Public Health England

Protecting and improving the nation's health

# SARS-CoV-2 variants of concern and variants under investigation in England

## Technical briefing 20

6 August 2021

This briefing provides an update on previous briefings up to 23 July 2021

# Contents

# Summary

There are 4 current variants of concern (VOCs) and 10 variants under investigation (VUIs) (Table 1).

This report has been published to continue to share the detailed variant surveillance analyses which contribute to the variant risk assessments and designation of new VOCs and VUIs. The specialist technical briefings contain early data and analysis on emerging variants and findings have a high level of uncertainty.

A new risk assessment for VUI-21JUL-01 (B.1.621) has been published and is available here. There are no updates to the Delta (B.1.617.2) risk assessment this week.

A separate report is published covering routine data on all other VOCs and VUIs.

Principal changes and findings are:

- there are no new VOCs or VUIs since the last briefing
- the proportion of cases sequenced and genotyped remains relatively low but has started to recover as case numbers fall and capacity expands
- Delta variant accounted for approximately 99% of sequenced and 98% genotyped cases from 25 July to 31 July 2021
- PCR cycle threshold (Ct) values from routinely undertaken tests in England show that Ct values (and by inference viral load) are similar between individuals who are unvaccinated and vaccinated.
- the UK Genotype to Phenotype Consortium reports new data relating to VUI-21JUL-01 (B.1.621). There is evidence of reduction in pseudovirus neutralisation by serum from individuals who have been vaccinated or previously infected with Delta

All risk assessments are published separately on the PHE webpage, Investigation of SARS-CoV-2 variants of concern, except for Gamma, which was published within Technical Briefing 7 and Alpha within Technical Briefing 9. As Delta is the dominant variant in the UK, epidemiological data in the weekly surveillance report is also relevant.

# Published information on variants

The collection page gives content on variants, including prior technical briefings. Definitions for variants of concern, variants under investigation, and signals in monitoring are detailed in technical briefing 8. Data on variants not detailed here is published in the variant data update. Variant risk assessments are available in prior technical briefings.

Public Health England (PHE) curated a repository on the 5 March 2021 containing the up-to-date genomic definitions for all VOCs and VUIs. The repository is accessible on GitHub.

World Health Organization (WHO) nomenclature from 31 May 2021 is incorporated. A table incorporating WHO and UK designations with Pango lineages is provided below (Table 1). Following the table, variants are referred to using their WHO designation where this exists and the UK designation where it does not.

Technical briefings are published periodically. From 15 onwards, briefings include variant diagnoses made by whole-genome sequencing and a genotyping PCR test, including the categorisation of sequenced and genotyped variant results and a rules-based decision algorithm (RBDA) to identify variant and mutation (VAM) profiles from genotype assay mutation profiles. Genotyping is used to identify variants Alpha, Beta, Delta, and Gamma. Targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha.

# Part 1: Surveillance overview

## 1.1 Variants under surveillance

Table 1 shows the current VOC, VUI, and variants in monitoring as of 2 August.

**Table 1. Variant lineage and designation as of 4 August 2021**

| WHO nomenclature as of 19 July 2021 | Lineage | Designation | Status | UK or International (not currently detected in UK) |
|---|---|---|---|---|
| Alpha | B.1.1.7 | VOC-20DEC-01 | VOC | UK |
| Beta | B.1.351 | VOC-20DEC-02 | VOC | UK |
| Gamma | P.1 | VOC-21JAN-02 | VOC | UK |
| Delta | B.1.617.2, AY.1, AY.2, and AY.3 | VOC-21APR-02 | VOC | UK |
| Zeta^ | P.2 | VUI-21JAN-01 | VUI | International |
| Eta | B.1.525 | VUI-21FEB-03 | VUI | UK |
| | B.1.1.318 | VUI-21FEB-04 | VUI | UK |
| Theta^ | P.3 | VUI-21MAR-02 | VUI | UK |
| Kappa | B.1.617.1 | VUI-21APR-01 | VUI | UK |
| | B.1.617.3 | VUI-21APR-03 | VUI | UK |
| | AV.1 | VUI-21MAY-01 | VUI | UK |
| | C.36.3 | VUI-21MAY-02 | VUI | UK |
| Lambda | C.37 | VUI-21JUN-01 | VUI | UK |
| | B.1.621 | VUI-21JUL-01 | VUI | UK |
| | B.1.1.7 with E484K | VOC-21FEB-02 | *Monitoring | International |
| Epsilon^ | B.1.427/B.1.429 | | Monitoring | |
| | B.1.1.7 with S494P | | Monitoring | |
| | A.27 | | Monitoring | |
| Iota | B.1.526 | | Monitoring | |
| | B.1.1.7 with Q677H | | Monitoring | |
| | B.1.620 | | Monitoring | |
| | B.1.214.2 | | Monitoring | |

| WHO nomenclature as of 19 July 2021 | Lineage | Designation | Status | UK or International (not currently detected in UK) |
|---|---|---|---|---|
| | R.1 | | Monitoring | |
| | B.1 with 214insQAS | | Monitoring | |
| | AT.1 | | Monitoring | |
| | Lineage A with R346K, T478R and E484K | | Monitoring | |
| | Delta like variant | | Monitoring | |
| | P.1 + N501T and E484Q | | Monitoring | |
| | B.1.629 | | Monitoring | |
| | B.1.619 | | Monitoring | |
| | C.1.2 | | Monitoring | |

Provisionally extinct variants are excluded from this table.

VOCs and VUIs are monitored weekly for observations within the last 12 weeks. If variants have not been detected in the UK within this period, they are moved to international status with continued monitoring. If a VOC or VUI has not been observed in the UK or international datasets within the preceding 12 weeks, it is designated as provisionally extinct, but monitoring remains in place.

VOC-21FEB-02 (B.1.1.7 with E484K) and VUI-21MAR-01 (B.1.324.1 with E484K) have not been observed in the UK or within the international GISAID dataset within the last 12 weeks. These variants are no longer included in the data update.

^Epsilon, Zeta and Theta were de-escalated by ECDC and by WHO.

# 1.2 Sequencing coverage

Sequencing capacity has been maintained, but the proportion of cases sequenced has fallen with increasing case numbers. Figure 1 shows the proportion of cases sequenced over time. Figure 2 shows the proportion of cases sequenced over time by regions. Figure 3 shows the proportion of cases sequenced amongst cases who tested positive while in hospital.

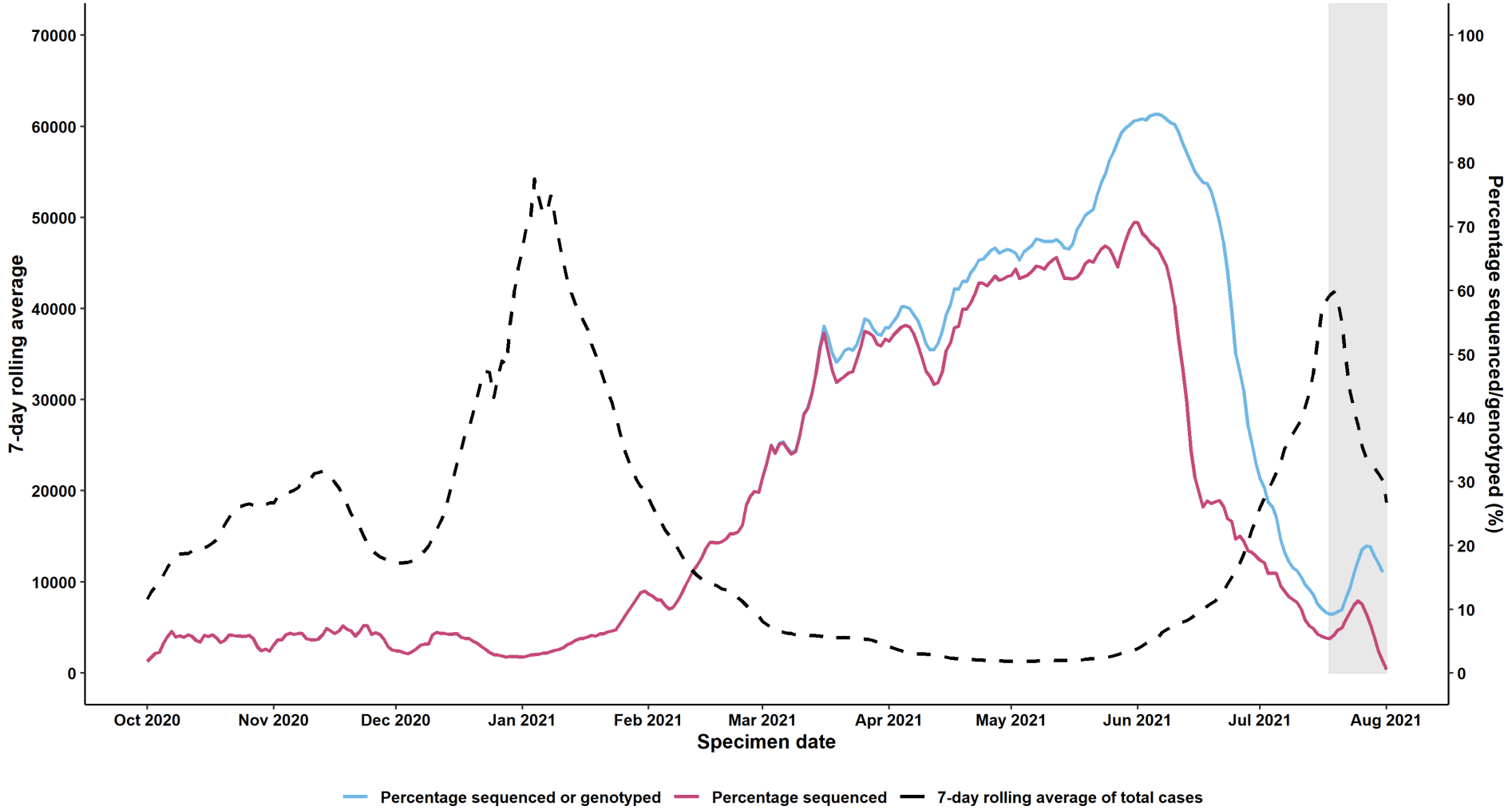
There is a reduction in overall sequencing coverage (Figure 1). Sequencing coverage is slightly higher for cases in hospital (Figure 3). During the current surge period, the sequencing strategy is:

- hospitalised cases and hospital staff
- cases among international travellers
- national core priority studies
- as near random a sample as possible from each region, to the maximum coverage allowed by laboratory capacity

The increase in cases observed in England since the middle of June 2021 has resulted in a lower proportion of samples being sent for whole-genome sequencing (WGS) and genotyping.

**Figure 1. Coverage of sequencing and genotyping over time (1 October 2020 to 2 August 2021)**

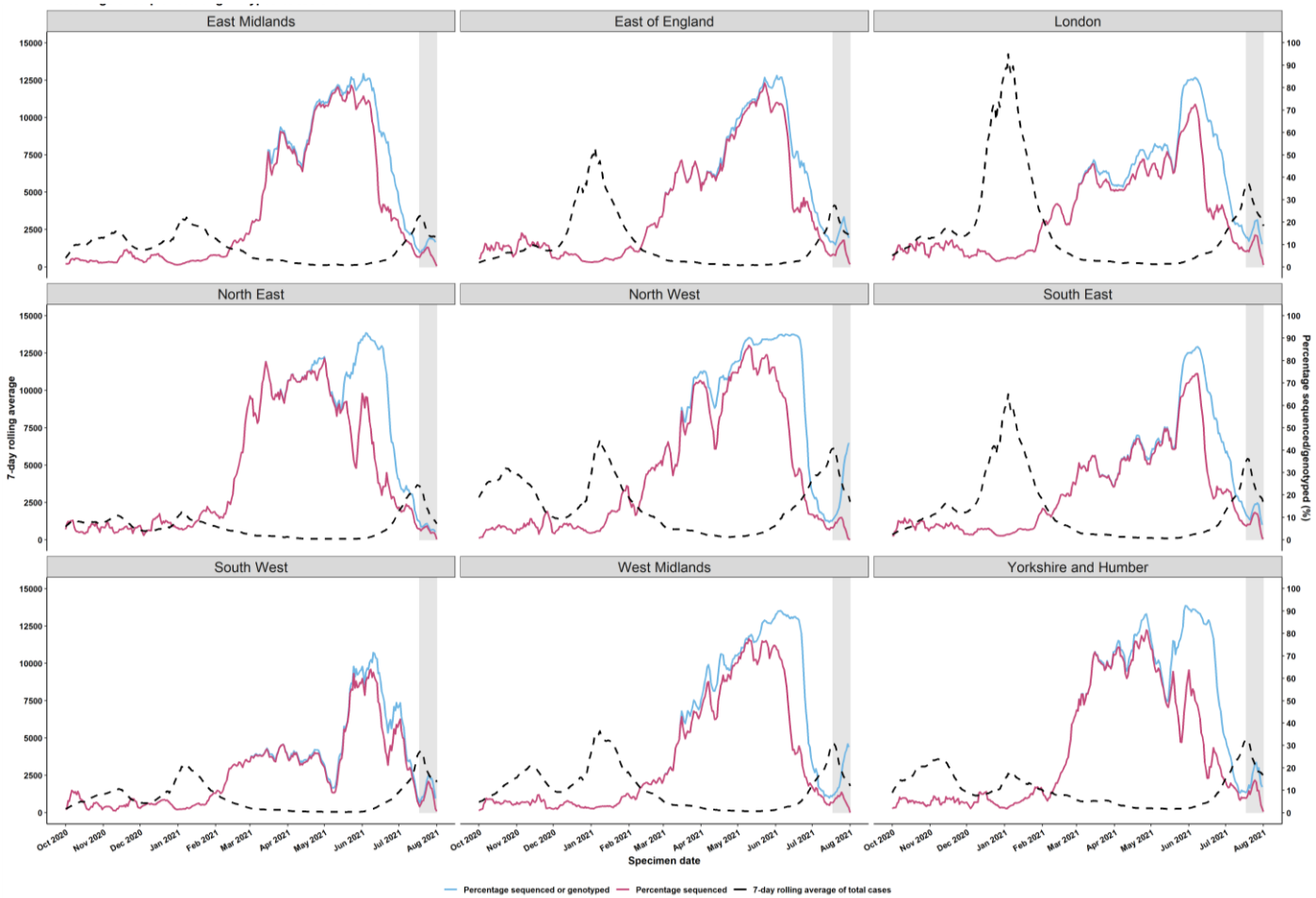
(Find accessible data used in this graph in underlying data)




Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

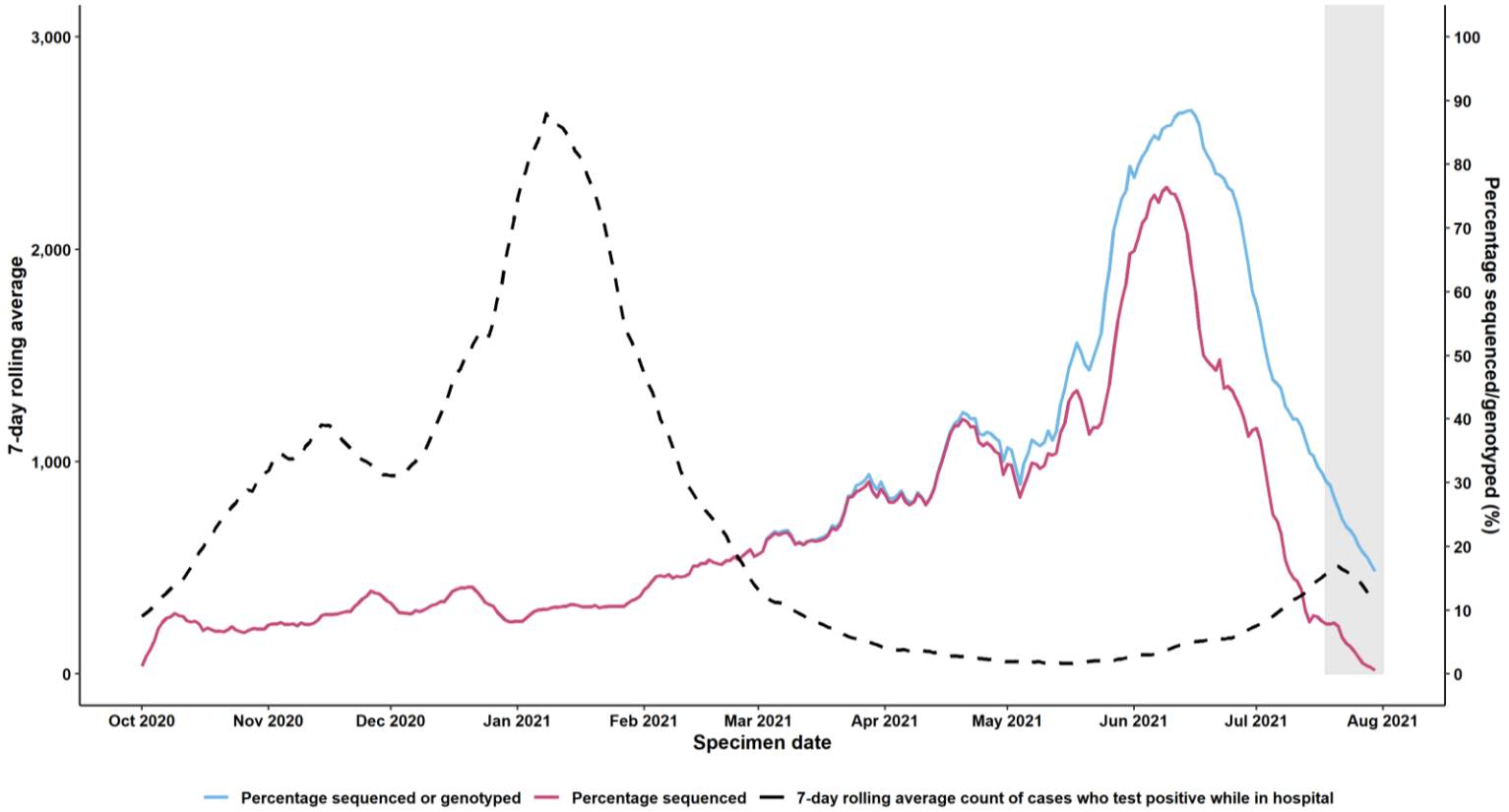
**Figure 2. Coverage of sequencing and genotyping over time by region (1 October 2020 to 2 August 2021)**

(Find accessible data used in this graph in underlying data)




Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.
There were 5493 cases with missing regional data that were excluded.

**Figure 3. Coverage of sequencing and genotyping for cases who test positive in hospital (1 October 2020 to 2 August 2021)**
(Find accessible data used in this graph in underlying data)




Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.
From 14 to 18 June 2021 an operational issue at a sequencing site resulted in a reduction in the number of samples with sequencing data of sufficient quality for variant assignment. There were 19,502 samples reported to PHE as impacted by the incident. PHE has received approximately 10,000 sample identifiers from the list of those affected of which sequencing data has been obtained for approximately 4,300 and genotyping data for 3,300 have a reflex assay result. For approximately 2,400 samples variant assignment is not possible. This issue resulted in a reduction in genome coverage for specimen dates 10 to 15 June 2021 and may impact variant counts in figures and tables for this limited period. The unusable samples were from locations distributed around the UK and the proportions of different variants by region should be correct. In addition, the genotyping results means that this has limited impact in the interpretation of the overall data.

# 1.3 VOC and VUI case numbers, proportion, deaths and case fatality rate

Summary epidemiology on Delta is shown in Table 2 and for each variant is shown in Table 3, case numbers are also updated online. Table 3 shows the number of sequenced, genotyped, and total cases and deaths for each variant. However, case fatality rates are not comparable across variants (see Table 3 footnote). Tables 4 and 5 show the number of cases who visited an NHS Emergency Department, were admitted, and died in any setting. The data is shown from 1 February 2021 onwards to enable comparisons across variants. Figure 4 shows the cumulative number of cases per variant indexed by days since the first report.

Information on attendance to emergency care is derived from the Emergency Care Data Set (ECDS), provided by NHS Digital. These data only show whether a case has attended hospital and was subsequently admitted as an inpatient. The data excludes cases currently in hospital or were directly admitted without first presenting to emergency care.

The crude analysis indicates that the proportion of Delta cases who present to emergency care is greater than that of Alpha, but a more detailed analysis indicates a significantly greater risk of hospitalisation among Delta cases compared to Alpha (see page 50 of Variant Technical Brief 15.

ECDS reporting is lagged as NHS trusts routinely provide monthly data by the 21st of the following month. However, some trusts report daily data, and the linkage between coronavirus (COVID-19) cases and ECDS data is updated twice-weekly.

**Table 2. Confirmed and provisional Delta cases by region as of 2 August 2021**

| Region | Confirmed cases | Provisional cases[1] | Total case number | Proportion of total cases |
|---|---|---|---|---|
| East Midlands | 11,069 | 6,270 | 17,339 | 5.8% |
| East of England | 13,200 | 7,893 | 21,093 | 7.0% |
| London | 25,646 | 18,227 | 43,873 | 14.6% |
| North East | 11,429 | 9,574 | 21,003 | 7.0% |
| North West | 41,693 | 40,354 | 82,047 | 27.3% |
| South East | 19,821 | 12,811 | 32,632 | 10.9% |
| South West | 16,808 | 4,340 | 21,148 | 7.0% |

[1] Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha.

| Region | Confirmed cases | Provisional cases[1] | Total case number | Proportion of total cases |
|---|---|---|---|---|
| West Midlands | 12,418 | 13,583 | 26,001 | 8.7% |
| Yorkshire and Humber | 16,922 | 16,315 | 33,237 | 11.1% |
| Unknown region | 759 | 985 | 1,744 | 0.6% |
| Total | 169,765 | 130,352 | 300,117 | - |

**Table 3. Number of confirmed and provisional cases by variant as of 2 August 2021**

| Variant | Confirmed (sequencing) case number | Provisional (genotyping) case number[2] | Total case number | Proportion of total cases | Deaths |
|---|---|---|---|---|---|
| Alpha | 220,754 | 5,692 | 226,446 | 42.8% | 4,284 |
| Beta | 901 | 71 | 972 | 0.2% | 13 |
| Delta | 169,765 | 130,352 | 300,117 | 56.7% | 743 |
| Eta | 443 | 0 | 443 | 0.1% | 12 |
| Gamma | 193 | 42 | 235 | 0.0% | 0 |
| Kappa | 447 | 0 | 447 | 0.1% | 1 |
| Lambda | 8 | 0 | 8 | 0.0% | 0 |
| Theta | 7 | 0 | 7 | 0.0% | 0 |
| Zeta | 54 | 0 | 54 | 0.0% | 1 |
| VUI-21FEB-01 (A.23.1 with E484K) | 79 | 0 | 79 | 0.0% | 2 |
| VOC-21FEB-02 (B.1.1.7 with E484K) | 45 | 0 | 45 | 0.0% | 1 |
| VUI-21FEB-04 (VUI-21FEB-04) | 295 | 0 | 295 | 0.1% | 1 |
| VUI-21MAR-01 (B1.324.1 with E484K) | 2 | 0 | 2 | 0.0% | 0 |
| VUI-21APR-03 (B.1.617.3) | 13 | 0 | 13 | 0.0% | 0 |

[2] Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha.

| Variant | Confirmed (sequencing) case number | Provisional (genotyping) case number[2] | Total case number | Proportion of total cases | Deaths |
|---|---|---|---|---|---|
| VUI-21MAY-01 (AV.1) | 184 | 0 | 184 | 0.0% | 1 |
| VUI-21MAY-02 (C.36.3) | 142 | 0 | 142 | 0.0% | 0 |
| VUI-21JUL-01 (B.1.621) | 32 | 0 | 32 | 0.0% | 0 |

