Public Health England

Protecting and improving the nation's health

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

Technical briefing 19

23 July 2021

This briefing provides an update on previous briefings up to 9 July 2021

Contents

Summary 3
Published information on variants 4
Part 1: Surveillance overview 5
1.1 Variants under surveillance 5
1.2 Sequencing coverage 7
1.3 VOC and VUI case numbers, proportion, deaths and case fatality rate 11
1.4 Variant prevalence 21
1.5 Antigenic change over time (international) 26
1.6 Secondary attack rates 29
1.7 Reinfections 35
1.8 Updates from Variant Technical Group Members 40
Part 2: Surveillance of individual variants 41
2.1 Delta (B.1.617.2) surveillance 41
2.2 VUI-21JUL-01 Surveillance 51
Sources and acknowledgments 53
Data sources 53
Variant Technical Group 53

Summar y

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 risk assessments updated this week are for Beta and Delta and there is one new VUI.

A separate report is published covering our routine data on all other variants of concern and variants under investigation. The specialist technical briefings contain early data and analysis on emerging variants and findings have a high level of uncertainty.

Principal changes and findings this week are:

- the number of genome sequence results available is maintained but the coverage has fallen with the increasing case numbers
- Delta variant accounted for approximately 99% of sequenced and 96% genotyped cases from 4 July to 10 July 2021
- distinct clades within Delta have been identified in the UK, which are primarily distinguished by changes outside spike ±additional spike mutations on Delta occur at relatively low frequencies at present
- preliminary analysis of national surveillance data finds an increased risk of reinfection with Delta, compared to Alpha
- B.1.621 has been designated a VUI on 21 July 2021, previously being a signal in monitoring. The new designation is based on international spread, importation to the UK, and mutations of concern
- one new variant in monitoring has been designated (C.1.2)

All risk assessments are published separately, except for Gamma, which was published within Technical Briefing 7 and Alpha within Technical Briefing 9.

All risk assessments are published separately here, except for Gamma, which was published within Technical Briefing 7, Alpha within Technical Briefing 9, and Delta in Technical Briefing 10. As Delta is the dominant variant in the UK, epidemiological data in the weekly surveillance report is highly relevant and available.

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 confirmed and probable 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 21 July. 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. Summary epidemiology on Delta is shown in Table 2 and for each variant is shown in Table 3, case numbers are also updated online.

Figure 4 shows cumulative cases of variants over time.

Table 1. Variant lineage and designation as of 21 July 2021

WHO nomenclature as of 19 July 2021	Lineage	Designation	Status
Alpha	B.1.1.7	VOC-20DEC-01	VOC
Beta	B.1.351	VOC-20DEC-02	VOC
Gamma	P.1	VOC-21JAN-02	VOC
Delta	B.1.617.2, AY.1 and AY.2	VOC-21APR-02	VOC
Zeta	P.2	VUI-21JAN-01	VUI
Eta	B.1.525	VUI-21FEB-03	VUI
	B.1.1.318	VUI-21FEB-04	VUI
Theta	P.3	VUI-21MAR-02	VUI
Kappa	B.1.617.1	VUI-21APR-01	VUI
	B.1.617.3	VUI-21APR-03	VUI
	AV.1	VUI-21MAY-01	VUI
	C.36.3	VUI-21MAY-02	VUI
Lambda	C.37	VUI-21JUN-01	VUI
	B.1.621	VUI-21JUL-01	VUI
	B.1.1.7 with E484K	VOC-21FEB-02	*Monitoring
Epsilon	B.1.427/B.1.429		Monitoring

WHO nomenclature as of 19 July 2021	Lineage	Designation	Status
	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
	R.1		Monitoring
	B.1 with 214insQAS		Monitoring
	AT.1		Monitoring
	Lineage A with R346K, T478R and E484K		Monitoring
	Delta like variant with E484A		Monitoring
	P.1 + N501T and E484Q		Monitoring
	B.1.629		Monitoring
	B.1.619		Monitoring
	C.1.2		Monitoring

Note that provisionally extinct variants are excluded from this table.

*VOC-21FEB-02 (B.1.1.7 with E484K). This specific clade of B.1.1.7 with E484K has not been detected in England since 1 March 2021. There is apparent transmission outside the UK based on international sequence data. It is no longer included in the data update but monitoring of international data continues.

