lighthouse Laboratory which are SGTF, and fraction of all sequenced samples which are the VUI lineage, or other lineages including the same deletion.

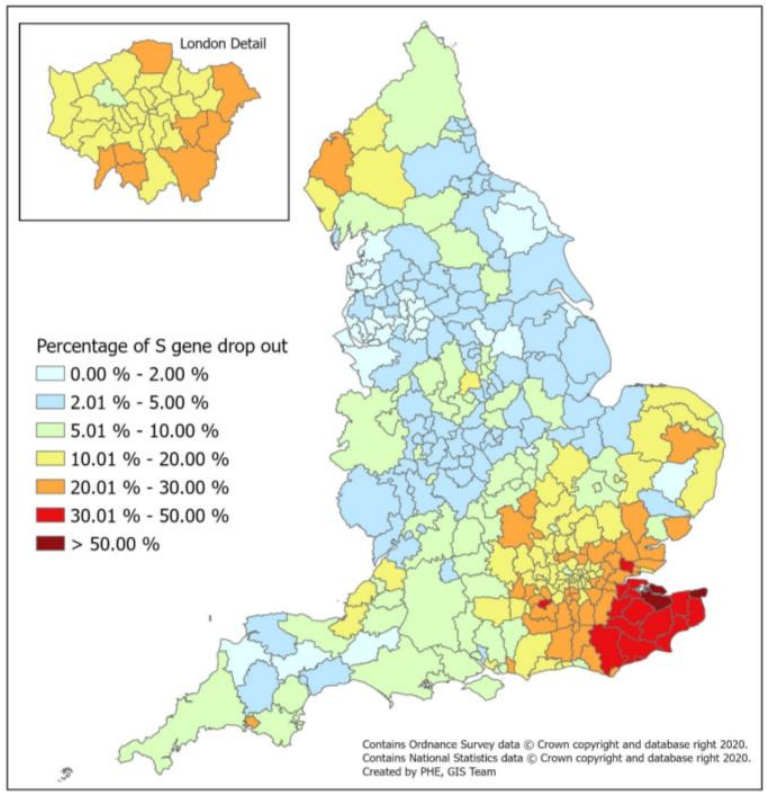
The proportion of cases that are SGTF at the Milton Keynes Lighthouse Laboratory has increased sharply. Of all pillar 2 samples that are sequenced, the proportion that are the VUI has shown the same trajectory, whereas other lineages with this deletion have stayed constant frequency.

Geographical distribution of S-gene target failure cases (n=67098 from 3 lighthouse laboratories)

Number of confirmed cases of S gene target failure reported by MK, AP and GG Light house labs (1 September – 13 December)



Proportion (%) of S-gene target failure cases in comparison to all COVID-confirmed cases from MK AP and GG Lighthouse labs (1 September – 13 December)