**Table 4. Attendance to emergency care and deaths of confirmed and provisional cases in England (1 February 2021 to 2 August 2021)**

| Variant | Age Group (years) | Cases Since 1 Feb | Cases with specimen date in past 28 days | | Cases with an A&E visit § (exclusion‡) | | Cases with an A&E visit§ (inclusion#) | | Cases where presentation to A&E resulted in overnight inpatient admission§ (exclusion‡) | | Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#) | | Deaths^ | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | n | % | n | % | n | % | n | % | n | % | n | % |
| Alpha | <50 | 118,178 | 75 | 0.1 | 4,982 | 4.2 | 5,828 | 4.9 | 1,239 | 1.0 | 1,689 | 1.4 | 66 | 0.1 |
| | ≥50 | 32,274 | 7 | 0.0 | 3,126 | 9.7 | 4,587 | 14.2 | 1,711 | 5.3 | 2,778 | 8.6 | 1,548 | 4.8 |
| | All cases | 150,541 | 82 | 0.1 | 8,108 | 5.4 | 10,415 | 6.9 | 2,950 | 2.0 | 4,467 | 3.0 | 1,614 | 1.1 |
| Beta | <50 | 596 | 10 | 1.7 | 26 | 4.4 | 28 | 4.7 | 5 | 0.8 | 8 | 1.3 | 1 | 0.2 |
| | ≥50 | 161 | - | 0.0 | 18 | 11.2 | 26 | 16.1 | 7 | 4.3 | 15 | 9.3 | 7 | 4.3 |
| | All cases | 766 | 10 | 1.3 | 44 | 5.7 | 54 | 7.0 | 12 | 1.6 | 23 | 3.0 | 8 | 1.0 |
| Gamma | <50 | 213 | 4 | 1.9 | 9 | 4.2 | 9 | 4.2 | 1 | 0.5 | 1 | 0.5 | - | 0.0 |
| | ≥50 | 21 | - | 0.0 | 1 | 4.8 | 1 | 4.8 | - | 0.0 | - | 0.0 | - | 0.0 |
| | All cases | 234 | 4 | 1.7 | 10 | 4.3 | 10 | 4.3 | 1 | 0.4 | 1 | 0.4 | - | 0.0 |
| Delta | <50 | 265,749 | 84,772 | 31.9 | 8,449 | 3.2 | 10,975 | 4.1 | 1,970 | 0.7 | 3,084 | 1.2 | 71 | 0.0 |
| | ≥50 | 33,736 | 13,803 | 40.9 | 1,940 | 5.8 | 3,342 | 9.9 | 1,059 | 3.1 | 2,074 | 6.1 | 670 | 2.0 |
| | All cases | 300,010 | 98,722 | 32.9 | 10,391 | 3.5 | 14,319 | 4.8 | 3,030 | 1.0 | 5,159 | 1.7 | 742 | 0.2 |
| Zeta | <50 | 16 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 |

| Variant | Age Group (years) | Cases Since 1 Feb | Cases with specimen date in past 28 days | | Cases with an A&E visit § (exclusion‡) | | Cases with an A&E visit§ (inclusion#) | | Cases where presentation to A&E resulted in overnight inpatient admission§ (exclusion‡) | | Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#) | | Deaths^ | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | n | % | n | % | n | % | n | % | n | % | n | % |
| | ≥50 | 8 | - | 0.0 | 1 | 12.5 | 1 | 12.5 | 1 | 12.5 | 1 | 12.5 | - | 0.0 |
| | All cases | 24 | - | 0.0 | 1 | 4.2 | 1 | 4.2 | 1 | 4.2 | 1 | 4.2 | - | 0.0 |
| Eta | <50 | 273 | - | 0.0 | 11 | 4.0 | 13 | 4.8 | 5 | 1.8 | 6 | 2.2 | - | 0.0 |
| | ≥50 | 114 | - | 0.0 | 4 | 3.5 | 7 | 6.1 | 1 | 0.9 | 3 | 2.6 | 6 | 5.3 |
| | All cases | 389 | - | 0.0 | 15 | 3.9 | 20 | 5.1 | 6 | 1.5 | 9 | 2.3 | 6 | 1.5 |
| VUI-21FEB-04 | <50 | 232 | 1 | 0.4 | 6 | 2.6 | 9 | 3.9 | 1 | 0.4 | 2 | 0.9 | - | 0.0 |
| | ≥50 | 55 | - | 0.0 | 1 | 1.8 | 2 | 3.6 | - | 0.0 | 1 | 1.8 | 1 | 1.8 |
| | All cases | 288 | 1 | 0.3 | 7 | 2.4 | 11 | 3.8 | 1 | 0.3 | 3 | 1.0 | 1 | 0.3 |
| Theta | <50 | 4 | - | 0.0 | 1 | 25.0 | 1 | 25.0 | - | 0.0 | - | 0.0 | - | 0.0 |
| | ≥50 | 3 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 |
| | All cases | 7 | - | 0.0 | 1 | 14.3 | 1 | 14.3 | - | 0.0 | - | 0.0 | - | 0.0 |
| Kappa | <50 | 383 | - | 0.0 | 9 | 2.3 | 10 | 2.6 | 1 | 0.3 | 2 | 0.5 | - | 0.0 |
| | ≥50 | 64 | - | 0.0 | 5 | 7.8 | 5 | 7.8 | 2 | 3.1 | 2 | 3.1 | 1 | 1.6 |
| | All cases | 447 | - | 0.0 | 14 | 3.1 | 15 | 3.4 | 3 | 0.7 | 4 | 0.9 | 1 | 0.2 |
| | <50 | 11 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 |

| Variant | Age Group (years) | Cases Since 1 Feb | Cases with specimen date in past 28 days | | Cases with an A&E visit § (exclusion‡) | | Cases with an A&E visit§ (inclusion#) | | Cases where presentation to A&E resulted in overnight inpatient admission§ (exclusion‡) | | Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#) | | Deaths^ | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | n | % | n | % | n | % | n | % | n | % | n | % |
| VUI-21APR-03 | ≥50 | 2 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 |
| | All cases | 13 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 |
| VUI-21MAY-01 | <50 | 161 | - | 0.0 | 1 | 0.6 | 2 | 1.2 | - | 0.0 | 1 | 0.6 | - | 0.0 |
| | ≥50 | 23 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | 1 | 4.3 |
| | All cases | 184 | - | 0.0 | 1 | 0.5 | 2 | 1.1 | - | 0.0 | 1 | 0.5 | 1 | 0.5 |
| VUI-21MAY-02 | <50 | 110 | - | 0.0 | 8 | 7.3 | 9 | 8.2 | 2 | 1.8 | 3 | 2.7 | - | 0.0 |
| | ≥50 | 31 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 |
| | All cases | 142 | - | 0.0 | 8 | 5.6 | 9 | 6.3 | 2 | 1.4 | 3 | 2.1 | - | 0.0 |
| Lambda | <50 | 8 | - | 0.0 | 1 | 12.5 | 1 | 12.5 | 1 | 12.5 | 1 | 12.5 | - | 0.0 |
| | ≥50 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| | All cases | 8 | - | 0.0 | 1 | 12.5 | 1 | 12.5 | 1 | 12.5 | 1 | 12.5 | - | 0.0 |
| VUI-21JUL-01 | <50 | 26 | 16 | 61.5 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 | - | 0.0 |
| | ≥50 | 6 | 3 | 50.0 | 1 | 16.7 | 1 | 16.7 | - | 0.0 | - | 0.0 | - | 0.0 |
| | All cases | 32 | 19 | 59.4 | 1 | 3.1 | 1 | 3.1 | - | 0.0 | - | 0.0 | - | 0.0 |

Data sources: Emergency care attendance and admissions from ECDS, deaths from PHE daily death data series (deaths within 28 days). NHS trusts are required to submit emergency care attendances by the 21st of each month. As a result, the number of cases with attendances may show substantial increases in technical briefs prepared after the monthly cut-off, compared with other briefs from the same month.
¥ Cases without specimen dates and unlinked sequences (sequenced samples that could not be matched to individuals) are excluded from this table.
* Cases are assessed for any emergency care attendance within 28 days of their positive specimen date. Cases still undergoing within 28-day period may have an emergency care attendance reported at a later date.
§ At least 1 attendance or admission within 28 days of positive specimen date
# Inclusion: Including cases with the same specimen and attendance dates
‡ Exclusion: Excluding cases with the same specimen and attendance dates. Cases where specimen date is the same as date of emergency care visit are excluded to help remove cases picked up via routine testing in healthcare settings whose primary cause of attendance is not COVID-19. This underestimates the number of individuals in hospital with COVID-19 but only includes those who tested positive prior to the day of their emergency care visit. Some of the cases detected on the day of admission may have attended for a diagnosis unrelated to COVID-19.
^ Total deaths in any setting (regardless of hospitalisation status) within 28 days of positive specimen date.

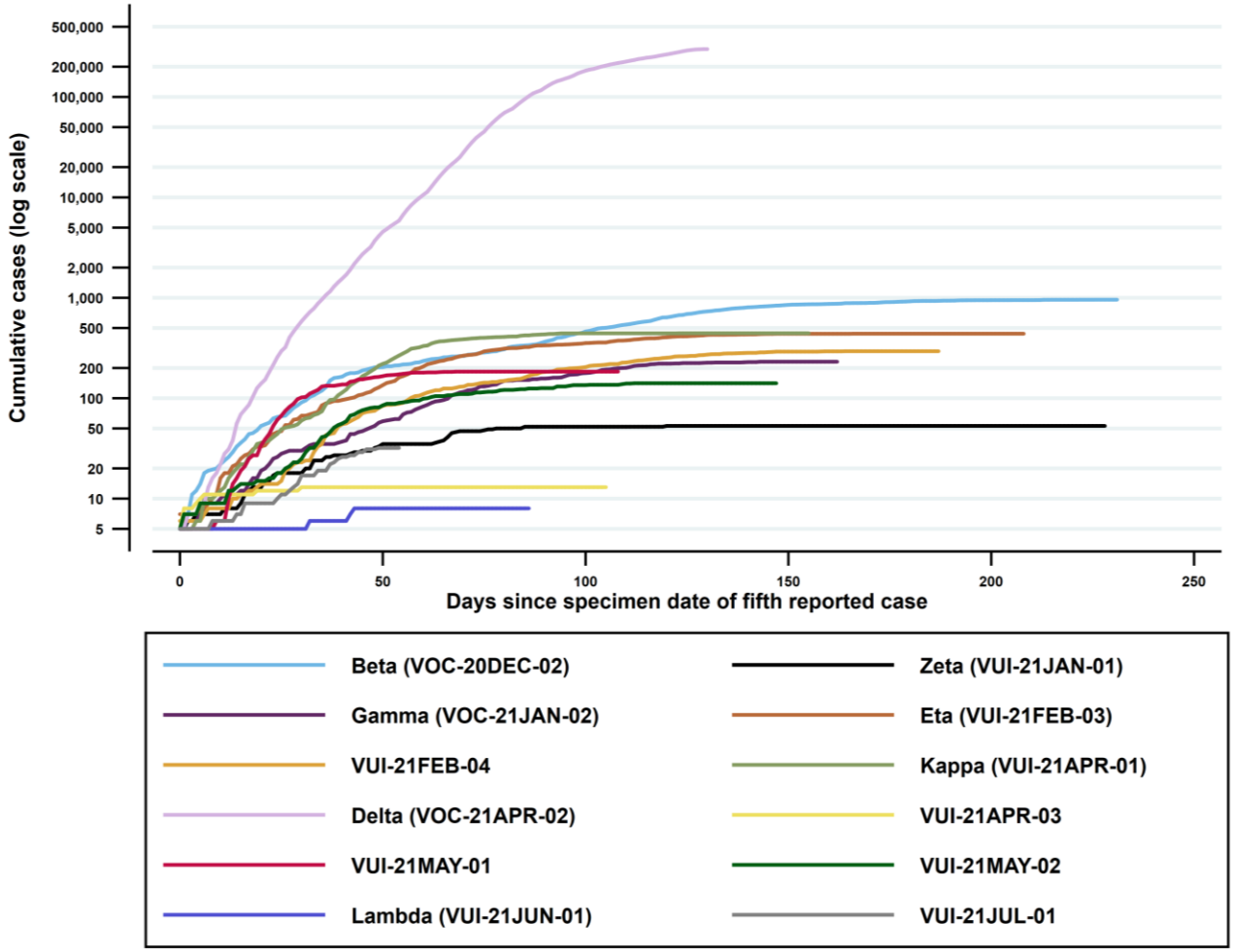
**Table 5. Attendance to emergency care and deaths of confirmed and provisional Delta cases in England by vaccination status (1 February 2021 to 2 August 2021)**

| Variant | Age group (years)** | Total | Cases with specimen date in past 28 days | Unlinked | <21 days post dose 1 | ≥21 days post dose 1 | Received 2 doses | Unvaccinated |
|---|---|---|---|---|---|---|---|---|
| Delta cases | <50 | 265,749 | 84,772 | 28,330 | 23,822 | 40,449 | 25,536 | 147,612 |
| | ≥50 | 33,736 | 13,803 | 2,989 | 195 | 5,640 | 21,472 | 3,440 |
| | All cases | 300,010 | 98,722 | 31,841 | 24,018 | 46,089 | 47,008 | 151,054 |
| Cases with an emergency care visit§ (exclusion‡) | <50 | 8,449 | N/A | 70 | 756 | 1,127 | 694 | 5,802 |
| | ≥50 | 1,940 | N/A | 10 | 15 | 326 | 1,098 | 491 |
| | All cases | 10,391 | N/A | 82 | 771 | 1,453 | 1,792 | 6,293 |
| Cases with an emergency care visit§ (inclusion#) | <50 | 10,975 | N/A | 119 | 953 | 1,368 | 864 | 7,671 |
| | ≥50 | 3,342 | N/A | 24 | 30 | 486 | 1,815 | 987 |
| | All cases | 14,319 | N/A | 145 | 983 | 1,854 | 2,679 | 8,658 |
| Cases where presentation to emergency care resulted in overnight inpatient admission§ ((exclusion‡) | <50 | 1,970 | N/A | 35 | 136 | 203 | 153 | 1,443 |
| | ≥50 | 1,059 | N/A | 7 | 12 | 125 | 620 | 295 |
| | All cases | 3,030 | N/A | 43 | 148 | 328 | 773 | 1,738 |
| Cases where presentation to emergency care resulted in overnight inpatient admission§ (inclusion#) | <50 | 3,084 | N/A | 61 | 211 | 298 | 224 | 2,290 |
| | ≥50 | 2,074 | N/A | 20 | 23 | 230 | 1,131 | 670 |
| | All cases | 5,159 | N/A | 82 | 234 | 528 | 1,355 | 2,960 |
| Deaths within 28 days of positive specimen date | <50 | 71 | N/A | 2 | 4 | 4 | 13 | 48 |
| | ≥50 | 670 | N/A | 5 | 6 | 65 | 389 | 205 |

| Variant | Age group (years)** | Total | Cases with specimen date in past 28 days | Unlinked | <21 days post dose 1 | ≥21 days post dose 1 | Received 2 doses | Unvaccinated |
|---|---|---|---|---|---|---|---|---|
| | All cases | 742 | N/A | 8 | 10 | 69 | 402 | 253 |