1.2 Sequencing coverage

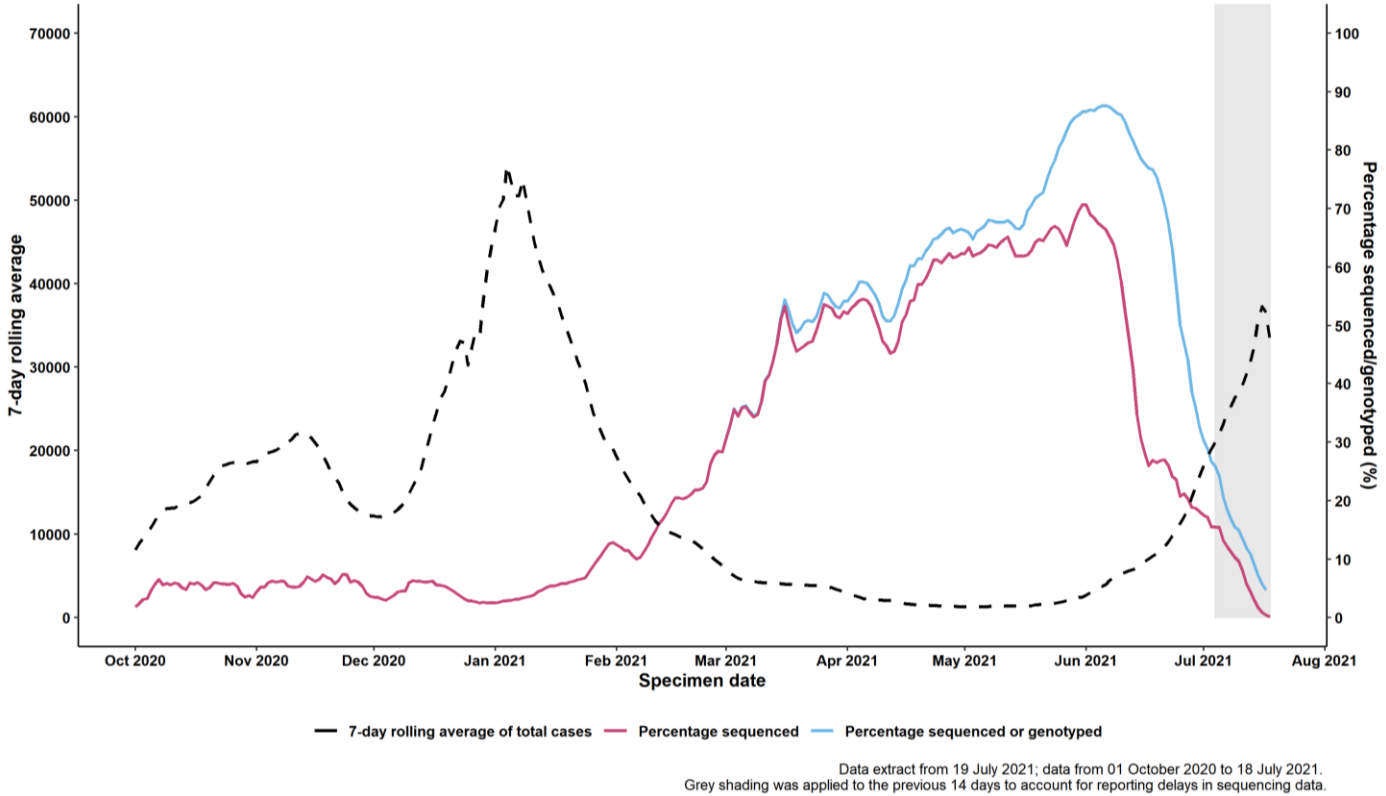
Sequencing capacity has been maintained, but the proportion of cases sequenced has fallen with increasing case numbers.

