Public Health England

Protecting and improving the nation's health

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

Technical briefing 21

20 August 2021

This briefing provides an update on previous briefings up to 6 August 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 separate report is published covering surveillance 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
- updated biological data are available suggesting that Delta with K417N (AY.1) is unlikely to show substantial antigenic change compared to Delta

All risk assessments are published separately here, 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 technical briefing 15, briefings include variant diagnoses identified 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 (or B.1.621), Delta, and Gamma. Targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha.

1 Surveillance overview

1.1 Variants under surveillance

Table 1 shows the current VOC, VUI, and variants in monitoring as of 16 August 2021.

Table 1. Variant lineage and designation as of 16 August 2021

WHO nomenclature	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	International
	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
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	

WHO nomenclature	Lineage	Designation	Status	UK or international (not currently detected in UK)
	B.1.620		Monitoring	
	B.1.214.2		Monitoring	
	R.1		Monitoring	
	B.1 with 214insQAS		Monitoring	
	AT.1		Monitoring	
	A.30		Monitoring	
	B.1.630		Monitoring	
	P.1 + N501T and E484Q		Monitoring	
	B.1.629		Monitoring	
	B.1.619		Monitoring	
	C.1.2		Monitoring	
	B.1.630		Monitoring	
	B.1.631/B.1.628		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.

The last documented case of VUI-21APR-03 (B.1.617.3) was on the 17 May 2021 in the UK, this variant was moved to international monitoring on the 16 August 2021.

VUI-21FEB-01 (A.23.1 with E484K), 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.

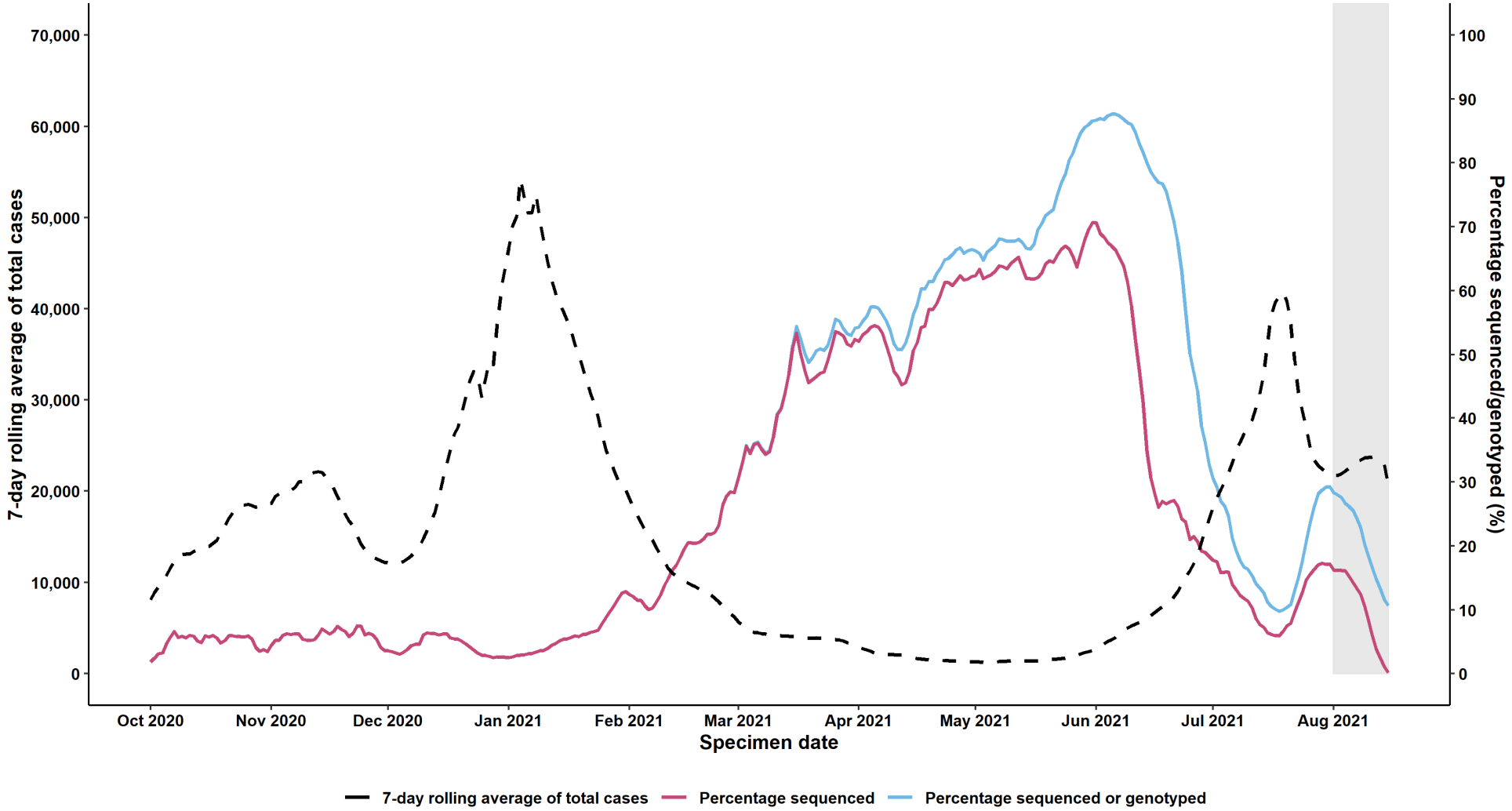
1.2 Sequencing coverage

Figure 1 shows the proportion of cases sequenced and genotyped over time. Figure 2 shows the proportion of cases sequenced and genotyped over time by regions. Figure 3 shows the proportion of cases sequenced and genotyped amongst cases who tested positive while in hospital. Figure 4 shows coverage of sequencing and genotyping for cases by age group.