Data sources: Emergency care attendance and admissions from ECDS, deaths from PHE daily death data series (deaths within 28 days). NHS trusts are required to submit emergency care attendances by the 21st of each month. As a result, the number of cases with attendances may show substantial increases in technical briefs prepared after the monthly cut-off, compared with other briefs from the same month.
¥ Cases without specimen dates and unlinked sequences (sequenced samples that could not be matched to individuals) are excluded from this table.
* Cases are assessed for any emergency care attendance within 28 days of their positive specimen date. Cases still undergoing within 28-day period may have an emergency care attendance reported at a later date.
§ At least 1 attendance or admission within 28 days of positive specimen date
# Inclusion: Including cases with the same specimen and attendance dates
‡ Exclusion: Excluding cases with the same specimen and attendance dates. Cases where specimen date is the same as date of emergency care visit are excluded to help remove cases picked up via routine testing in healthcare settings whose primary cause of attendance is not COVID-19. This underestimates the number of individuals in hospital with COVID-19 but only includes those who tested positive prior to the day of their emergency care visit. Some of the cases detected on the day of admission may have attended for a diagnosis unrelated to COVID-19.
^ Total deaths in any setting (regardless of hospitalisation status) within 28 days of positive specimen date.
** Age <50 + >50 do not total 'all cases' per category as some cases lack reported age data

**Figure 4. Cumulative cases in England of variants indexed by days since the fifth reported case as of 2 August 2021**
(Find accessible data used in this graph in underlying data)



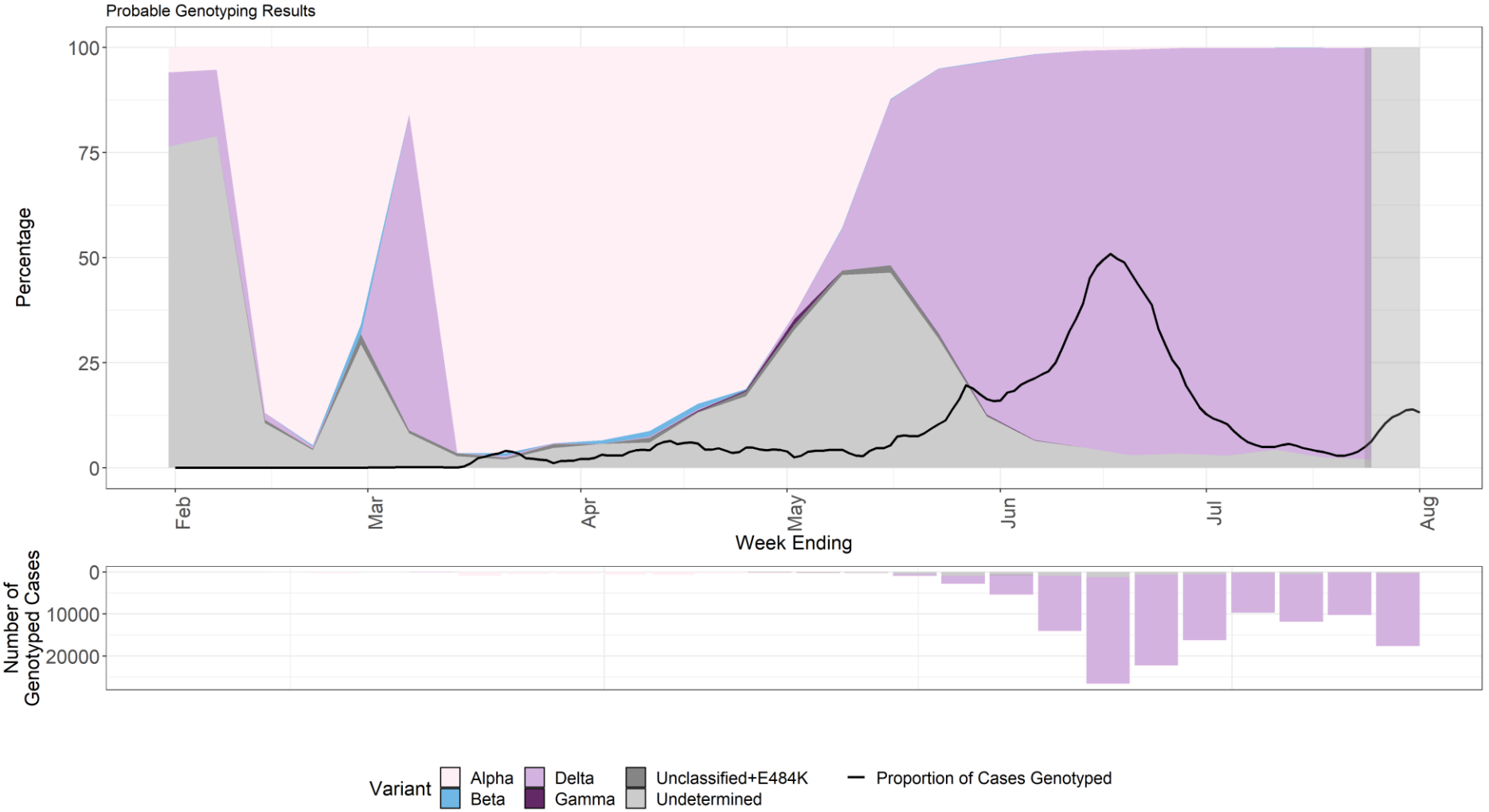
# 1.4 Variant prevalence

The prevalence of different variants amongst genotyped and sequenced cases is presented in Figures 5 and 6 and split by region in Figures 7 and 8. Genotyping provides probably variant result with a shorter turnaround time of 12 to 24 hours after initial confirmation of COVID-19. The initial panel of targets began trials in March 2021, using single nucleotide polymorphisms that included N501Y, E484K, K417N, and K417T. Results have been reported and used for public health action since 29 March 2021. On 11 May 2021, after rapid validation of targets to allow identification of Delta variant, P681R was introduced in the panel to replace N501Y. Genotyping results have now been fully integrated into the variant data reports and analyses. Changes in the use of genotyping over time should be considered when interpreting prevalence from genotyped data.

The ‘Other’ category in Figures 6 and 8 includes genomes where the quality is insufficient to determine variant status and genomes that do not meet the current definition for a VUI or VOC. Sequencing numbers and coverage fall in the last week shown due partly to sequencing lag time, and new sequences are still being produced relating to sample dates in that week. The supplementary data for figures are available.

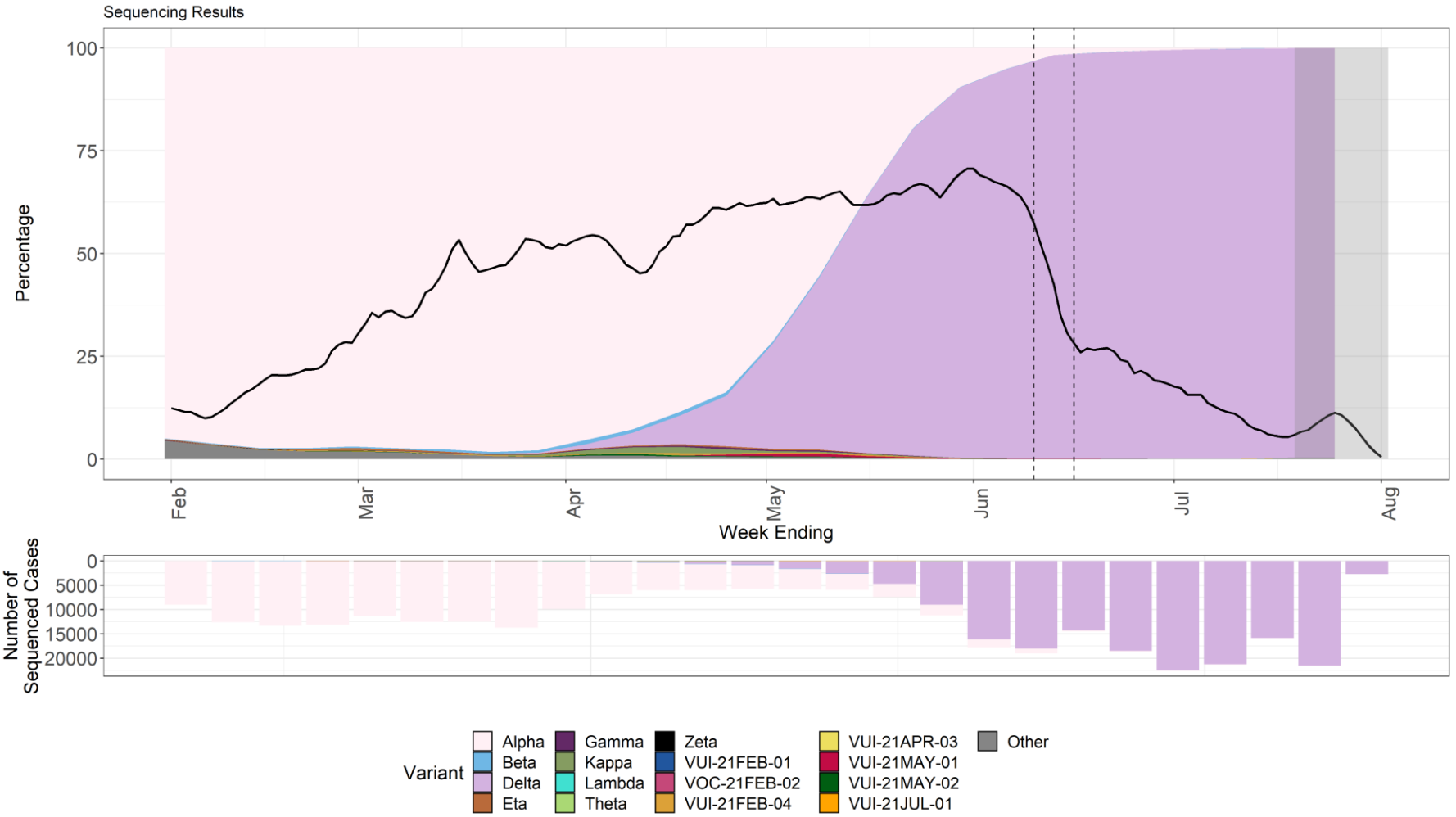
Delta variant accounted for approximately 99% of sequenced and 98% genotyped cases from 25 July to 31 July 2021.

**Figure 5. Variant prevalence for available genotyped cases in England (1 February 2021 to 2 August 2021)**
(Find accessible data used in this graph in underlying data)