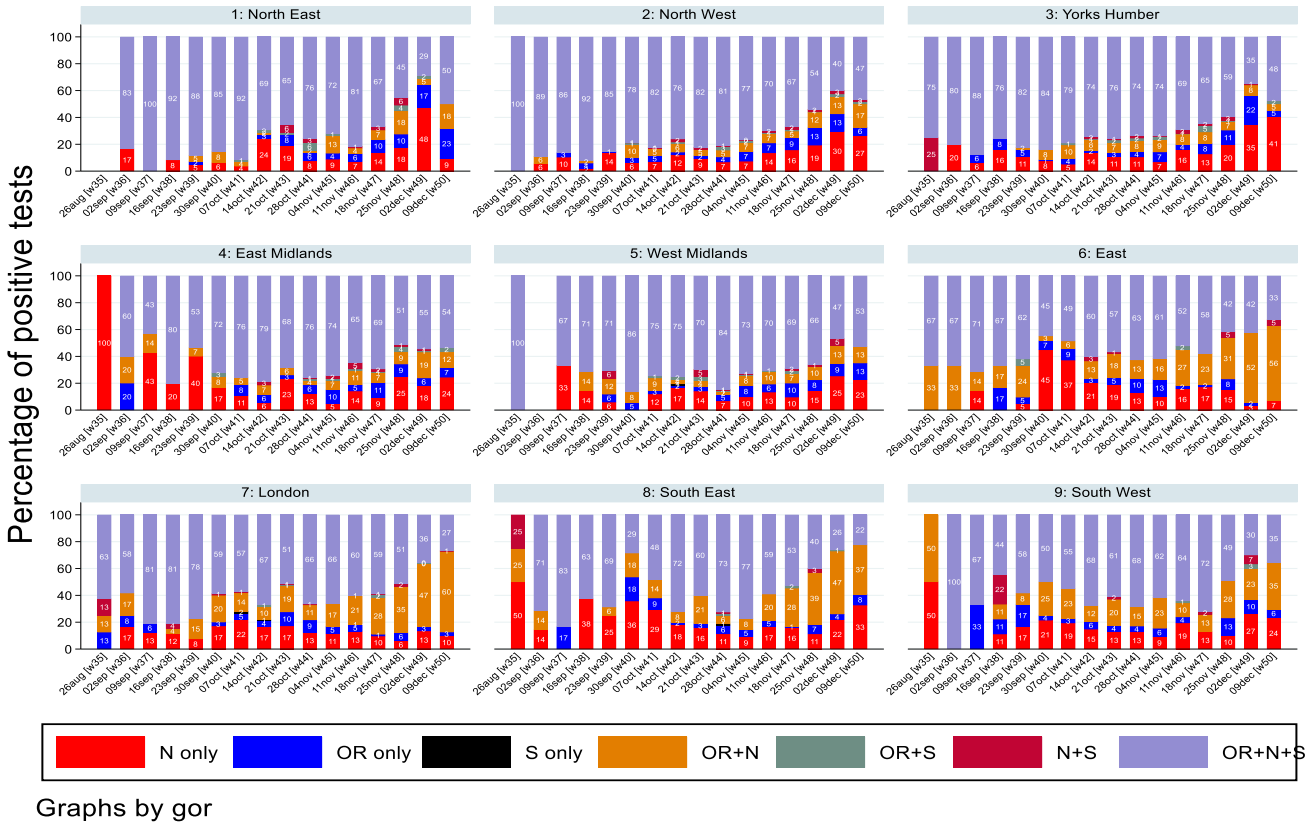
England only

5.4a

England Ad hoc (5.4) Ct Monitoring (ONS SURVEY: SHARED WITH PERMISSION)

Infectiousness within households – initial analysis

- From monitoring patterns in which genes are found to be present in the PCR test we can identify where cases of the new variant are likely to be increasing. This is because the new variant has genetic changes in the S gene, meaning that it is no longer detected by the current test.
- Samples that would previously have been positive on all three genes (purple bar on plot) are now positive only on the ORF1ab and N genes (orange bar on plot).
- Evidence suggests that the new variant is comprising an increasing proportion of positives over the last 3 weeks.
- This analysis shows that the new variant is now dominant in London and the East of England. It is also spreading to the South East and South West.
- When monitoring Ct patterns by age, there was no evidence to suggest that OR and N gene positives were more common in certain age groups than others. Whilst there was some variation by age in the whole sample, as well as in London and the East of England, this was compatible with chance.
- This analysis is presented for the whole study period up to 9 December in England regions and the Devolved Administrations on the following slide.



UK confirmed case numbers

*Cases confirmed by sequencing are likely to underrepresent total number of cases

**No new genomics data reported from COG-UK in the last 24 hours

VUI-202012/01 cases identified* (data correct as of 15:00 hrs 16/12/2020).

Total confirmed cases in the UK	New cases	% change
1439	4	<0.01

Total presumptive cases in the UK	New presumptive cases	% change
36	0	0

N501Y cases identified* (data correct as of 15:00 hrs 16/12/2020).