Sequencing coverage is improving (Figure 1). During the current surge period, the sequencing strategy for both Pillar 1 and 2 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

Figure 1. Coverage of sequencing and genotyping over time (1 October 2020 to 15 August 2021)
(Find accessible data used in this graph in underlying data)



Data extract from 16 August 2021; data from 01 October 2020 to 15 August 2021.
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 15 August 2021)
(Find accessible data used in this graph in underlying data)

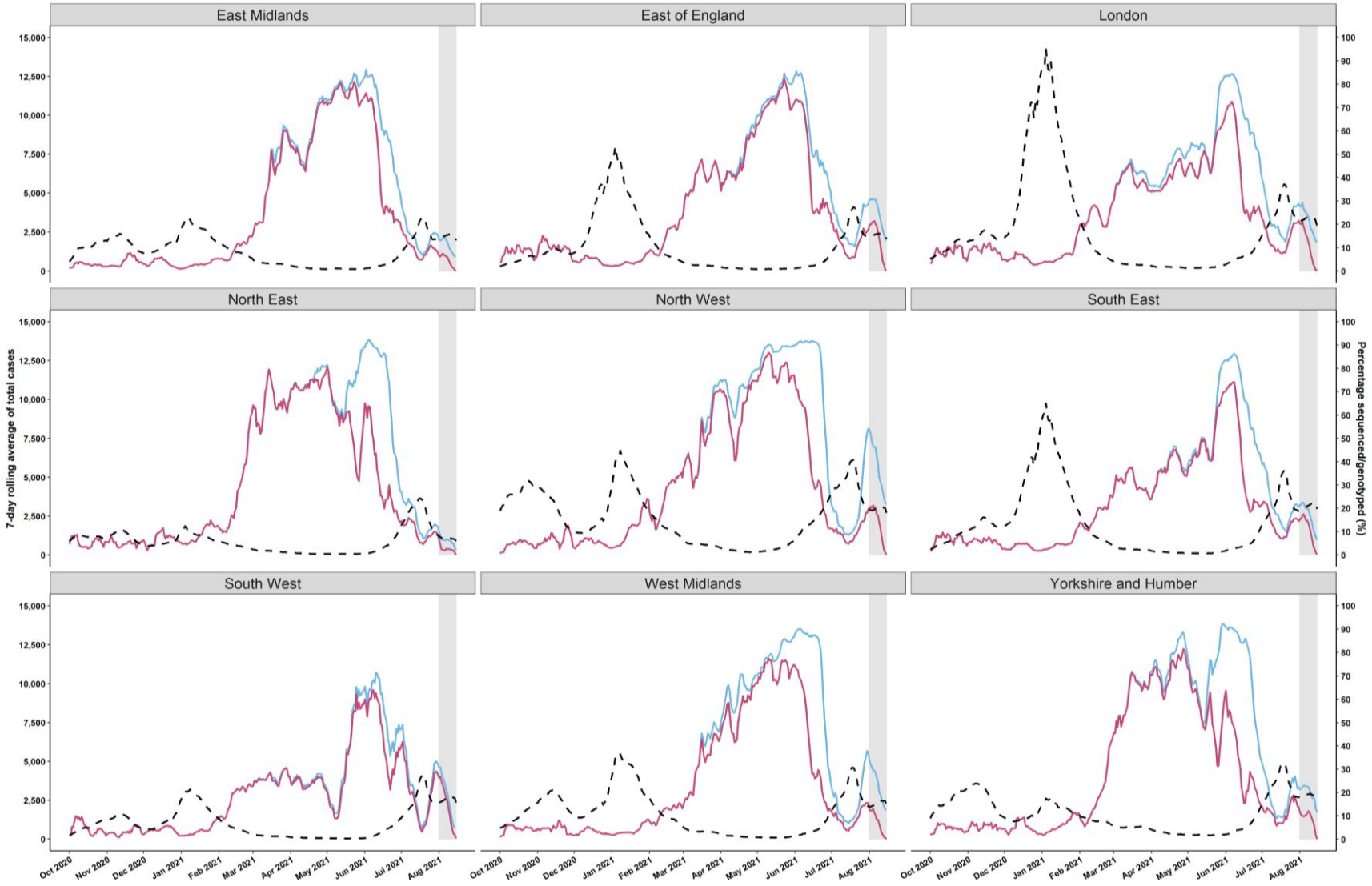
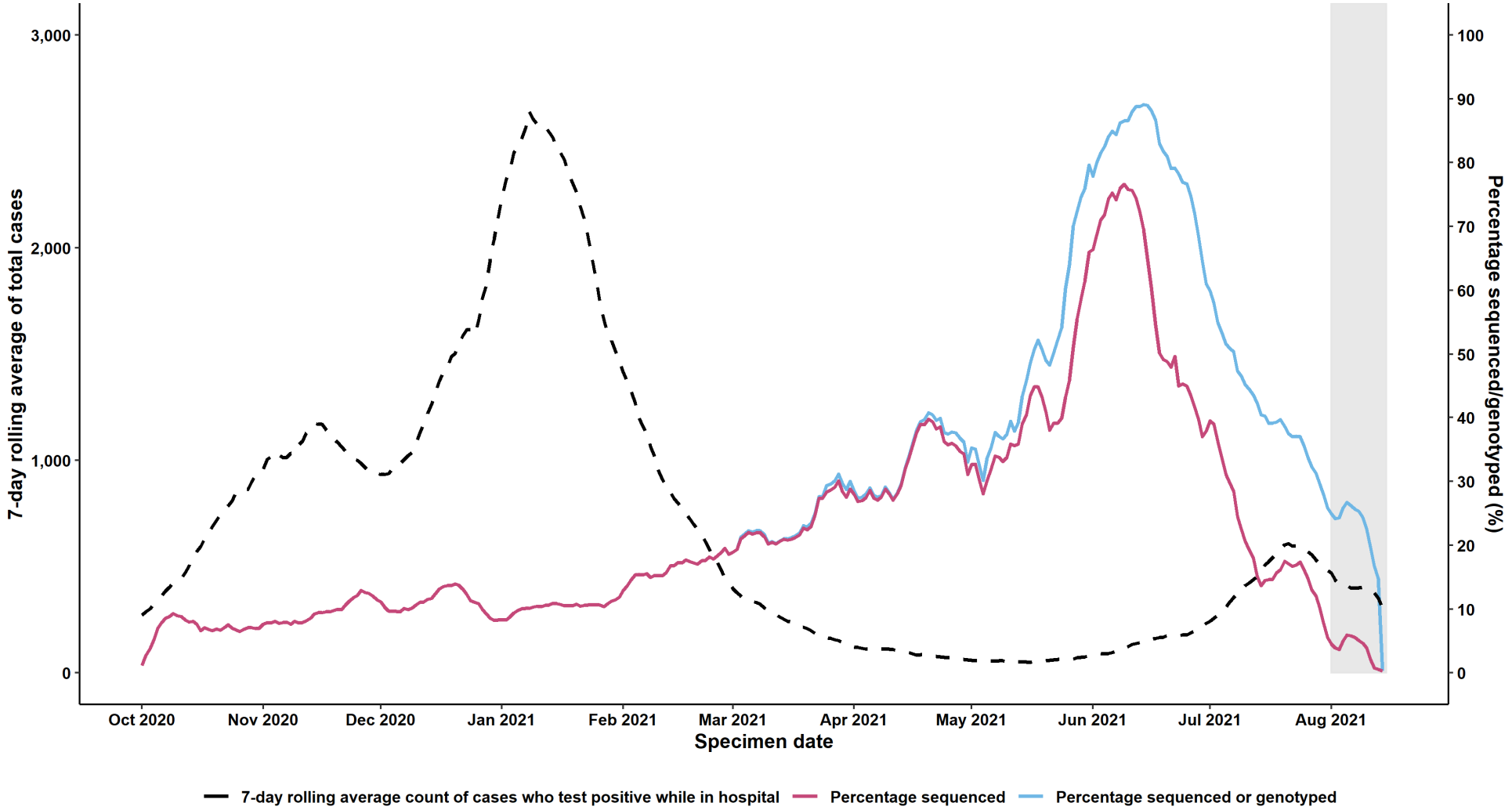
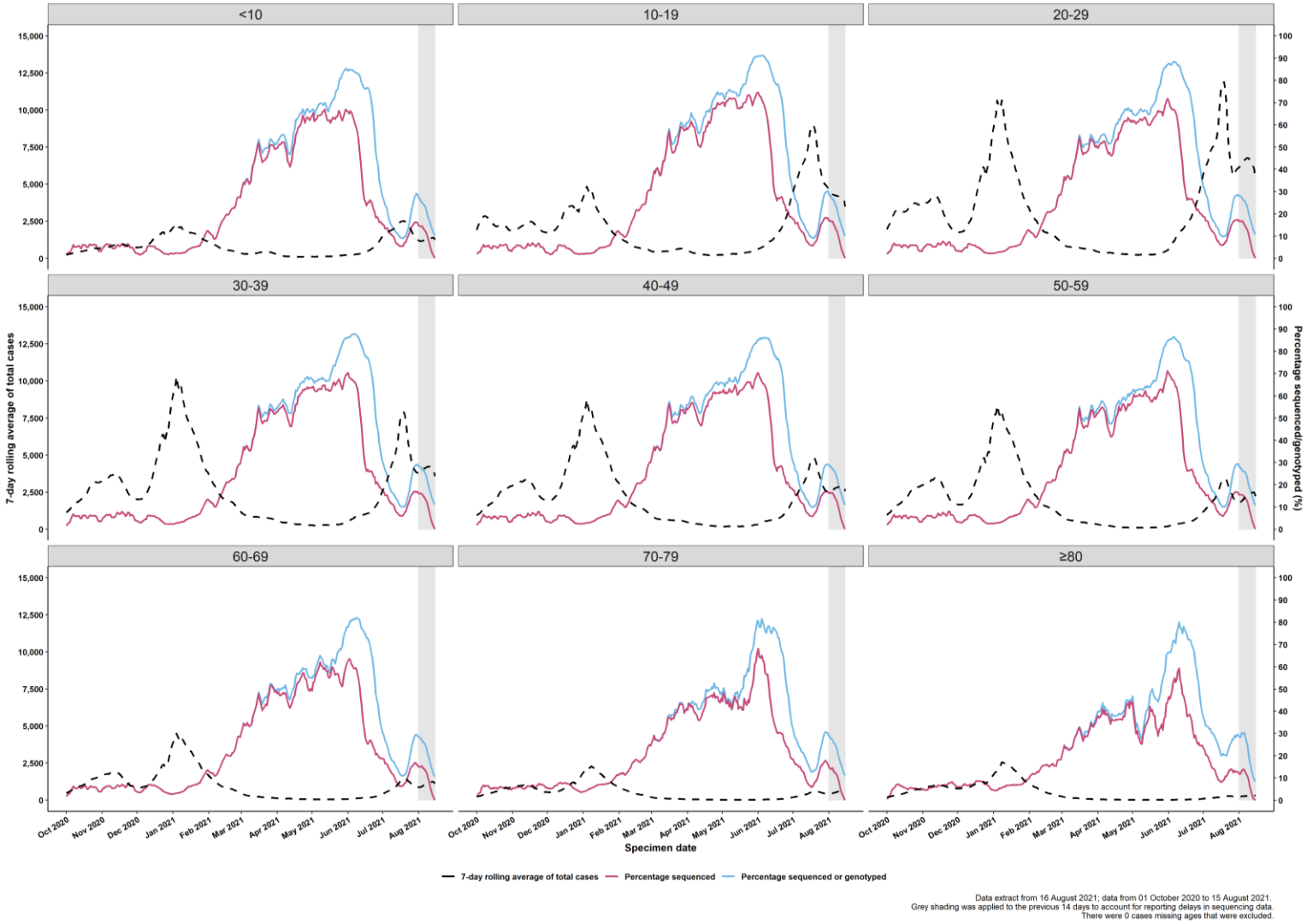