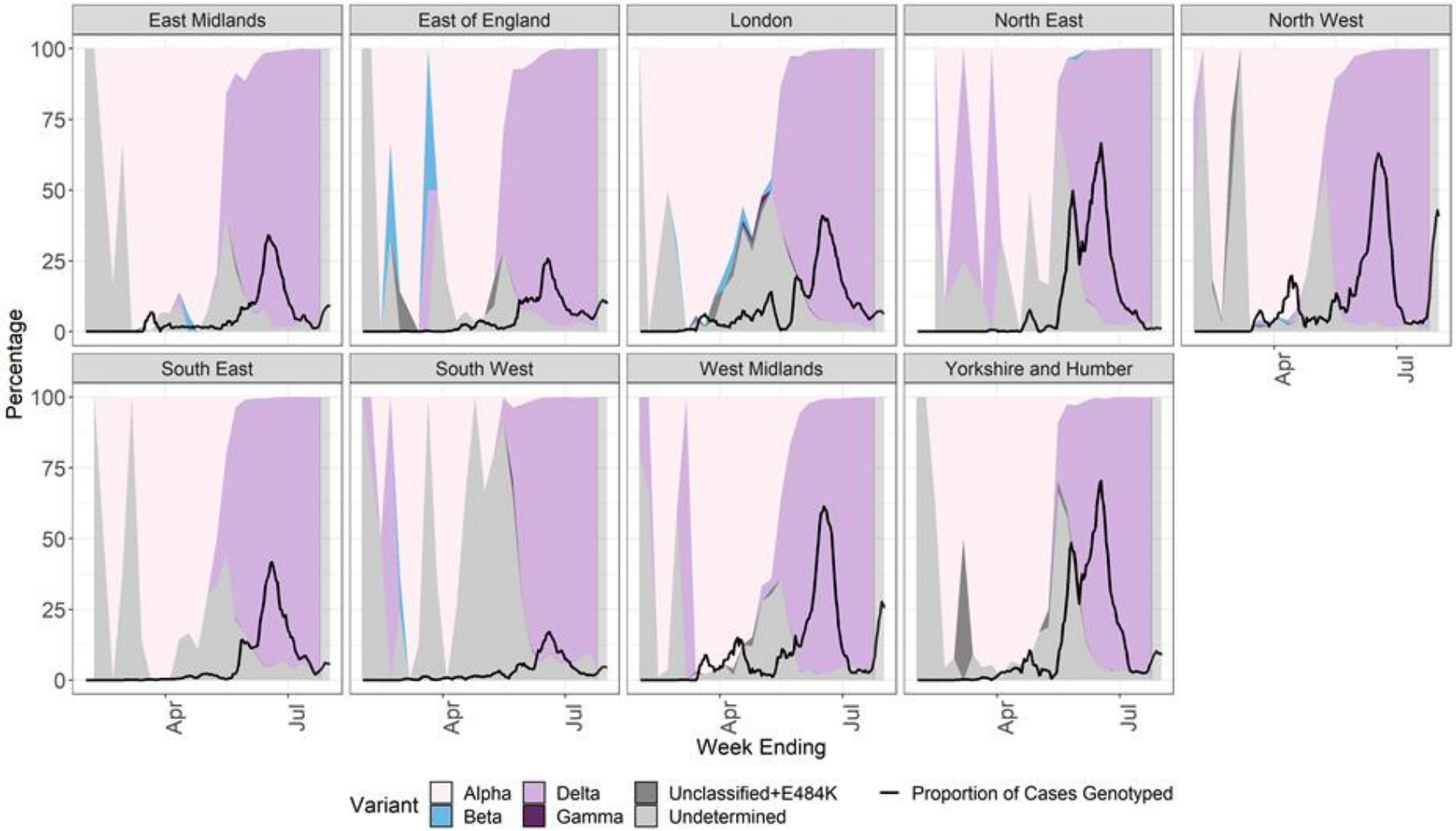

A small number of cases identified as Beta (B.1.351) on genotyping since May 2021 without confirmatory sequencing may be VUI-21JUL-01 (B.1.621) with an additional K417N mutation.

**Figure 6. Variant prevalence for available sequenced cases in England (1 February 2021 to 2 August 2021)**
Find accessible data used in this graph in underlying data).



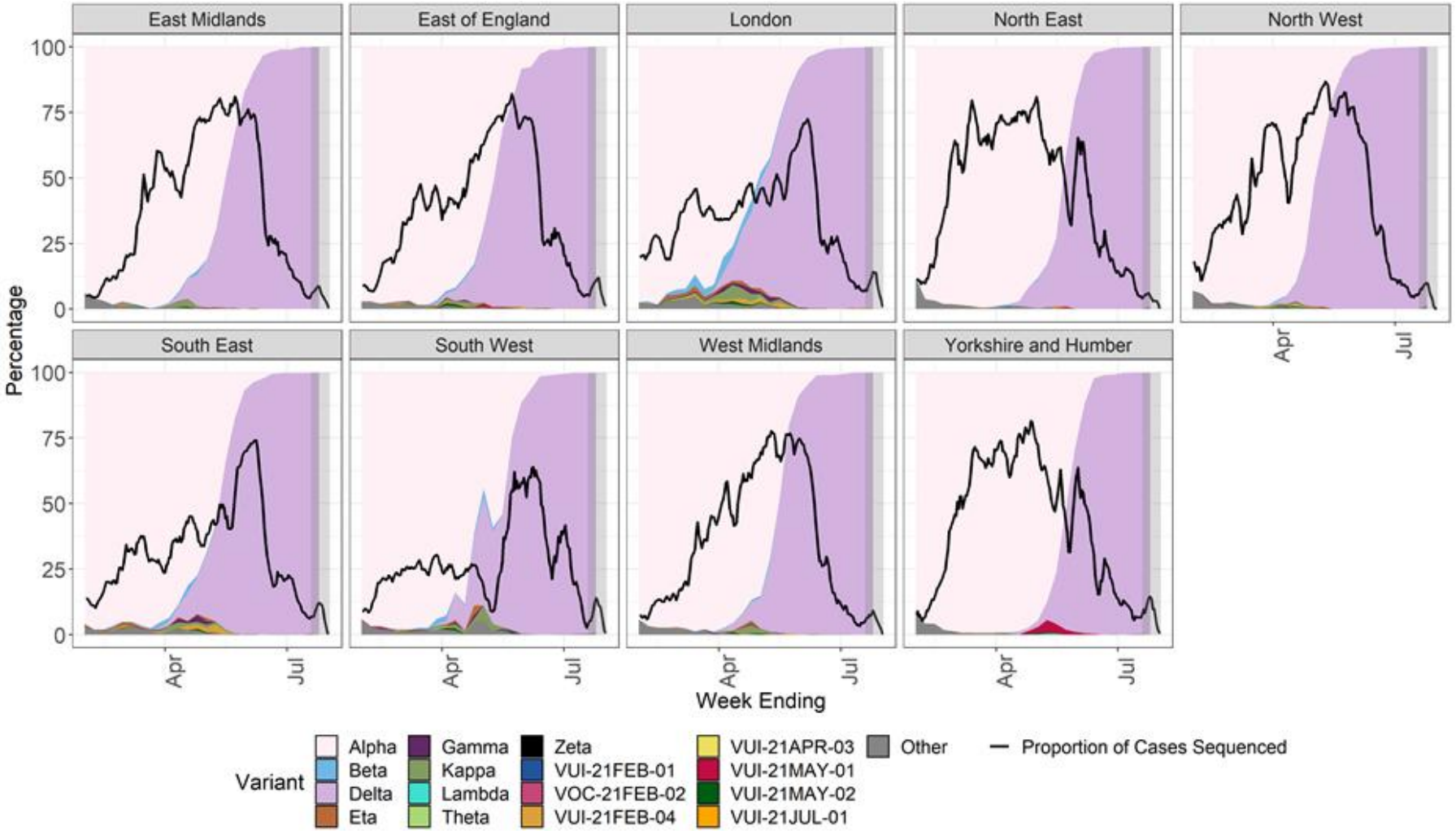

Dashed lines indicate period incorporating issue at a sequencing site.

**Figure 7. Variant prevalence for genotyped cases in England by region (1 February 2021 to 2 August 2021)**
(Find accessible data used in this graph in underlying data)




Note that 1,253 cases were excluded due to missing region or specimen date information.

**Figure 8. Variant prevalence for sequenced cases in England by region (1 February 2021 to 2 August 2021)**
(Find accessible data used in this graph in underlying data)




Note that 1,512 cases were excluded due to missing region or specimen date information.

# 1.5 Antigenic change over time (international)

A list of mutations of potential antigenic significance has been compiled using the available published evidence. The full list of mutations of potential antigenic significance is compiled and continuously updated by an expert group comprising members of the variant technical group, COG-UK, and UK-G2P using literature searches and data mining from publicly available datasets. Data analysis includes GISAID data uploaded before 4 August 2021 (excluding UK data). The increase in the number of antigenic mutations over time is illustrated for all variants in Figure 9 and for variants excluding VOCs and VUIs in Figure 10.

The plots in Figures 9 and 10 were obtained by first counting the number of high confidence antigenic mutations for each sequence. The sequences were then grouped and the prevalence for each number of mutations was estimated weekly from March 2020 until 1 July 2021. All non-synonymous mutations at positions in the spike protein that have been associated with antigenicity were considered antigenic. VOCs or VUIs were identified by analysing their spike mutation profile to deal with low-quality and partial sequences.

Table 6 shows additional spike mutations with a potential impact on antigenicity, avidity, or the furin cleavage site significance acquired by Delta in the UK. This data uses the numbers of genomes in the national genomic data set rather than case numbers. Only mutations associated with antigenic change are presented here, such as those identified by published research. The unlinked sequences represent the number of sequences not present within the English surveillance system. These sequences include those samples from the Devolved Administrations and cannot be associated with a date by PHE.

**Table 6. Additional spike mutations of interest detected in Delta genomes in the UK as of 3 August 2021**

| Amino acid change | Delta sequences in UK (COG UK) | Delta sequences outside UK (GISAID) | Delta sequences 4 May to 3 June 2021 | | Delta sequences 4 June to 3 July 2021 | | Delta sequences 4 July to 3 August 2021 | |
|---|---|---|---|---|---|---|---|---|
| | | | England | Outside UK | England | Outside UK | England | Outside UK |
| P251L | 1,585 | 1,700 | 7 | 44 | 141 | 272 | 312 | 1,373 |
| G446V | 665 | 211 | 48 | 34 | 132 | 65 | 119 | 80 |
| V483F | 92 | 66 | 2 | 13 | 19 | 10 | 48 | 33 |
| Q493E | 62 | 51 | 0 | 12 | 5 | 23 | 51 | 12 |
| K417N | 60 | 1,223 | 30 | 251 | 3 | 722 | 7 | 207 |
| S494L | 42 | 38 | 5 | 7 | 9 | 18 | 20 | 3 |
| V445I | 40 | 3 | 0 | 2 | 0 | 1 | 32 | 0 |
| L455F | 33 | 39 | 0 | 11 | 14 | 13 | 16 | 11 |
| N501Y | 29 | 128 | 0 | 20 | 8 | 85 | 9 | 15 |
| S494P | 25 | 25 | 0 | 9 | 5 | 6 | 13 | 7 |
| K458N | 23 | 10 | 0 | 0 | 18 | 5 | 5 | 5 |
| K444N | 21 | 38 | 4 | 15 | 6 | 8 | 5 | 15 |
| F490L | 20 | 4 | 0 | 2 | 1 | 0 | 15 | 1 |
| E484Q | 15 | 155 | 1 | 17 | 4 | 90 | 6 | 43 |
| P681H | 13 | 28 | 1 | 11 | 1 | 8 | 4 | 1,373 |
| R246I | 11 | 12 | 1 | 1 | 0 | 1 | 10 | 2 |
| P499L | 11 | 5 | 0 | 0 | 3 | 1 | 6 | 1 |
| E484G | 9 | 3 | 0 | 0 | 2 | 0 | 5 | 1 |
| E484A | 7 | 15 | 1 | 1 | 2 | 13 | 0 | 1 |
| D80A | 2 | 61 | 1 | 10 | 0 | 29 | 1 | 8 |
| E484K | 1 | 25 | 0 | 3 | 1 | 21 | 0 | 1 |
| Total Delta | 229,588 | 135,609 | 31,820 | 16,970 | 81,079 | 48,553 | 65,865 | 57,899 |

**Figure 9. Prevalence of antigenic mutations over time for all genomes in GISAID (excluding UK data) as of 4 August 2021**
(Find accessible data used in this graph in underlying data)