Total confirmed cases in the UK	New cases	% change
550	53	10.7

Four nations

Proposed risk assessment

Risk Assessment

Indicator	Risk assessment framework				Assessment (Confidence*) and rationale
Zoonotic emergence	Animal reservoir identified but no evidence of transmission from animals to humans	Sporadic transmission from animals to humans	Frequent transmission from animals to humans		**NOT APPLICABLE** **No evidence of a zoonotic reservoir at present.**
Transmissibility between humans	No demonstrated person to person transmission	Limited human case clusters	Established human to human transmission, which appears similar to wild type virus	Transmissibility appears greater than the wild type virus	**RED (LOW CONFIDENCE OR MODERATE CONFIDENCE?)** **Preliminary modelling suggests this lineage has a high growth rate, potentially higher than other lineages co-circulating. This is biologically plausible since N501Y is in a position which could affect the receptor binding affinity of spike protein. Additional epidemiological investigations, continued surveillance and phenotypic studies are required to increase the confidence in this finding.**
Infection severity	Evidence of less severe clinical picture or lower infection fatality than from wild type SARS-CoV-2 infections	Similar clinical picture and infection fatality to wild type SARS-CoV-2 infections OR experimental animal data suggesting potential for increased disease severity humans	More severe clinical picture or higher infection fatality than from wild type SARS-CoV-2 infections (limited to specific risk groups)	More severe clinical picture or higher infection fatality than from wild type SARS-CoV-2 infections	**INSUFFICIENT INFORMATION** **There is no systematic data on this at present, and investigations are being urgently undertaken into deaths and hospital admissions amongst cases infected with the variant.**
Susceptibility and immunity – natural infection	Evidence of no antigenic difference from other circulating wild type virus	Structural data suggesting antigenic difference from other circulating wild type virus	Experimental evidence of functional evasion of naturally acquired immunity	Evidence of frequent infection in humans with known prior infection with earlier virus variant.	**AMBER (LOW CONFIDENCE)** **The N501Y variant in the spike receptor binding domain suggests that this variant may be antigenically distinct. There is no neutralisation data from polyclonal sera. The small number of possible reinfections in the variant cluster may support this but comparisons to reinfection rate in other lineages are required. Urgent neutralisation data is required.**
Vaccines	Evidence of no structural or antigenic difference in vaccine targets	Structural data suggesting difference in vaccine target epitopes	Experimental evidence of functional evasion of vaccine derived immunity	Evidence of frequent vaccine failure or decreased effectiveness in humans	**INSUFFIENT INFORMATION** **There is insufficient information to assess the risk of evasion of vaccine derived immunity. Urgent neutralisation data is required.**
Drugs and therapeutics	Evidence of no structural or antigenic difference in therapeutic targets	Structural data suggesting difference in therapeutic target epitopes	Experimental evidence of reduced drug susceptibility	Evidence of frequent drug or therapeutic failure or decreased effectiveness in humans	**INSUFFICIENT INFORMATION** **There is insufficient information to assess the risk of reduced drug susceptibility. Consideration should be given to evaluation.**

VUI-202012/01 Risk assessment part 2

Overall assessment of level and nature of risk, and level of confidence

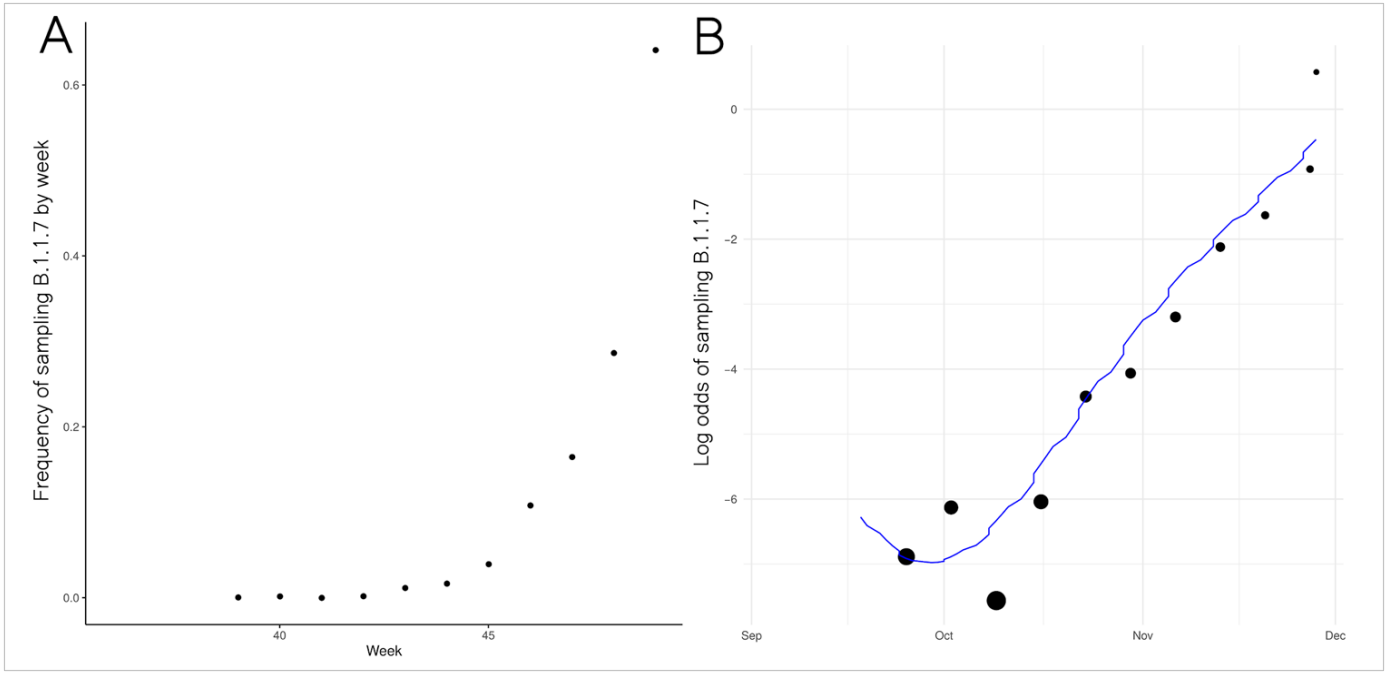
PHE and NERVTAG consider this variant to require urgent investigation. It may be more transmissible than wild type virus, has multiple mutations, and the location of the mutations raises the possibility of antigenic change which could affect natural or vaccine derived immunity. The cluster is spreading rapidly and the lag in genomic data, combined with changes in performance in lighthouse laboratory assays, suggests it may already be widespread. This assessment is based on preliminary data. At present although experts agree, the evidence base is rapidly evolving and the current assessment has low confidence and is likely to change rapidly.