Figure 3. Coverage of sequencing and genotyping for cases who test positive in hospital (1 October 2020 to 15 August 2021)
(Find accessible data used in this graph in underlying data)



Data extract from 16 August 2021; data from 01 October 2020 to 15 August 2021.
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

Figure 4. Coverage of sequencing and genotyping for cases by age group (1 October 2020 to 11 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.

Footnote to figures 1 to 4:
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 and deaths

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 5 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 emergency care at an NHS hospital and was subsequently admitted as an inpatient. The data does not include cases who 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 Briefing 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 COVID-19 cases and ECDS data is updated twice-weekly.

Table 2. Sequenced and genotyped Delta cases by region as of 16 August 2021

Region	Sequenced cases	Genotyped cases[1]	Total case number	Proportion of total cases
East Midlands	13,477	8,098	21,575	5.6%
East of England	19,697	11,509	31,206	8.1%
London	34,586	23,319	57,905	15.0%
North East	12,748	10,469	23,217	6.0%
North West	50,726	49,281	100,007	25.9%
South East	26,797	15,460	42,257	10.9%
South West	25,207	5,489	30,696	7.9%
West Midlands	16,816	17,934	34,750	9.0%
Yorkshire and Humber	22,530	20,482	43,012	11.1%
Unknown region	980	1,247	2,227	0.6%
Total	223,564	163,288	386,852	-

[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

Table 3. Number of sequenced and genotyped cases by variant as of 16 August 2021

Variant	Confirmed (sequencing) case number	Provisional (genotyping) case number[1]	Total case number	Proportion of total cases	Deaths
Alpha	221,027	5,705	226,732	36.8%	4,323
Beta	906	71	977	0.2%	13
Delta	223,564	163,288	386,852	62.7%	1,192
Eta	443	0	443	0.1%	12
Gamma	198	42	240	0.0%	0
Kappa	448	0	448	0.1%	2
Lambda	8	0	8	0.0%	0
Theta	7	0	7	0.0%	0
VOC-21FEB-02	45	0	45	0.0%	1
VUI-21APR-03	13	0	13	0.0%	0
VUI-21FEB-01	79	0	79	0.0%	2
VUI-21FEB-04	300	0	300	0.0%	1
VUI-21JUL-01	37	0	37	0.0%	0
VUI-21MAR-01	2	0	2	0.0%	0
VUI-21MAY-01	184	0	184	0.0%	1
VUI-21MAY-02	142	0	142	0.0%	0
Zeta	54	0	54	0.0%	1

[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

Table 4. Attendance to emergency care and deaths of sequenced and genotyped cases in England (1 February 2021 to 15 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	118,236	55	0.0	5,005	4.2	5,835	4.9	1,239	1.0	1,676	1.4	67	0.1
	≥50	32,286	9	0.0	3,150	9.8	4,581	14.2	1,725	5.3	2,761	8.6	1,552	4.8
	All cases	150,620	64	0.0	8,155	5.4	10,416	6.9	2,964	2.0	4,437	2.9	1,619	1.1
Beta	<50	599	5	0.8	26	4.3	28	4.7	5	0.8	8	1.3	1	0.2
	≥50	164	2	1.2	18	11.0	26	15.9	7	4.3	15	9.1	7	4.3
	All cases	772	7	0.9	44	5.7	54	7.0	12	1.6	23	3.0	8	1.0
Gamma	<50	218	4	1.8	9	4.1	9	4.1	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	239	4	1.7	10	4.2	10	4.2	1	0.4	1	0.4	-	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	%
Delta	<50	337,834	106,718	31.6	11,195	3.3	14,676	4.3	2,538	0.8	4,112	1.2	113	0.0
	≥50	48,264	20,295	42.0	2,952	6.1	5,098	10.6	1,593	3.3	3,173	6.6	1,076	2.2
	All cases	386,735	127,091	32.9	14,147	3.7	19,774	5.1	4,131	1.1	7,285	1.9	1,189	0.3
Zeta	<50	16	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	≥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	10	3.7	12	4.4	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	14	3.6	19	4.9	6	1.5	9	2.3	6	1.5

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-21FEB-04	<50	235	2	0.9	6	2.6	9	3.8	1	0.4	2	0.9	-	0.0
	≥50	57	-	0.0	1	1.8	2	3.5	-	0.0	1	1.8	1	1.8
	All cases	293	2	0.7	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	384	1	0.3	9	2.3	10	2.6	1	0.3	2	0.5	-	0.0
	≥50	65	-	0.0	6	9.2	6	9.2	3	4.6	3	4.6	2	3.1
	All cases	449	1	0.2	15	3.3	16	3.6	4	0.9	5	1.1	2	0.4

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	11	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	≥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

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	%
Lambda	<50	8	-	0.0	1	12.5	1	12.5	1	12.5	1	12.5	-	0.0
	≥50	7	2	29	1	14	1	14	-	-	-	-	-	-
	All cases	8	-	0.0	1	12.5	1	12.5	1	12.5	1	12.5	-	0.0
VUI-21JUL-01	<50	30	4	13.3	1	3.3	1	3.3	-	0.0	-	0.0	-	0.0
	≥50	7	2	28.6	1	14.3	1	14.3	-	0.0	-	0.0	-	0.0
	All cases	37	6	16.2	2	5.4	2	5.4	-	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 sequenced and genotyped Delta cases in England by vaccination status (1 February 2021 to 15 August 2021)