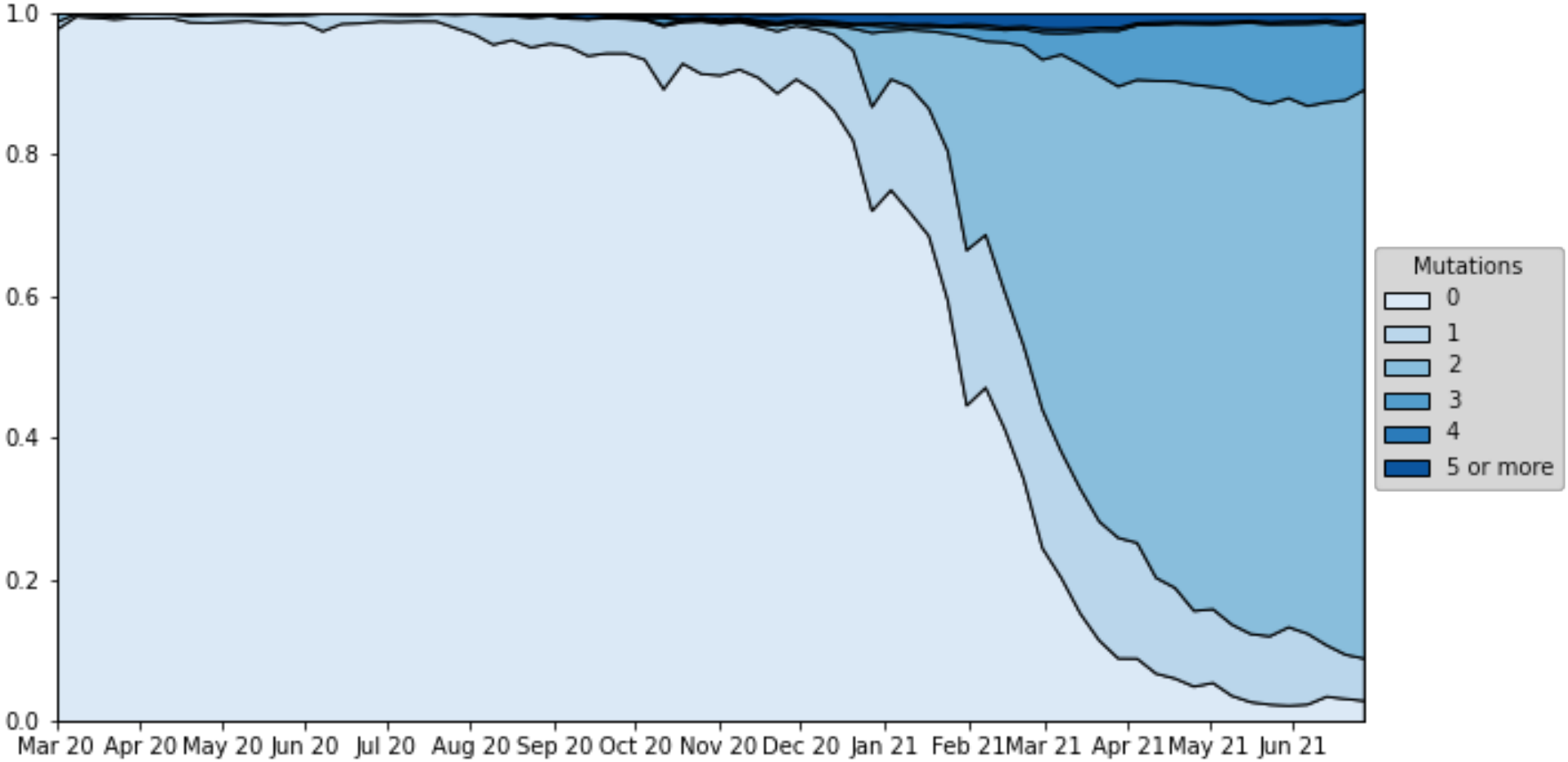
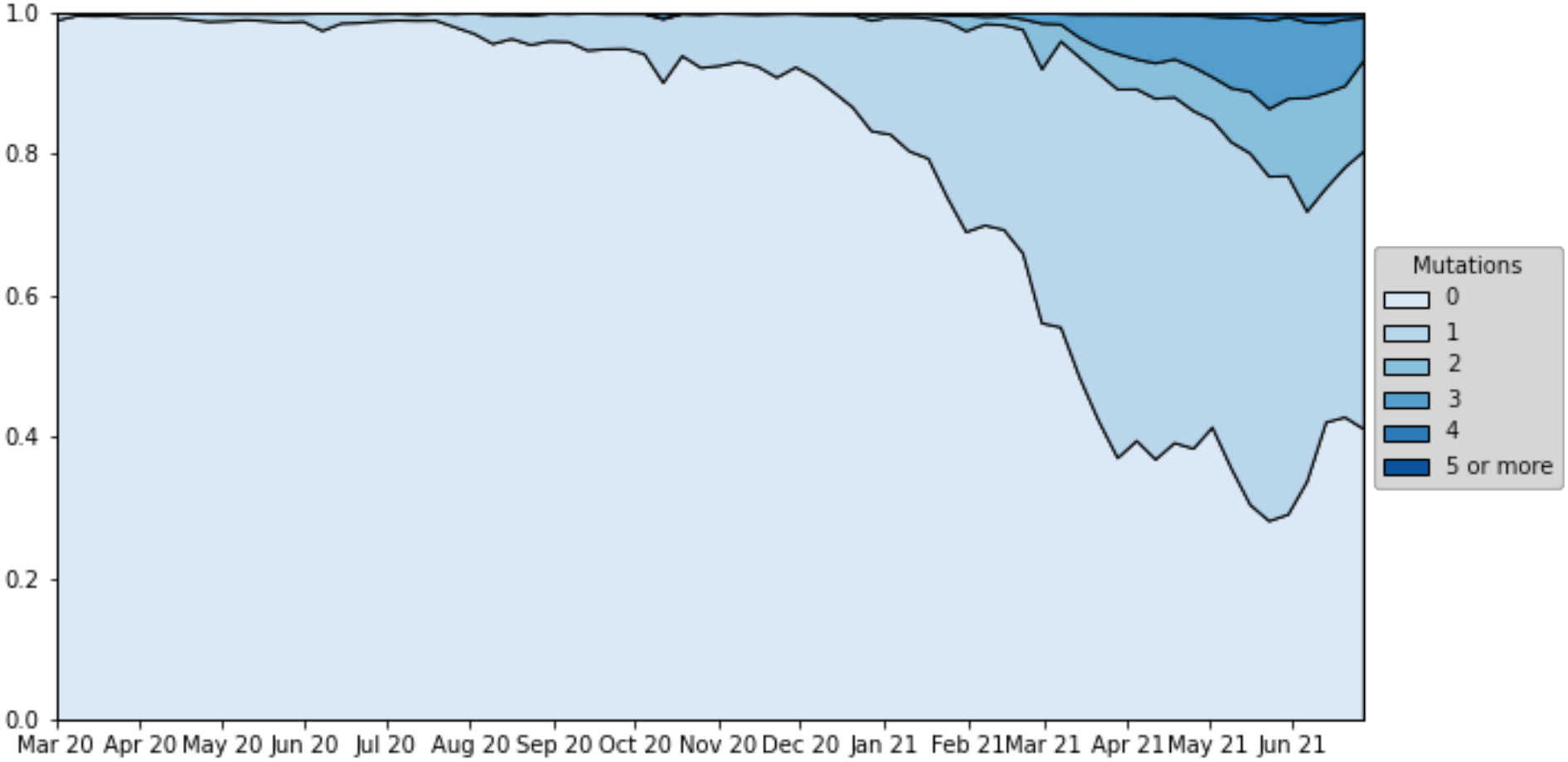


**Figure 10. Prevalence of antigenic mutations over time for all genomes in GISAID (excluding UK data), excluding VOCs and VUIs, as of 4 August 2021**

(Find accessible data used in this graph in underlying data)



# 1.6 Secondary attack rates

This section includes secondary attack rates for traveller and non-traveller cases, and separate household contact rates, including new analysis of rates for household and non-household contacts of non-traveller cases over time for Delta and Alpha variants.

Secondary attack rates are based on positive tests amongst contacts named to NHS Test and Trace by an original case identified with a sequenced or genotyped VOC or VUI. Variant cases are identified using sequencing results supplemented with genotyping results as of 26 July 2021 and exclude low-quality results.

Secondary attack rates are shown for cases with and without travel history. In non-travel settings, only close contacts named by the original case are included, that is, household members, face-to-face contact, people within one metre of the case for one minute or longer, or people within 2 metres for 15 minutes. In travel settings, the contacts reported are not restricted to only close contacts named by the case. For example, they may include contacts on a plane linked by additional contact tracing efforts. This likely deflates secondary attack rates amongst travellers compared to non-travellers. In addition, people recently returning from overseas are subject to stricter quarantine measures and may moderate their behaviour towards contacts. Travel history suggests where infection of the original case may have occurred.

Table 7 shows secondary attack rates for all variants between 5 January 2021 and 13 July 2021, which was a period chosen to capture data for all variants. Direct comparisons between variants are not valid as vaccination levels and social restrictions in England have varied over this period. Estimates of secondary attack rates for travel-related contacts with VOCs or VUIS were considerably lower than non-travel cases due to differences in contact definitions.

Figure 11 shows the secondary attack rates amongst household and non-household contacts of non-travel cases with Delta and Alpha between 29 March 2021 to 11 July 2021. Secondary attack rates amongst household and non-household contacts of cases with Delta appear steady over the last 6 weeks, with estimates of 10.4% (95% CI: 10.1% - 10.7%) for household contacts and 6.2% (95% CI: 5.8% - 6.7%) for non-household contacts from exposure events after 5 July 2021. Secondary attack rate estimates for contacts of cases with Alpha have not been produced for the most recent week due to low case numbers.

**Table 7. Secondary attack rates for all variants**
(5 January 2021 to 13 July 2021, variant data as of 26 July 2021, and contact tracing data as of 3 August 2021)

| Variant | Travel-related cases (with contacts) | Non-travel cases (with contacts) | Travel-related case proportions | Secondary attack rate in contacts of travel-related cases (95% CI) [secondary cases /contacts] | Secondary attack rate in household contacts of non-travel or unknown cases (95% CI) [secondary cases/contacts] | Secondary attack rate in non-household contacts of non-travel or unknown cases (95% CI) [secondary cases/contacts] |
|---|---|---|---|---|---|---|
| Alpha | 4,430 (76.5% with contacts) | 185,060 (75.1% with contacts) | 2.3% | 1.5% (1.4% to 1.6%) [1,260/83,413] | 10.2% (10.1% to 10.3%) [34,603/338,503] | 5.6% (5.5% to 5.8%) [3,305/58,659] |
| Beta | 344 (70.1% with contacts) | 427 (68.1% with contacts) | 44.6% | 1.9% (1.5% to 2.2%) [113/6,095] | 9.9% (7.9% to 12.2%) [74/751] | 2.9% (1.3% to 6.2%) [6/206] |
| Zeta | 4 (75.0% with contacts) | 27 (77.8% with contacts) | 12.9% | Unavailable [0/160] | 7.7% (3.0% to 18.2%) [4/52] | Unavailable [0/1] |
| Gamma | 74 (66.2% with contacts) | 148 (70.9% with contacts) | 33.3% | 1.1% (0.6% to 1.9%) [10/946] | 10.3% (7.1% to 14.8%) [25/242] | 3.4% (1.2% to 9.4%) [3/89] |

| | | | | | | |
|---|---|---|---|---|---|---|
| VUI-21FEB-01 | 0 (0 with contacts) | 63 (60.3% with contacts) | 0.0% | Unavailable [0/0] | 9.9% (5.1% to 18.3%) [8/81] | Unavailable [1/12] |
| Eta | 196 (70.4% with contacts) | 198 (73.2% with contacts) | 49.7% | 1.1% (0.8% to 1.5%) [47/4,282] | 9.8% (7.1% to 13.4%) [33/337] | Unavailable [1/43] |
| VUI-21FEB-04 | 117 (68.4% with contacts) | 159 (79.2% with contacts) | 42.4% | 0.5% (0.3% to 0.8%) [17/3,246] | 8.5% (5.8% to 12.1%) [26/307] | 6.5% (3.0% to 13.4%) [6/93] |
| Theta | 5 (40.0% with contacts) | 1 (100.0% with contacts) | 83.3% | Unavailable [0/5] | Unavailable [0/3] | Unavailable [0/0] |
| Kappa | 233 (77.3% with contacts) | 173 (77.5% with contacts) | 57.4% | 1.9% (1.5% to 2.3%) [83/4,453] | 9.7% (7.1% to 13.0%) [38/392] | Unavailable [3/45] |
| Delta | 1913 (67.0% with contacts) | 223,061 (77.9% with contacts) | 0.9% | 1.7% (1.6% to 1.9%) [573/32,990] | 10.8% (10.7% to 10.9%) [45,289/418,463] | 5.8% (5.6% to 5.9%) [8,515/147,684] |
| VUI-21APR-03 | 7 (14.3% with contacts) | 5 (100.0% with contacts) | 58.3% | Unavailable [1/201] | Unavailable [1/12] | Unavailable [0/0] |
| VUI-21MAY-01 | 2 (0.0% with contacts) | 176 (84.7% with contacts) | 1.1% | Unavailable [0/0] | 8.0% (5.8% to 11.1%) [33/411] | 2.4% (0.8% to 6.9%) [3/124] |

| | | | | | | |
|---|---|---|---|---|---|---|
| VUI-21MAY-02 | 70 (74.3% with contacts) | 54 (81.5% with contacts) | 56.5% | 0.8% (0.5% to 1.5%) [11/1,325] | 8.2% (4.4% to 14.8%) [9/110] | Unavailable [0/13] |
| Lambda) | 8 (62.5% with contacts) | 0 (0 with contacts) | 100.0% | Unavailable [1/194] | Unavailable [0/0] | Unavailable [0/0] |
| VUI-21JUL-01 | 6 (50.0% with contacts) | 9 (77.8% with contacts) | 40.0% | Unavailable [2/75] | Unavailable [1/15] | Unavailable [0/3] |