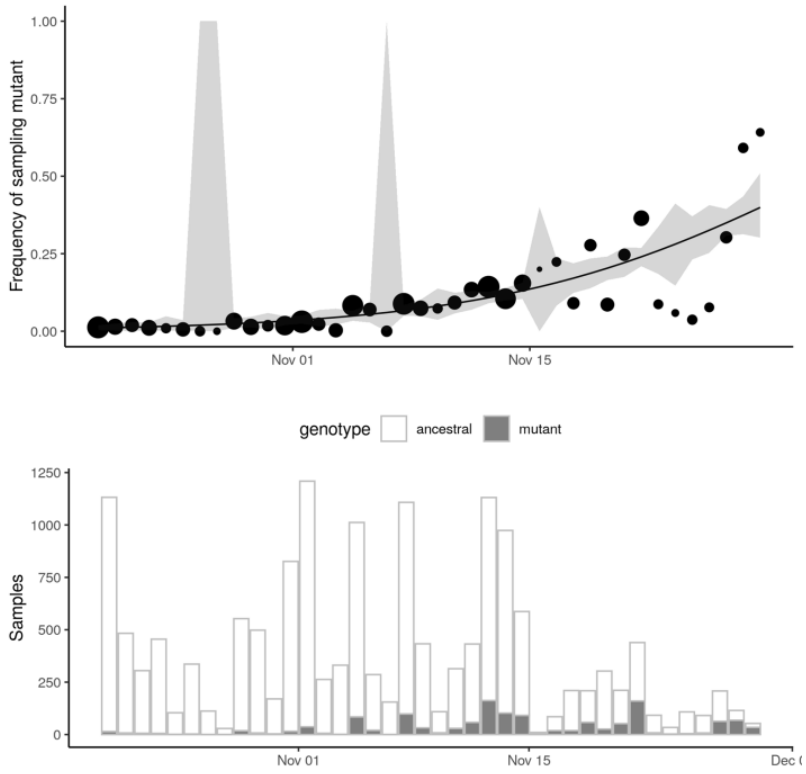
Recommendations of PHE and NERVTAG

1. Further investigations should be undertaken with urgency.
2. Surveillance should be enhanced.
3. Material should be rapidly obtained for viral culture.
4. Fitness of the mutant should be assessed in primary human airway cultures
5. Assessment of antigenicity through virus neutralisation should be made using both wild type virus and pseudovirus technical approaches.
6. Information should be sought on the genomes present in international data in GISAID with variants at position 501
7. Investigation should be undertaken to provide reassurance that Lateral Flow Devices in common use will identify this variant
8. DHSC should consider the need for enhanced control measures to limit the spread of this variant pending the availability of additional information
9. DHSC should consider the communications needed locally, nationally and internationally.

Questions for NERVTAG: Addition of diagnostics to the RA? Low or moderate confidence in increased trasnsmissibility ?

Growth in sample frequency of VUI

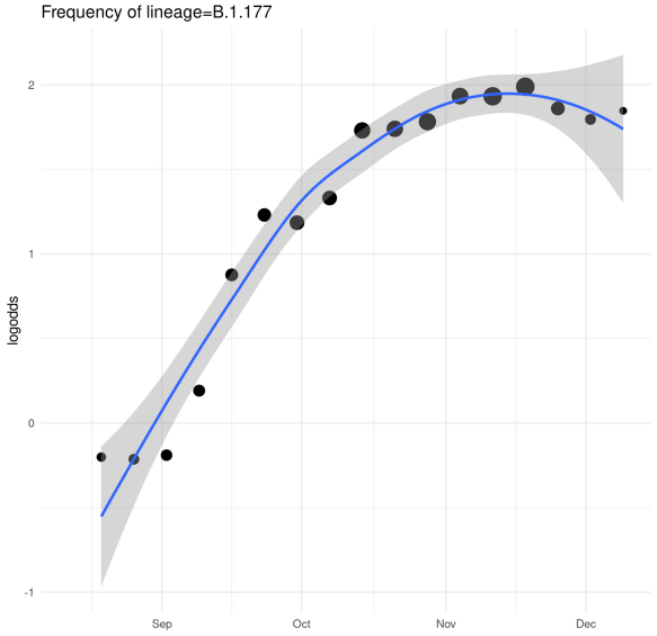




- Frequency of VUI in sequences from Pillar 2 sampling has increased exponentially since late November
- Change in frequency consistent with but not indicative of a constant selective advantage of VUI
- Logistic growth model indicates VUI grows +71% (95%CI: 67%-75%) faster per generation (6.5 days)
    - Limitations: Sample frequency is noisy & overdispersed in ways not captured by this model