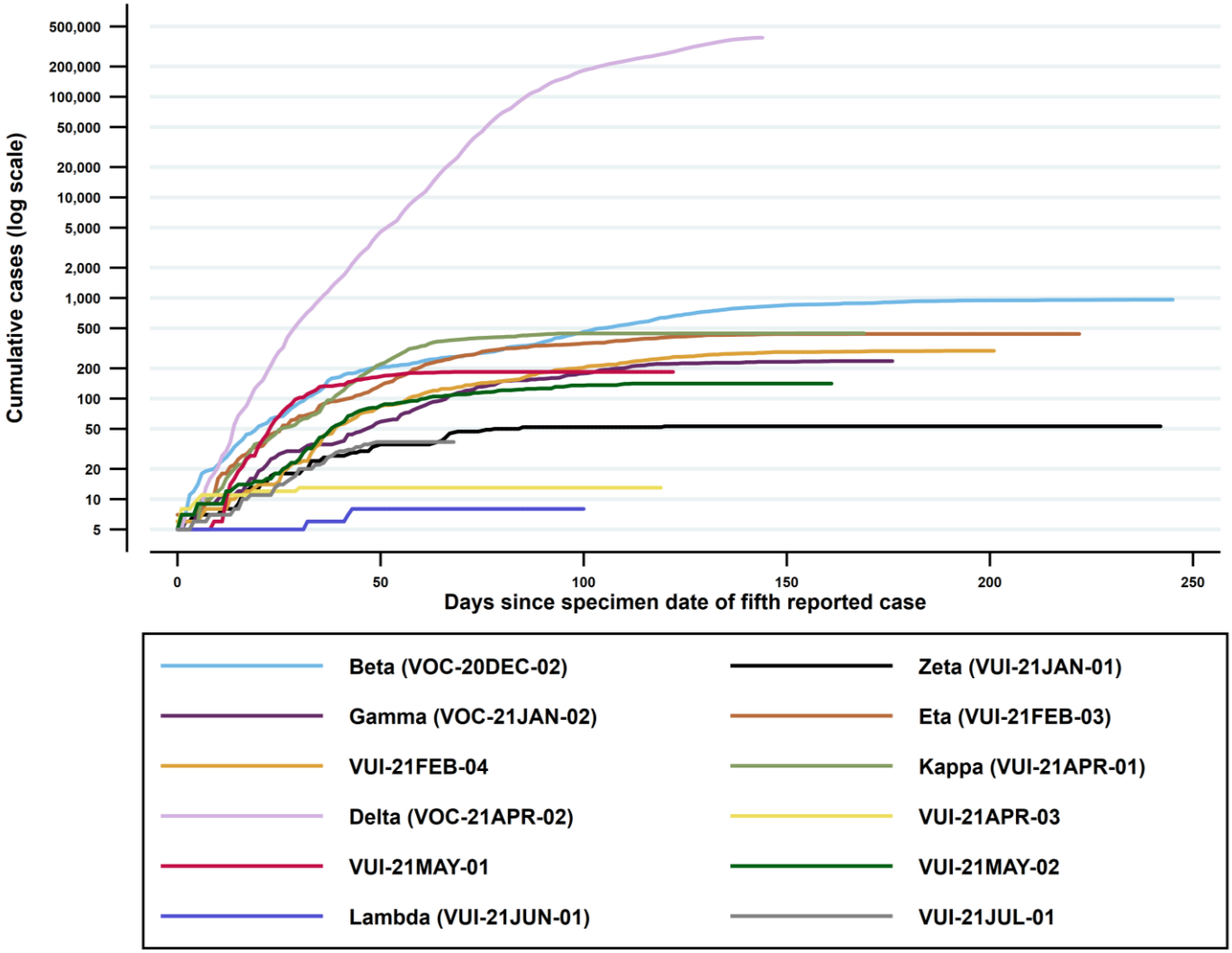
Variant	Age group (years)**	Total	Cases with specimen date in past 28 days	Unlinked	<21 days post dose 1	≥21 days post dose 1	≥14 days post dose 2	Unvac-cinated
Delta cases	<50	337,834	106,718	35,397	25,965	57,688	40,544	178,240
	≥50	48,264	20,295	4,242	228	6,075	32,828	4,891
	All cases	386,735	127,091	40,273	26,194	63,763	73,372	183,133
Cases with an emergency care visit§ (exclusion‡)	<50	11,195	N/A	88	886	1,581	1,161	7,479
	≥50	2,952	N/A	18	19	372	1,803	740
	All cases	14,147	N/A	106	905	1,953	2,964	8,219
Cases with an emergency care visit§ (inclusion#)	<50	14,676	N/A	154	1,111	1,926	1,447	10,038
	≥50	5,098	N/A	36	43	574	2,956	1,489
	All cases	19,774	N/A	190	1,154	2,500	4,403	11,527

Cases where presentation to emergency care resulted in overnight inpatient admission§ ((exclusion‡)	<50	2,538	N/A	41	144	267	246	1,840
	≥50	1,593	N/A	11	13	149	990	430
	All cases	4,131	N/A	52	157	416	1,236	2,270
Cases where presentation to emergency care resulted in overnight inpatient admission§ (inclusion#)	<50	4,112	N/A	71	229	402	366	3,044
	≥50	3,173	N/A	28	31	287	1,838	989
	All cases	7,285	N/A	99	260	689	2,204	4,033
Deaths within 28 days of positive specimen date	<50	113	N/A	3	6	5	27	72
	≥50	1,076	N/A	13	8	85	652	318
	All cases	1,189	N/A	16	14	90	679	390

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 5. Cumulative cases in England of variants indexed by days since the fifth reported case as of 15 August 2021
(Find accessible data used in this graph in underlying data)