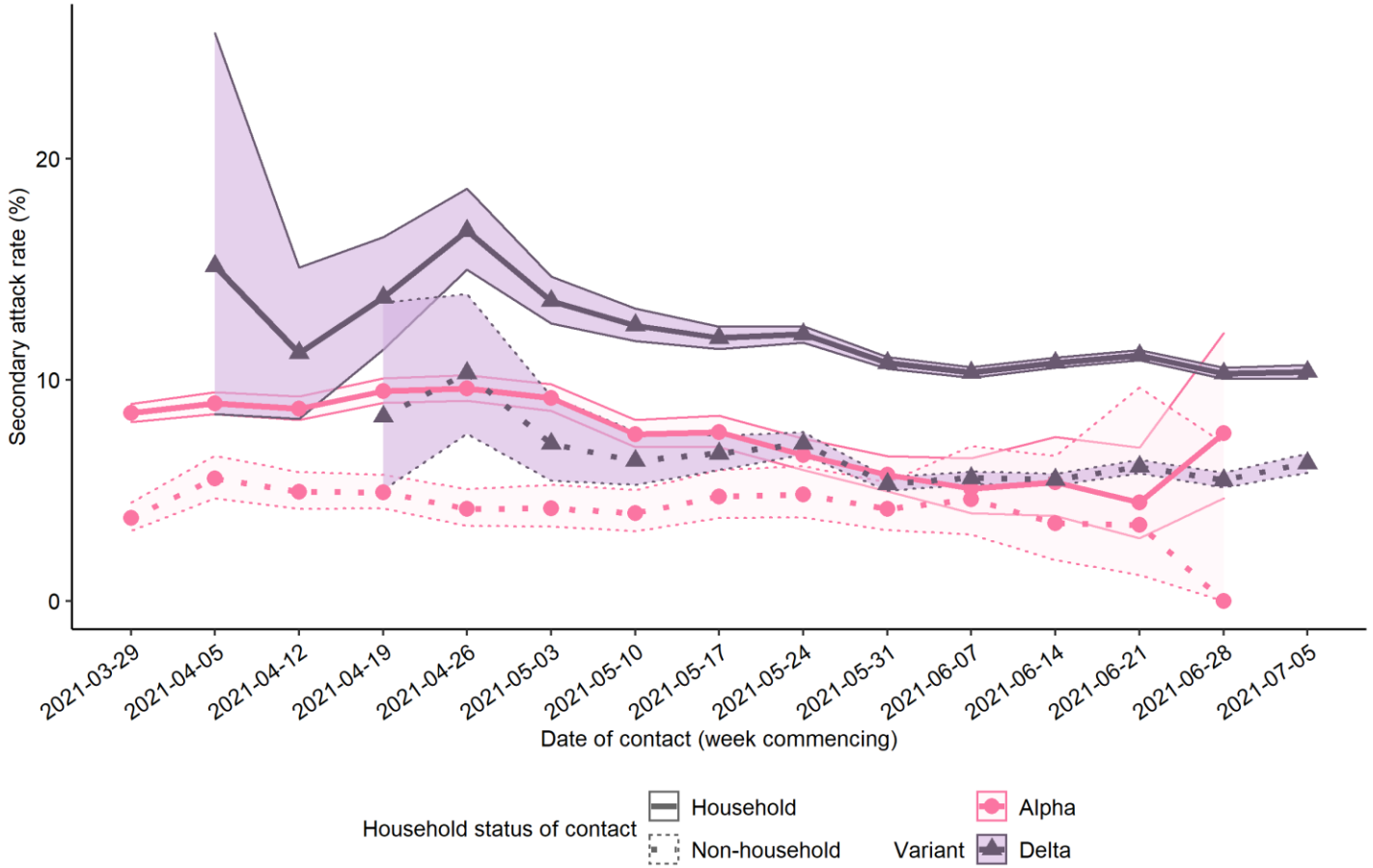
Footnote to table 7

Secondary attack rates are marked as 'Unavailable' when count of contacts is fewer than 50 or count of cases is fewer than 20. Travel-linked cases for secondary attack rates are identified positively in NHS Test and Trace data using multiple PHE sources. A case is considered as being travel-linked if EpiCell or Health Protection Teams have found evidence of international travel, their NHS Test and Trace record mentions an event associated with international travel, their NHS Test and Trace record was created after notification via International Health Regulations National Focal Point, their contacts were traced by the international contact tracing team, or they have been marked for priority contact tracing in NHS Test and Trace for reasons of travel. Some travel-linked cases may be missed by these methods and would be marked as non-travel-linked or unknown.

Secondary attack rates from NHS Test and Trace should generally be considered lower bounds due to the nature of contact tracing and testing. Data provided is for period until 13 July 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Cases are included in case counts if their onset or (if asymptomatic) test is during the period of study, contacts are included in secondary attack rates if their exposure date or onset or test of exposing case if the contact is a household contact is during the period of study. Secondary attack rates are suppressed when count of contacts is less than 50 or count of cases is less than 20. Probable (genotyping) results are included, low quality genomic results are not.

**Figure 11. Secondary attack rates in household and non-household contacts of non-travel Alpha and Delta cases, with 95% confidence intervals (29 March 2021 to 11 July 2021, variant data as of 26 July 2021, contact tracing data as of 3 August 2021)**

(Find accessible data used in this graph in underlying data)



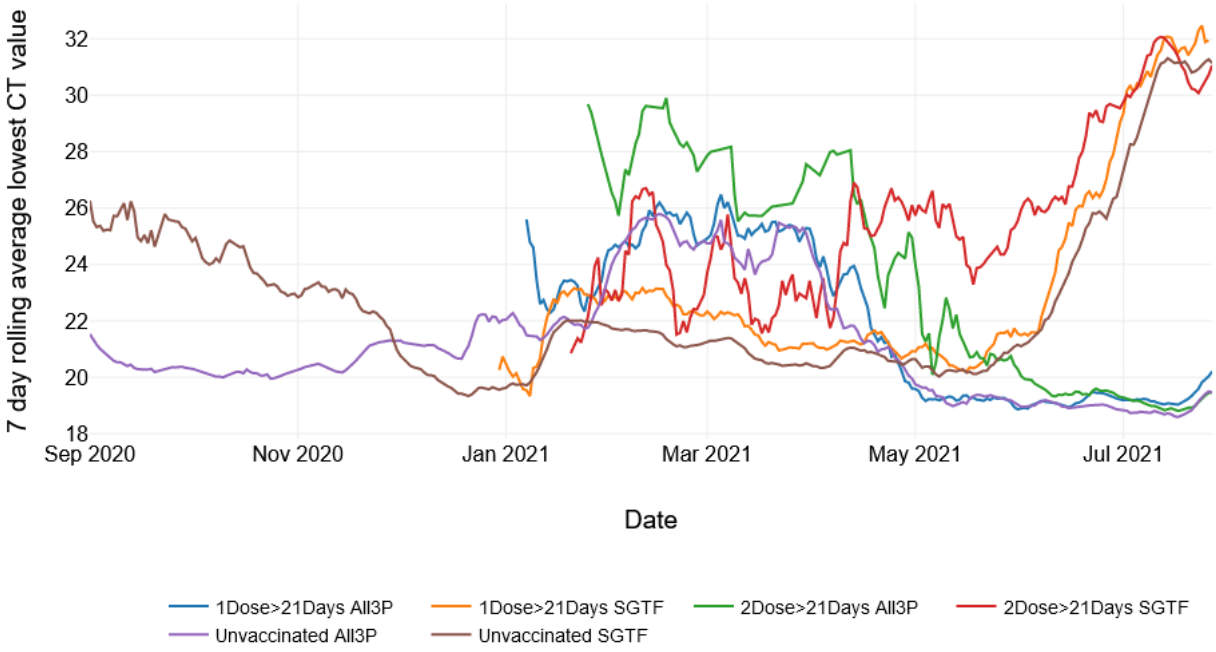

Please see footnote to Table 7. Data provided is for period until 11 July 2021 in order to allow time for contacts to become cases and complete weeks to be shown.

# 1.7 Vaccination

## 1.7.1. Comparison of viral load Ct by vaccination status

In the NHS Test and Trace (NHSTT) case data, the mean and median lowest Ct values for all cases with Delta, where Ct data are available, since the 14 June 2021 are similar, with a median of 17.8 for unvaccinated and 18.0 for those with 2 vaccine doses (Figure 12). This means that whilst vaccination may reduce an individual's overall risk of becoming infected, once they are infected there is limited difference in viral load (and Ct values) between those who are vaccinated and unvaccinated. Given they have similar Ct values, this suggests limited difference in infectiousness. To note, this analysis is undertaken on case data and are not age-stratified. Findings can be influenced by test-seeking behaviour, as well as true changes in the data, for example the age distribution of cases, which can also influence Ct values.

**Figure 12. Average daily lowest Ct values for vaccinated vs. unvaccinated cases, by variant from NHSTT data from 1 September 2020 until 25 July 2021[1]**




Notes

This Figure shows the Ct values (higher count for lower viral loads) in people who catch the Alpha variant (referred to as SGTF, shown in red, yellow and brown), or Delta variant (Delta compatible referred to as All3P or S+, shown in green, blue and purple). For each variant, a comparison is shown between Ct values of unvaccinated cases, cases with 1 vaccination dose more than 21 days ago, and cases with 2 vaccination doses more than 21 days ago. Since May 2021 the average Ct values for Delta cases overall in the NHSTT case data (using the S gene as a proxy), have decreased (meaning average viral loads have become higher), which is a known pattern in an increasing epidemic (and was previously seen when the original 'wild type' virus was no longer prevalent).

# 1.8 Updates from Variant Technical Group members

This section contains summaries of key information reported by Variant Technical Group members for use in the variant risk assessments. Links to full published data will be provided once available.

## 1.8.1 Genotype to Phenotype (G2P) Consortium

Preliminary pseudovirus neutralisation data indicates that:

- sera from vaccinees shows decreased ability to neutralize B.1.621 compared to first wave virus and Alpha, with a magnitude of change similar to Beta
- sera from individuals who have been infected with Delta does not have strong neutralising activity against either Beta or B.1.621
- sera from individuals who have been vaccinated and have had subsequent recent Delta infection have a high level of neutralising activity against all variants tested (including beta and B.1.621)

# Part 2: Surveillance of individual variants

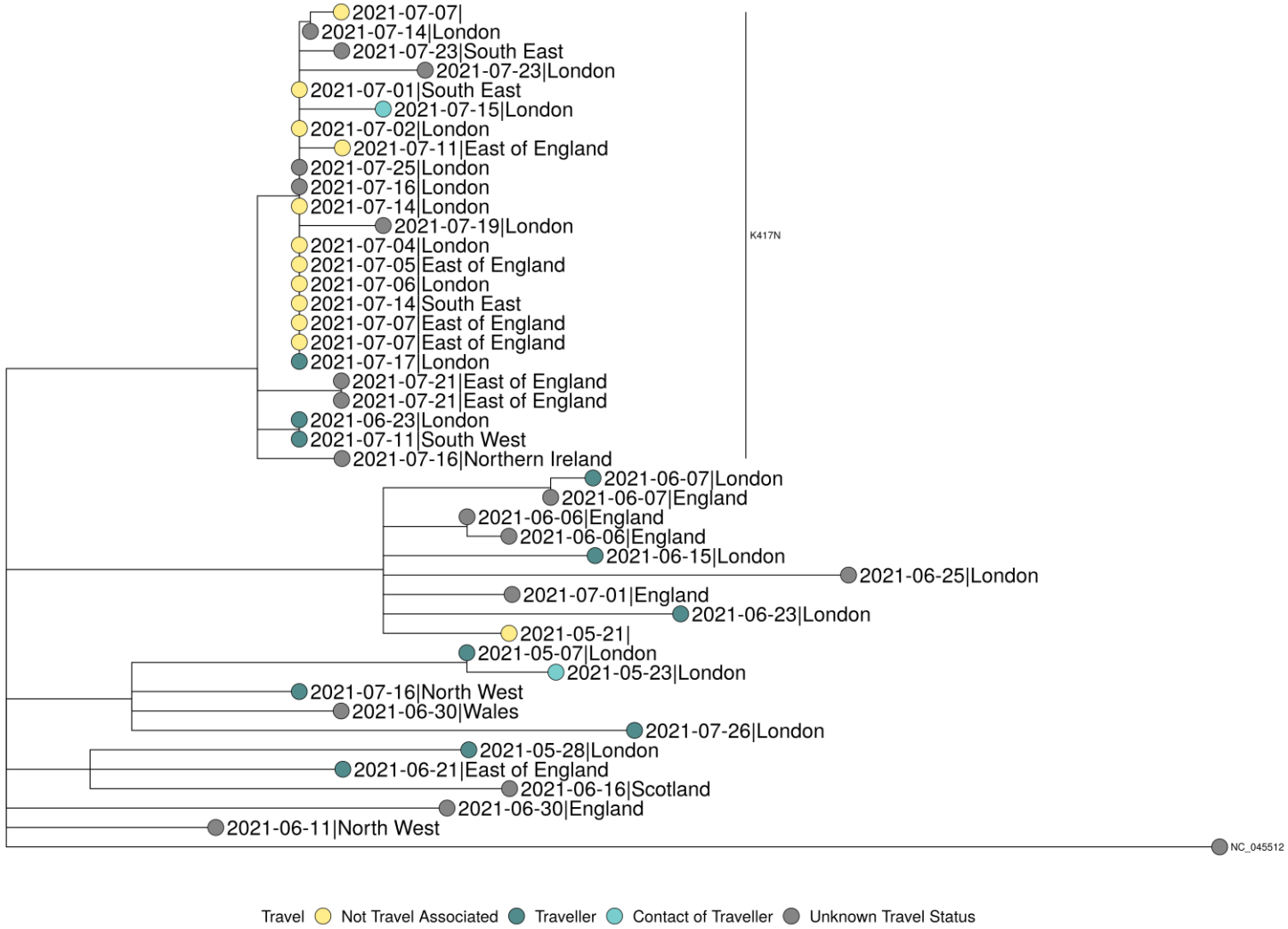
## 2.1 VUI-21JUL-01 (B.1.621) Surveillance

VUI-21JUL-01 was identified through international variant horizon scanning and was made a signal in monitoring by PHE on 7 June 2021 (lineage B.1.621 at the time). On 21 July 2021, PHE designated lineage B.1.621 as a new variant under investigation, VUI-21JUL-01, based on apparent spread into multiple countries, importation to the UK and mutations of concern.