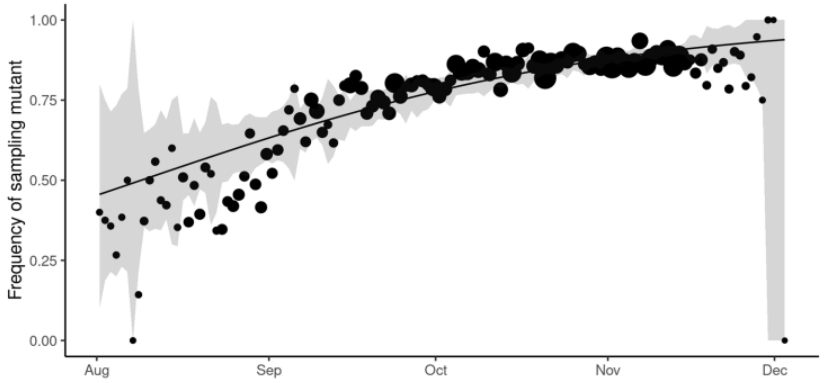
Limitations: Genetic variants can achieve high frequency even if selectively neutral

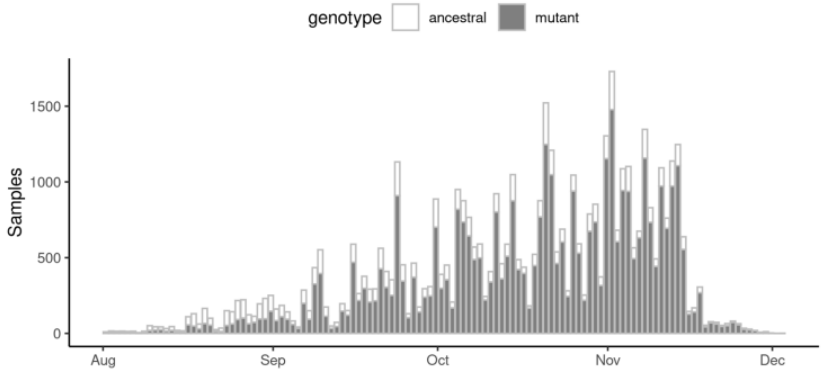
Recent Example: Frequency of B.1.177 lineage in UK with A222V variant, Multiple introductions to UK in August-October 2020