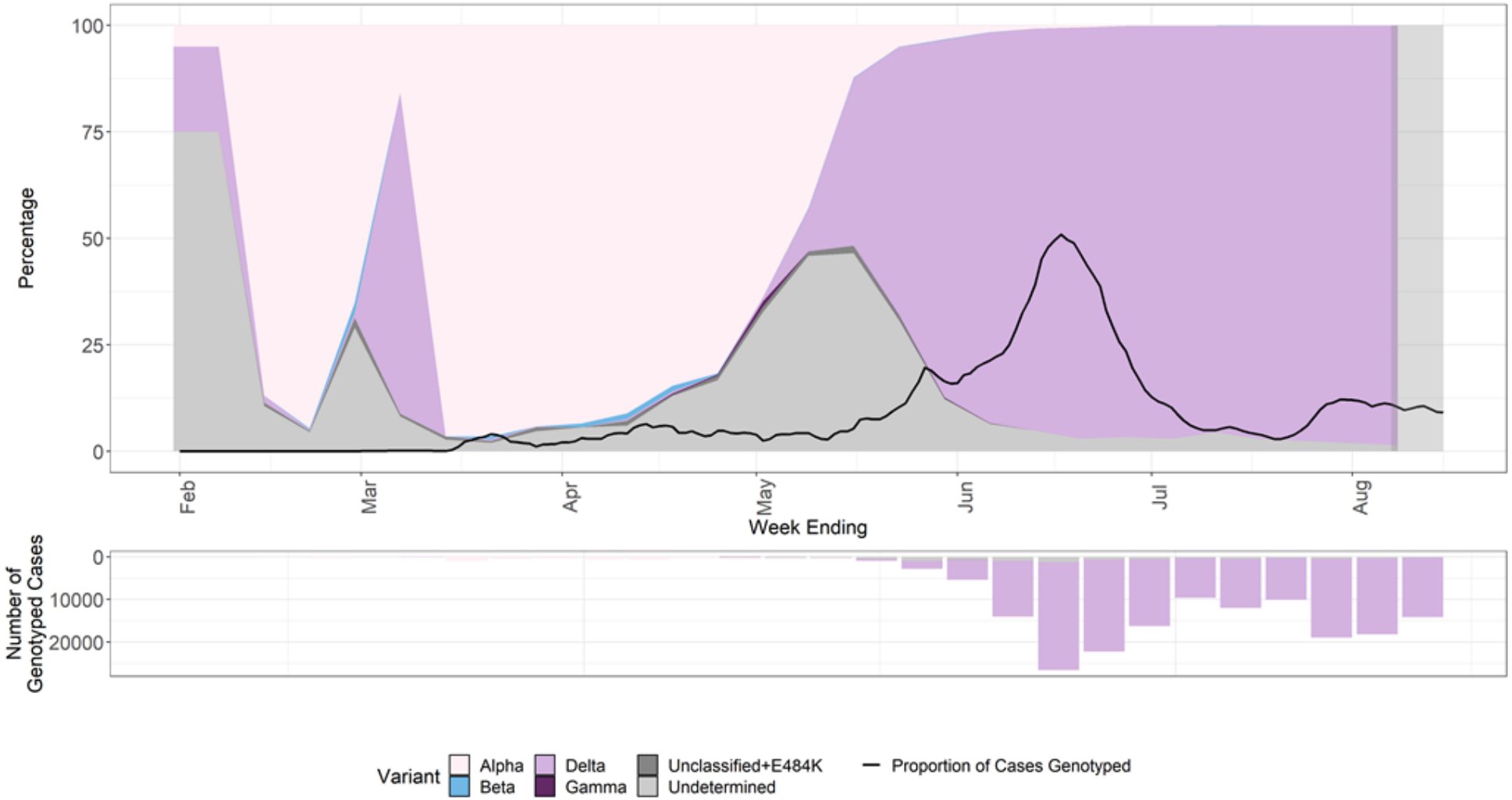
1.4 Variant prevalence

The prevalence of different variants amongst genotyped and sequenced cases is presented in Figures 6 and 7 and split by region in Figures 8 and 9. 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 7 and 9 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. The supplementary data for figures are available.

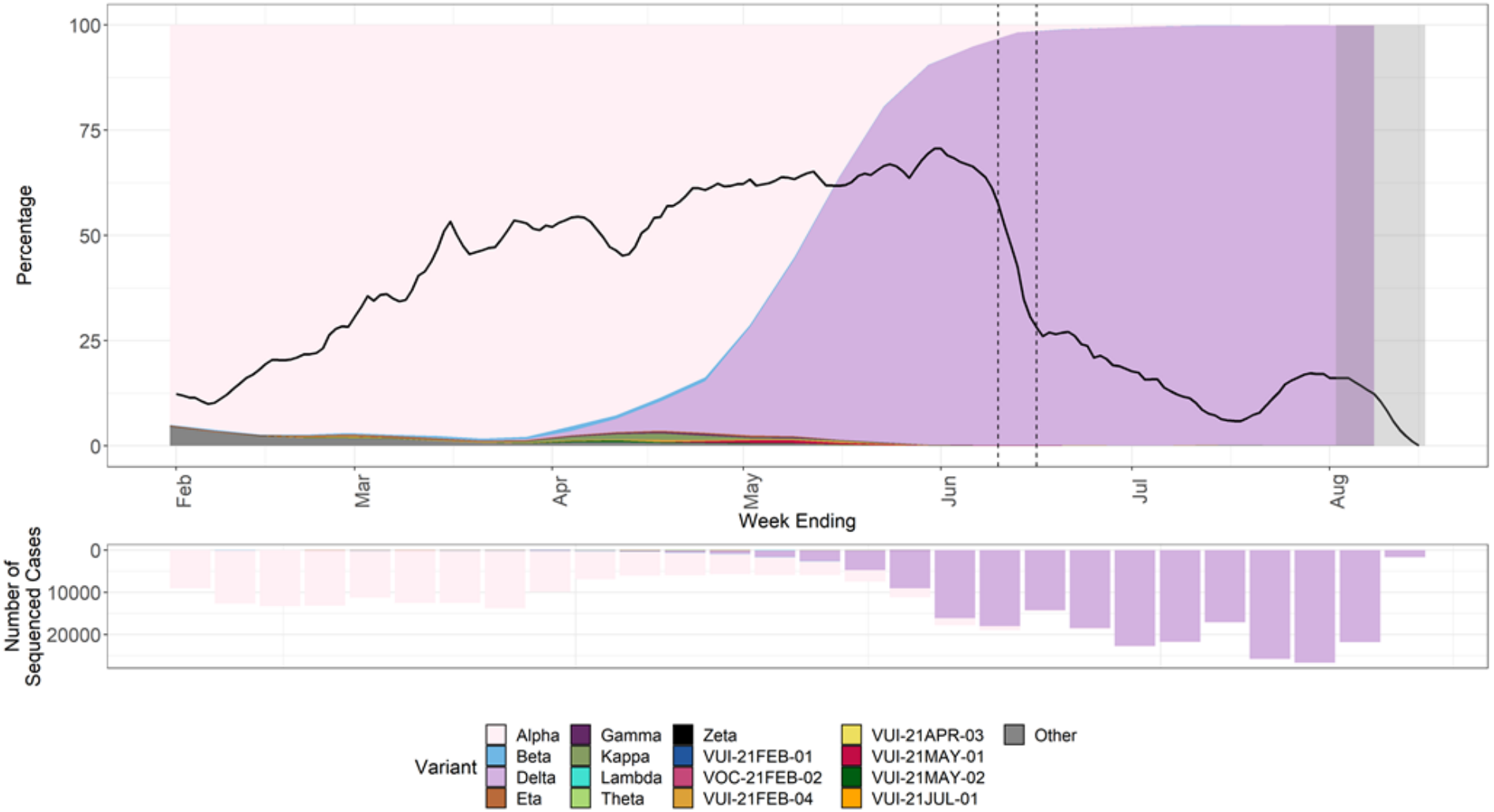
Delta variant accounted for approximately 99% of sequenced and 99% genotyped cases from 8 August to 14 August 2021.