VUI-21JUL-01 is characterised by the non-synonymous mutations NSP3; T237A, T720I. NSP4; T492I. NSP6; Q160R. NSP12; P323L. NSP13; P419S, T95I. S; R346K, E484K, N501Y, D614G, P681H, D950N. ORF3a; Q57H, ORF8; T11K, P38S, S67F, and N; T205I as well as an insertion in S at 144. Recent sequences identified as B.1.621 have also contained the spike K417N mutation.

The phylogenetic tree of UK VUI-21JUL-01 (B.1.621) cases is shown in Figure 13, which supports multiple importation events.

**Figure 13: Maximum likelihood tree of UK VUI-21JUL-01 (B.1.621) cases. Travel information is indicated by tip colour. Sample date and location of case is shown in the label for each tip. Clade containing the K417N is shown. Tree is rooted on NC_045512**



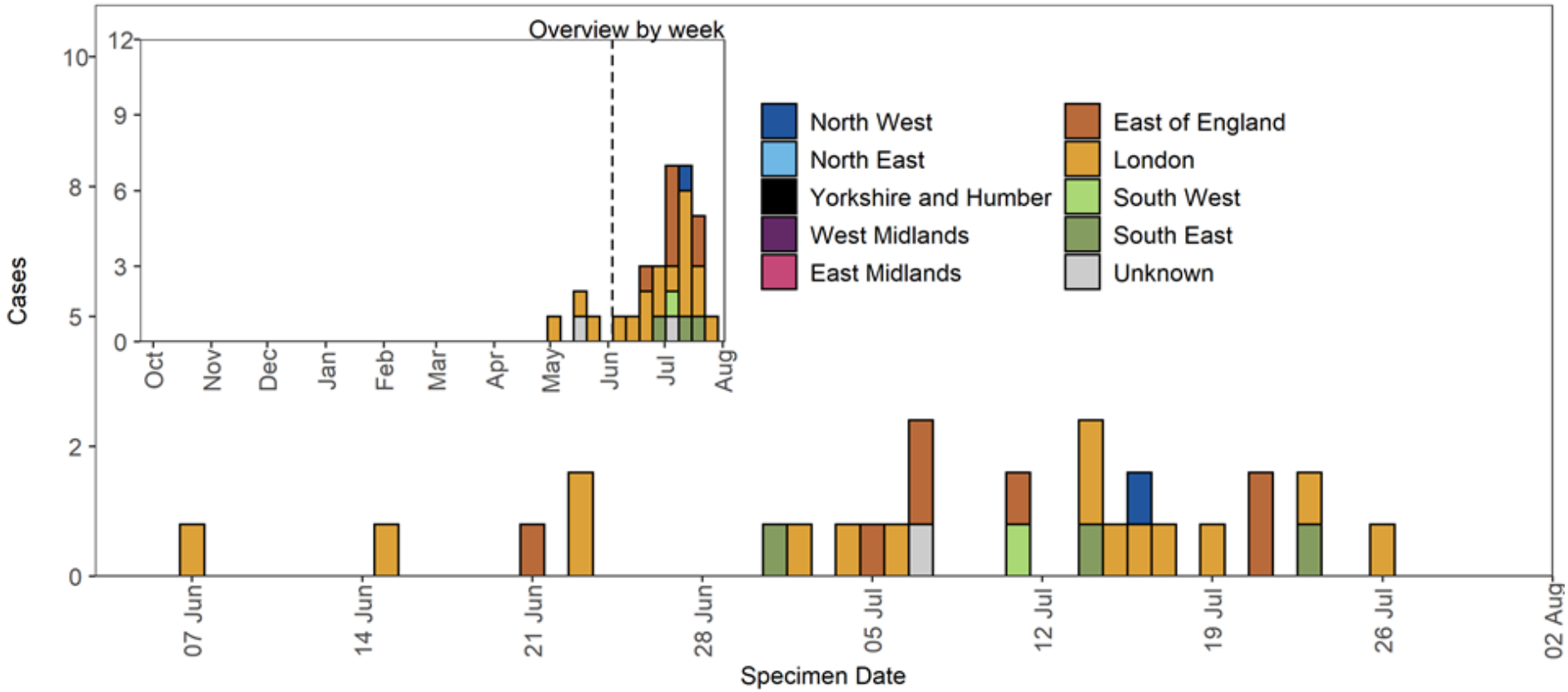
### 2.1.1 Epidemiology in England

As of 2 August 2021, there are 32 VUI-21JUL-01 cases in England and 4 genomes for which case data is being sought. Cases have been detected across 6 English regions, with most cases in London (18, 56%). The most frequent age group was the under 20 age group, with 11 cases. Seven of the 32 cases have history of travel which include travel from or transit through Mexico, Spain, Dominican Republic, and Colombia.

**Table 8. Confirmed and provisional VUI-21JUL-01 cases in England by region as of 2 August 2021**

| Region | Total case number | Proportion of total cases |
|---|---|---|
| East Midlands | 0 | 0.0% |
| East of England | 7 | 21.9% |
| London | 18 | 56.2% |
| North East | 0 | 0.0% |
| North West | 1 | 3.1% |
| South East | 3 | 9.4% |
| South West | 1 | 3.1% |
| West Midlands | 0 | 0.0% |
| Yorkshire and Humber | 0 | 0.0% |
| Unknown region | 2 | 6.2% |
| Total | 32 | - |

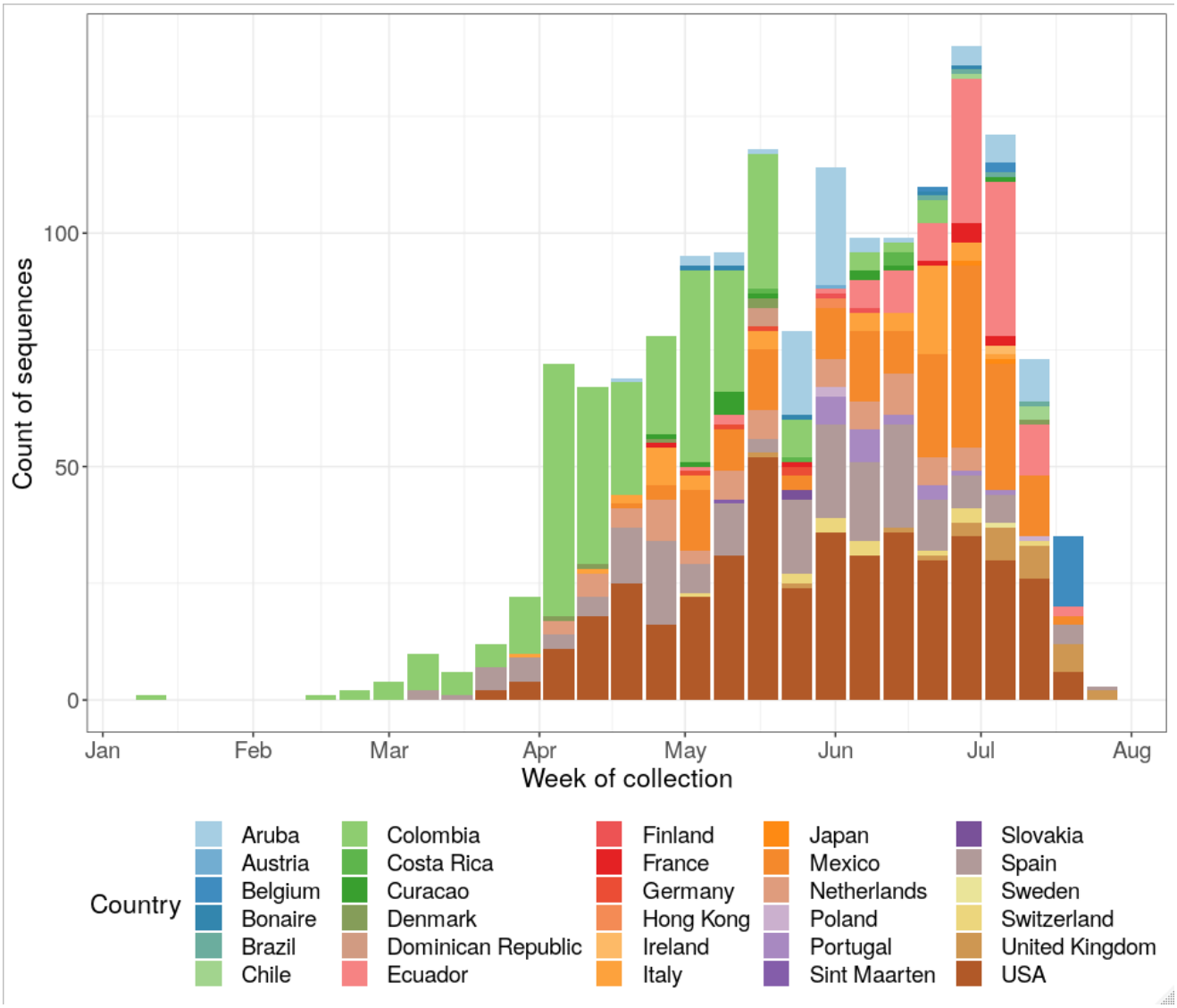
**Figure 14. Cases of VUI-21JUL-01 in England by region as of 2 August 2021**
(Find accessible data used in this graph in underlying data.)



## 2.1.2. International epidemiology

As of 2 August 2021, 3,854 sequences on GISAID have been assigned to the B.1.621 lineage. B.1.621 sequences have been uploaded from Aruba (76), Austria (49), Belgium (29), Bonaire (5), Brazil (5), Chile (1), Colombia (398), Costa Rica (5), Curacao (17), Denmark (5), Dominican Republic (9), Ecuador (107), Finland (3), France (9), Germany (15), Hong Kong (2), Ireland (4), Italy (61), Japan (2), Luxembourg (1), Malta (1), Mexico (193), Netherlands (64), Poland (3), Portugal (23), Saint Martin (2), Slovakia (3), Spain (258), Switzerland (35), USA (542). Figure 15 shows the distribution of case per country over time, based on GISAID data, indicating that an increasing number of countries reported cases in June and July.

**Figure 15. Count of B.1.621 classified sequences by week of collection uploaded to GISAID by week as of 2 August 2021**
(Find accessible data used in this graph in underlying data.)



# Sources and acknowledgments

## Data sources

Data used in this investigation is derived from the COG-UK dataset, the PHE Second Generation Surveillance System (SGSS), NHS Test and Trace, the Secondary Uses Service (SUS) dataset, Emergency Care Data Set (ECDS), and the PHE Case and Incident Management System (CIMS). Data on international cases are derived from reports in GISAID, the media and information received via the International Health Regulations National Focal Point (IHRNFP) and Early Warning and Response System (EWRS).

### Repository of human and machine-readable genomic case definitions

Genomic definitions for all VOC and VUI are provided in order to facilitate standardised VOC and VUI calling across sequencing sites and bioinformatics pipelines and are the same definitions used internally at PHE. Definition files are provided in YAML format so are compatible with a range of computational platforms. The repository will be regularly updated. The genomic and biological profiles of VOC and VUI are also detailed on first description in prior technical briefings.

## Variant Technical Group

### Authors of this report

PHE Genomics Cell
PHE Outbreak Surveillance Team
PHE Epidemiology Cell
PHE Contact Tracing Data Team
PHE International Cell
JBC Public Health Science Team
Contributions from the Variant Technical Group Members including the Genotype to Phenotype Consortium

### Variant Technical Group members and contributors

The PHE Variant Technical Group includes members and contributors from the following organisations: Public Health England, Public Health Wales, Public Health Scotland, Public Health Agency Northern Ireland, the Department of Health and Social Care, Imperial College London, London School of Hygiene and Tropical Medicine, University of Birmingham, University of Cambridge (including the MRC Biostatistics Unit), University of Edinburgh, University of Liverpool, the Wellcome Sanger Institute, the NHS Test and Trace Joint Biosecurity Centre, Genotype to Phenotype Consortium, SPI-M

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# About Public Health England

Public Health England exists to protect and improve the nation's health and wellbeing, and reduce health inequalities. We do this through world-leading science, research, knowledge and intelligence, advocacy, partnerships and the delivery of specialist public health services. We are an executive agency of the Department of Health and Social Care, and a distinct delivery organisation with operational autonomy. We provide government, local government, the NHS, Parliament, industry and the public with evidence-based professional, scientific and delivery expertise and support.

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