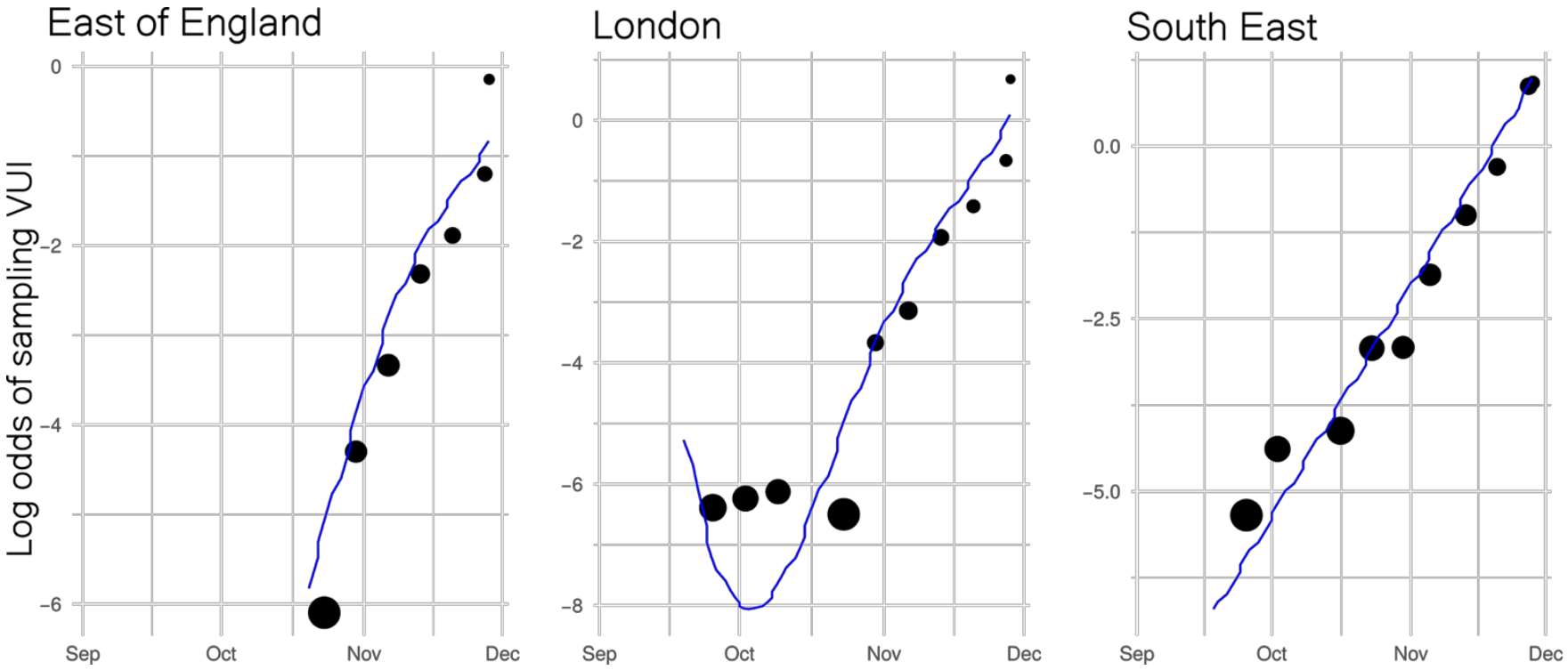


Currently >70% frequency in UK

Initial growth fuelled by holiday travel in Europe. Growth has declined with reduced travel.





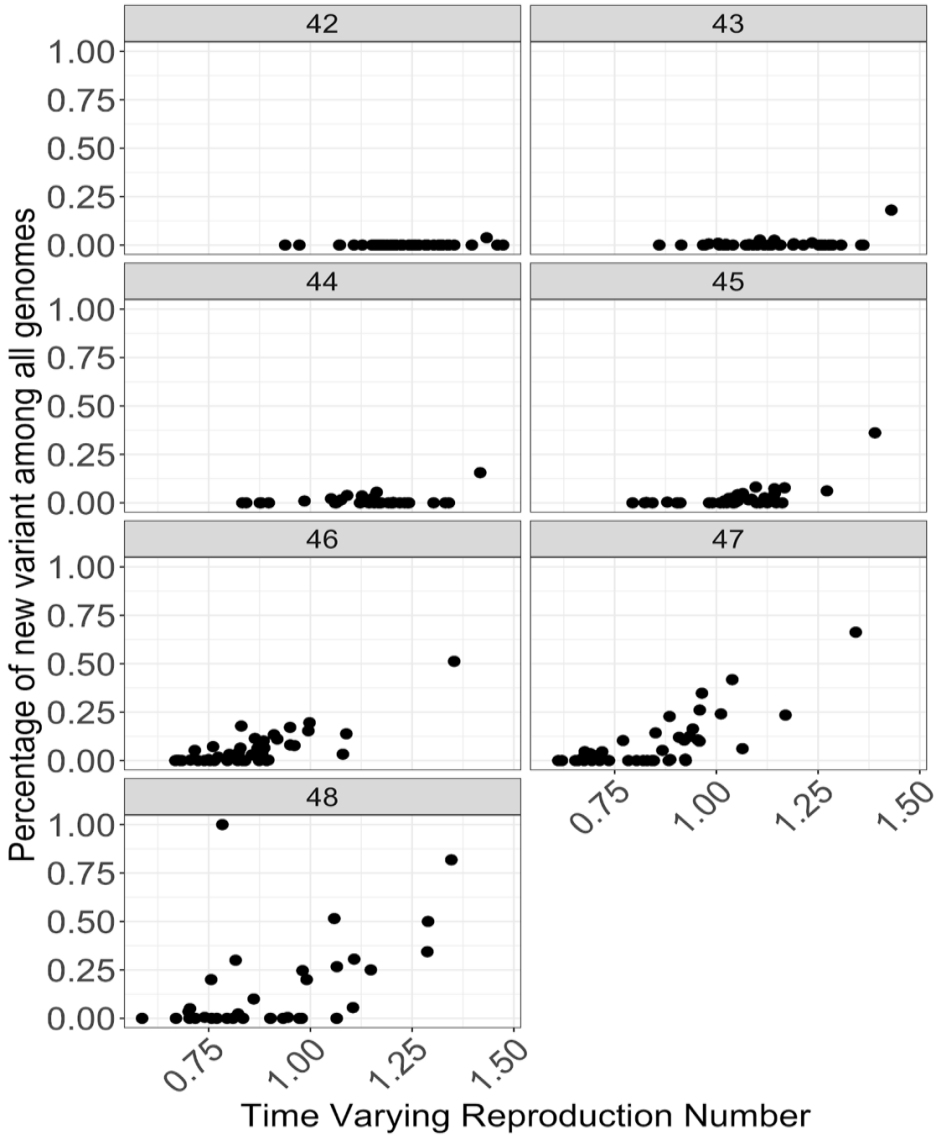


Similar rates of growth observed in different regions. Relative difference in growth rate between B.1.1.7 and other lineages:

- East of England: +72% (95%CI: 62%-82%)
- London: +86% (95%CI: 78%-94%)
- South East: +71% (95%CI: 65%-78%)

Relationship with transmission

- Time varying reproduction number[1] is correlated with the increase in fraction of new variant at many places
- Figure shows relationship between fraction of new variant among all genomes plotted against the time varying reproduction number for each week. Each datapoint is an STP area.



Coalescent phylogenetic estimate

Data
1007 genomes from London and Kent sampled by Pillar 2 from 20-Sep to 30-Nov. A second analysis performed with samples up until 21-Nov to remove potential biases from lag in sequencing and non-representative sampling towards the present.
Analysis
Analysis using BEAST v1.10.4, exponential growth coalescent model, strict molecular clock.

Results - Samples from 20-Sep to 30-Nov:
Growth rate (per year): 31.96 [95% credible interval: 25.53, 38.90]
Doubling time (days): 7.9 [6.5, 9.9]
R: 1.57 [1.45, 1.69]

Results - Samples from 20-Sep to 21-Nov:
Growth rate (per year): 40.43 [95% credible interval: 30.66, 53.21]
Doubling time (days): 6.3 [4.8, 8.3]
R: 1.72 [1.55, 1.95]

Caveats
Lag in sequencing from pillar 2 results in a drop off of sequences towards the end of November -
If this is non-random then this may cause an underestimation of the growth rate.
R estimate assumes a serial interval of 6.5 days

Data

- Sequence of S:N501Y and deletion at 69-70 were used as a proxy for membership in lineage B.1.1.7
- 1451 unique pillar 2 samples collected from Sep 2nd to Nov 29 2020 across 163 local authorities areas in England
- Pillar 2 cases, deaths and new hospital admissions taken from UK dashboard
- Data aggregated by STP regions and week

Methods

- R_t for each STP per week modelled as a weekly random walk process and estimated using a semi-mechanistic Bayesian model from case and death data
(Mishra, et al, medRxiv 2020.11.24.20236661; doi: https://doi.org/10.1101/2020.11.24.20236661)

- Then regress R_t for each STP against the fraction of the new variant, with categorical variables for each STP area and for each week to account for spatiotemporal effects (two variants – unweighted and weighted)

  ➔ Additive model : estimate the exact amount of increase or decrease in R_t by using R_t as response in the linear model

  ➔ Multiplicative model : estimate the relative increase or decrease in R_t by using $\log(R_t)$ as the response variable in the linear model

Results

- Additive model (unweighted): increase in R_t of 0.39 [0.24-0.55]

  ➔ For example, under the additive assumption, an area with an R_t of 0.8 without the new variant would have an R_t of 1.19 [1.04-1.35] if only N501Y was present

- Additive model (weighted): increase in R_t of 0.93 [0.73-1.13]

- Multiplicative model: relative increase in R_t of 48% [27%-74%]

  ➔ For example, under the multiplicative assumption, an area with an R_t of 0.8 without the new variant would have an R_t of 1.18 [1.02-1.40] if only N501Y was present

Limitations and assumptions

- Frequency may be underestimated from genomic data
- Confidence intervals assume independence of the observations, homoscedasticity and normality of the observations
- Spatial correlation has not be taken into consideration
- Population is considered homogeneous and all age bands are considered equally
- No causal relationship established. Only associative effects are estimated

Risk Assessment

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References

[1] A COVID-19 Model for Local Authorities of the United Kingdom
Swapnil Mishra, Jamie Scott, Harrison Zhu, Neil M. Ferguson, Samir Bhatt, Seth Flaxman, Axel Gandy
medRxiv 2020.11.24.20236661; doi: https://doi.org/10.1101/2020.11.24.20236661

Speech

Prime Minister's statement on coronavirus (COVID-19): 19 December 2020

Prime Minister Boris Johnson gave a statement at the coronavirus press conference.

Published 19 December 2020
From: Prime Minister's Office, 10 Downing Street and The Rt Hon Boris Johnson MP

Delivered on: **19 December 2020 (Transcript of the speech, exactly as it was delivered)**

Good afternoon,

I am sorry to report that the situation has deteriorated since I last spoke to you three days ago.