Figure 6. Variant prevalence for all England available genotyped cases from 1 February 2021 as of 16 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 7. Variant prevalence for all England available sequenced cases from 1 February 2021 as of 16 August 2021 (excluding 172 cases where the specimen date was unknown). (Find accessible data used in this graph in underlying data).



Dashed lines indicate period incorporating issue at a sequencing site.

Figure 8. Variant prevalence from 1 February 2021 as of 16 August 2021 by region for all genotyped cases in England (excluding 1540 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data)

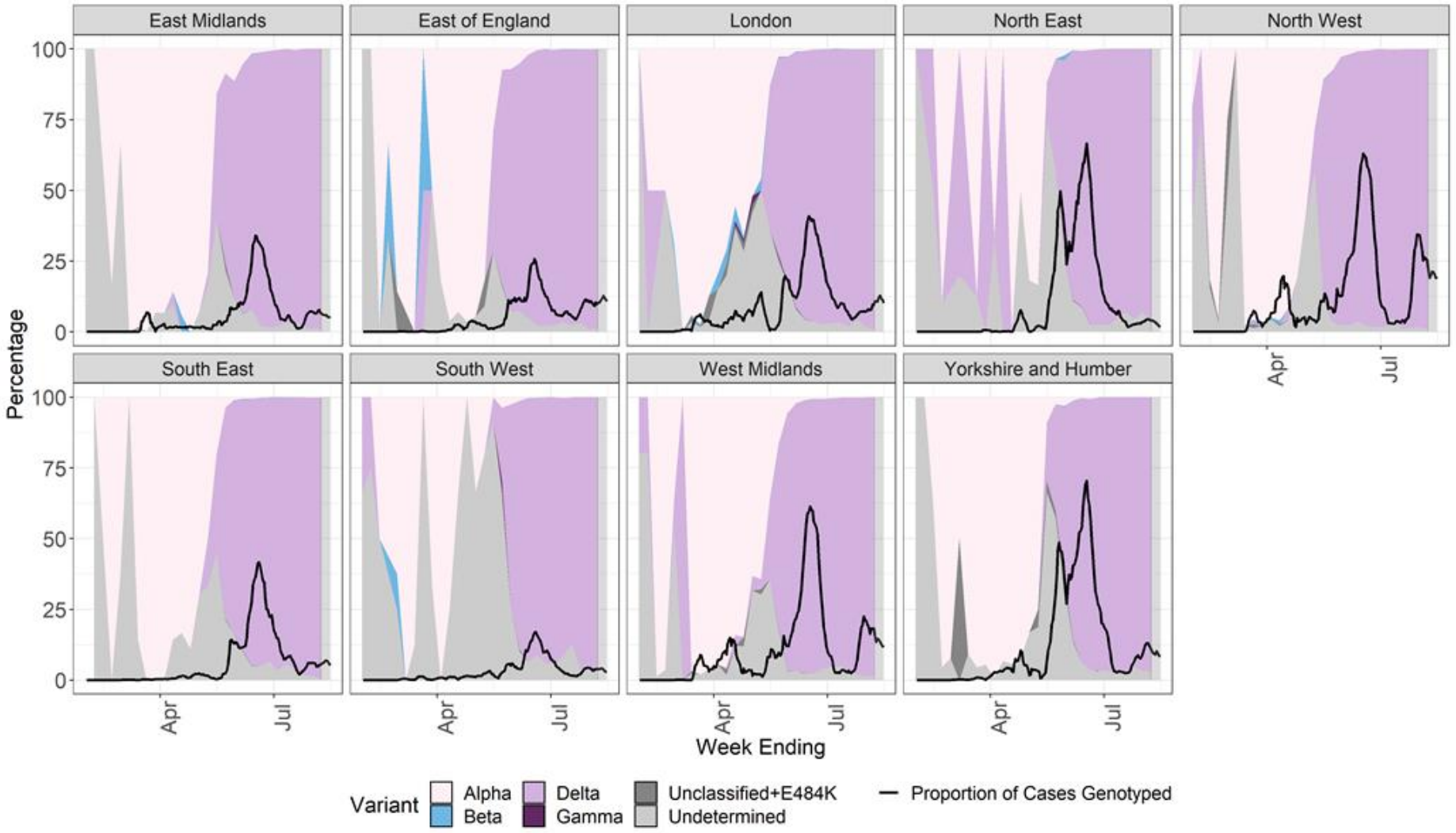
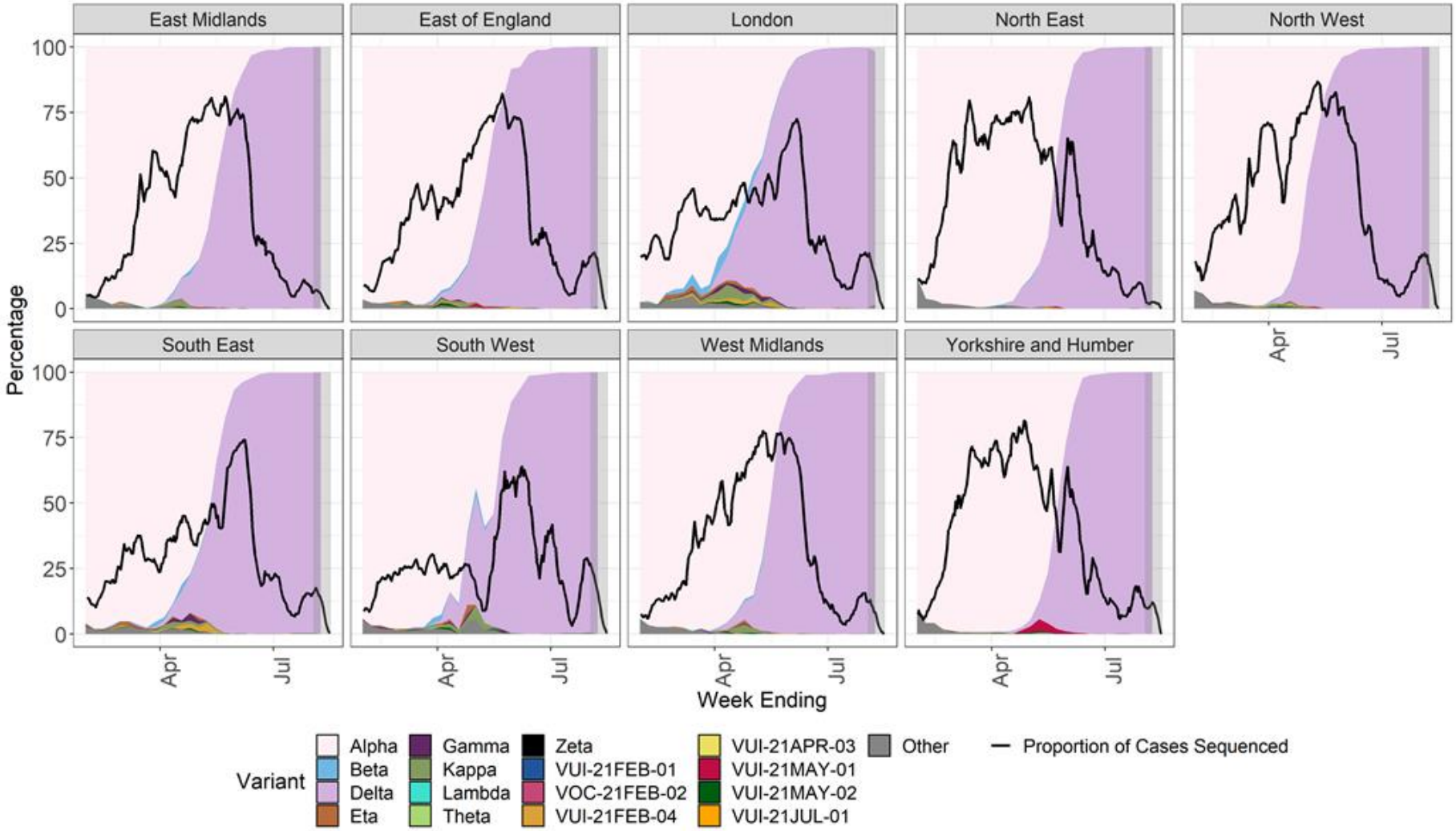