Yesterday afternoon, I was briefed on the latest data showing the virus spreading more rapidly in London, the South East and the East of England than would be expected given the tough restrictions which are already in place.

I also received an explanation for why the virus is spreading more rapidly in these areas. It appears this spread is now being driven by the new variant of the virus, which we first learned about earlier this week.

Our advisory group on New and Emerging Respiratory Virus Threats – NERVTAG – has spent the last few days analysing the new variant.

There is no evidence the variant causes more severe illness or higher mortality, but it does appear to be passed on significantly more easily.

NERVTAG's early analysis suggests the new variant could increase R by 0.4 or greater. Although there is considerable uncertainty, it may be up to 70% more transmissible than the old variant.

This is early data. It is subject to review. It is the best we have at the moment, and we have to act on information as we have it because this is now spreading very fast.

The U.K. has by far the best genomic sequencing ability in the world, which means we are better able to identify new strains like this than any other country.

The Chief Medical Officer last night submitted our findings so far to the World Health Organisation and we will continue to be totally transparent with our global partners.

There is still much we don't know. While we are fairly certain the variant is transmitted more quickly, there is no evidence to suggest that it is more lethal or causes more severe illness. Equally there is no evidence to suggest the vaccine will be any less effective against the new variant.

Our experts will continue their work to improve our understanding of the variant.

So we are learning more about this variant as we go.

But we know enough already to be sure that we must act now.

I met ministers on the Covid Operations Committee last night and again first thing this morning, and Cabinet met at lunchtime to agree the following actions.

First, we will introduce new restrictions in the most affected areas – specifically those parts of London, the South East and the East of England which are currently in tier 3.

These areas will enter a new tier 4, which will be broadly equivalent to the national restrictions which were in place in England in November.

That means:

Residents in those areas must stay at home, apart from limited exemptions set out in law. Non-essential retail, indoor gyms and leisure facilities, and personal care services must close. People must work from home if they can, but may travel to work if this is not possible, for example in the construction and manufacturing sectors. People should not enter or leave tier 4 areas, and tier 4 residents must not stay overnight away from home. Individuals can only meet one person from another household in an outdoor public space.

Unlike the November national restrictions, communal worship can continue to take place in tier 4 areas.

These measures will take effect from tomorrow morning.

All tiers will continue to be regularly reviewed in line with the approach previously set out, with the next formal review point taking place on 30 December.

Second, we are issuing new advice on travel.

Although the new variant is concentrated in tier 4 areas, it is nonetheless present at lower levels around the country.

We are asking everyone, in all tiers, to stay local.

People should carefully consider whether they need to travel abroad and follow the rules in their tier.

Those in tier 4 areas will not be permitted to travel abroad apart from limited exceptions, such as for work purposes.

Third, we must, I am afraid, look again at Christmas.

As Prime Minister, it is my duty to take the difficult decisions, to do what is right to protect the people of this country.

Given the early evidence we have on this new variant of the virus, and the potential risk it poses, it is with a heavy heart that I must tell you we cannot continue with Christmas as planned.

In England, those living in tier 4 areas should not mix with anyone outside their own household at Christmas, though support bubbles will remain in place for those at particular risk of loneliness or isolation.

Across the rest of the country, the Christmas rules allowing up to three households to meet will now be limited to Christmas Day only, rather than the five days as previously set out.

As before, there will be no relaxation on 31 December, so people must not break the rules at New Year.

I know how much emotion people invest in this time of year, and how important it is for grandparents to see their grandchildren, and for families to be together.

So I know how disappointing this will be, but we have said throughout this pandemic that we must and we will be guided by the science.

When the science changes, we must change our response.

When the virus changes its method of attack, we must change our method of defence.

As your Prime Minister, I sincerely believe there is no alternative open to me. Without action, the evidence suggests infections would soar, hospitals would become overwhelmed and many thousands more would lose their lives.

I want to stress we are not alone in this fight – many of our European friends and neighbours are being forced to take similar action.

We are working closely with the devolved administrations to protect people in every part of the UK.

Of course there is now hope – real hope – that we will soon be rid of this virus.

That prospect is growing with every day that passes and every vaccine dose administered.

The UK was the first country in the western world to start using a clinically approve vaccine.

So please, if the NHS contacts you then get your vaccine – and join the 350,000 people across the UK who have already had their first dose.

Yes, Christmas this year will be very different, but we must be realistic.

We are sacrificing our chance to see loved ones this Christmas, so we have a better chance of protecting their lives so we can see them at future Christmases.

As sure as night follows day, we will beat back this virus.

We will defeat it.

And we will reclaim our lives.

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