Figure 9. Variant prevalence from 1 February 2021 as of 16 August 2021 by region for all sequenced cases in England (excluding 1767 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data)



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 17 August 2021 (excluding UK data).

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 17 August 2021

Amino acid change	Delta Number of sequences (COG UK)	Delta Number of sequences GISAID (outside UK)	Delta Number of sequences 18 May to 17June 2021		Delta Number of sequences 18 June to 17 July 2021		Delta Number of sequences 18 July to 17 August 2021	
			England	Outside UK	England	Outside UK	England	Outside UK
P251L	1,982	3,288	32	99	277	1,581	383	1,586
G446V	889	437	101	44	152	169	161	176
V483F	182	92	5	7	40	34	72	31
Q493E	104	71	2	19	28	27	59	17
K417N	87	1,929	15	449	2	997	28	373
S494L	77	82	5	15	14	21	43	41
L455F	67	92	2	17	21	17	36	51
V445I	62	5	0	3	10	1	40	1
E484Q	57	404	1	33	7	218	30	140
K444N	42	61	4	14	3	22	17	19
N501Y	39	476	0	44	12	118	13	301
F490L	34	6	0	1	11	0	17	2
S494P	32	37	2	9	10	12	11	10
K458N	28	12	0	4	22	3	6	5
P681H	22	96	2	14	0	11	8	69
R246I	21	18	1	0	4	3	15	6
K444R	18	4	0	0	5	2	9	2
P499L	11	9	2	0	2	5	5	3
F490S	9	18	0	3	1	6	7	8
Q493L	8	24	0	0	2	15	3	9
E484A	7	26	1	12	2	13	0	1
E484K	2	99	0	5	1	34	1	59
D80A	2	72	0	18	0	35	1	4
Total	**299,969**	**248,481**	**60,269**	**27,613**	**85,356**	**110,785**	**80,676**	**91,869**

1.6 Reinfections

Population data based on the first time that individuals tested positive for SARS-CoV-2 through PCR and/or lateral flow device testing in England together with those who have tested positive for SARS-CoV-2 through PCR and/or lateral flow testing with an interval of at least 90 days between 2 consecutive positive tests show, to the end of week 30 in 2021 (to 1 August 2021), there have been 5.2 million first infections with 35,124 possible reinfections identified, of which 137 have been confirmed by identification of genetically distinct specimens from each illness episode. See surveillance report for further details.

1.7 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.

1.7.1 Updates on Delta with K417N (AY.1 and AY.2)

- Data from the Genotype to Phenotype (G2P) consortium demonstrated that Delta with K417N (AY.1) does not show increased replication in human airway culture compared to Delta (B.1.617.2)
- G2P also reports that when sera from healthcare workers who had been double vaccinated are tested in a live virus neutralization assay against Delta or Delta with K417N isolate, there was no significant difference in titres.
- Oxford University report that when sera from individuals who had been infected with SARS-CoV-2 early in the pandemic are tested, there is no reduction in ability to neutralise Delta with K417N pseudovirus compared to Delta pseudovirus. Delta with K417N demonstrated a 1.9-fold mean reduction and Delta a 2.8-fold mean reduction compared to original SAR-CoV-2 pseudovirus.
- PHE Porton Down report that sera from individuals who had been infected with SARS-CoV-2 early in the pandemic show no reduction in ability to neutralise Delta with K417N wild virus compared to Delta wild virus.
- PHE Colindale reports that using peptide-based assays, a single point mutation at 417 was not associated with significant antigenic variation and is therefore unlikely to contribute significantly to antigenic escape.

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

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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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