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
- imported cases
- national core priority studies
- as near random a sample as possible from each region, to the maximum coverage allowed by laboratory capacity

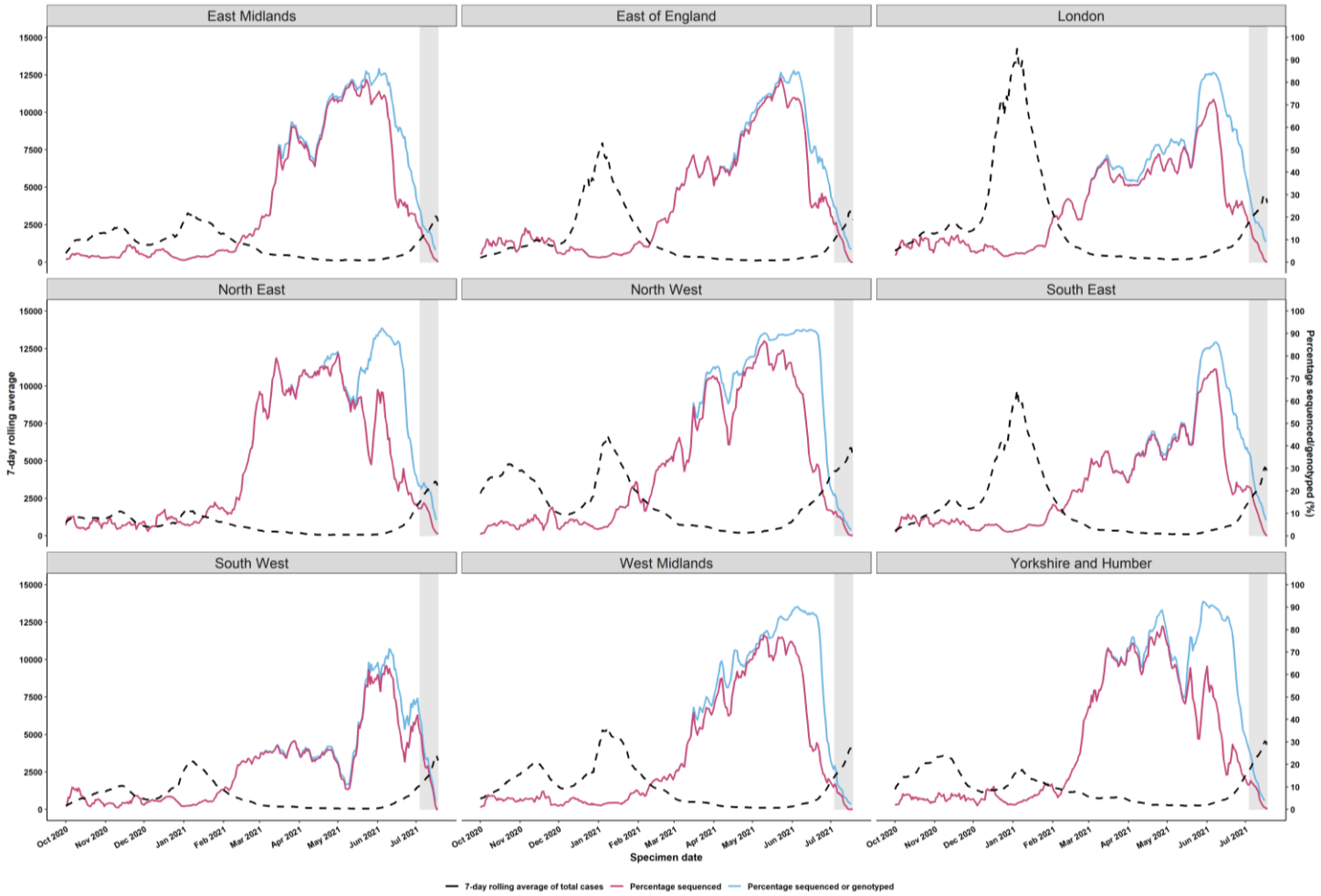
The increase in cases observed in England since the middle of June has resulted in a lower proportion of samples being sent for whole-genome sequencing (WGS) and genotyping. On July 4, 2021, 25.8% of new samples had further typing information of which 15.5 % of which was derived from WGS and an additional 10.3% provided by genotyping.

Figure 1 . Coverage of s equencing and genotyping : percentage of SARS -CoV-2 cases sequenced over time as of 19 July 2021 (Find accessible data used in this graph in underlying data)[1]



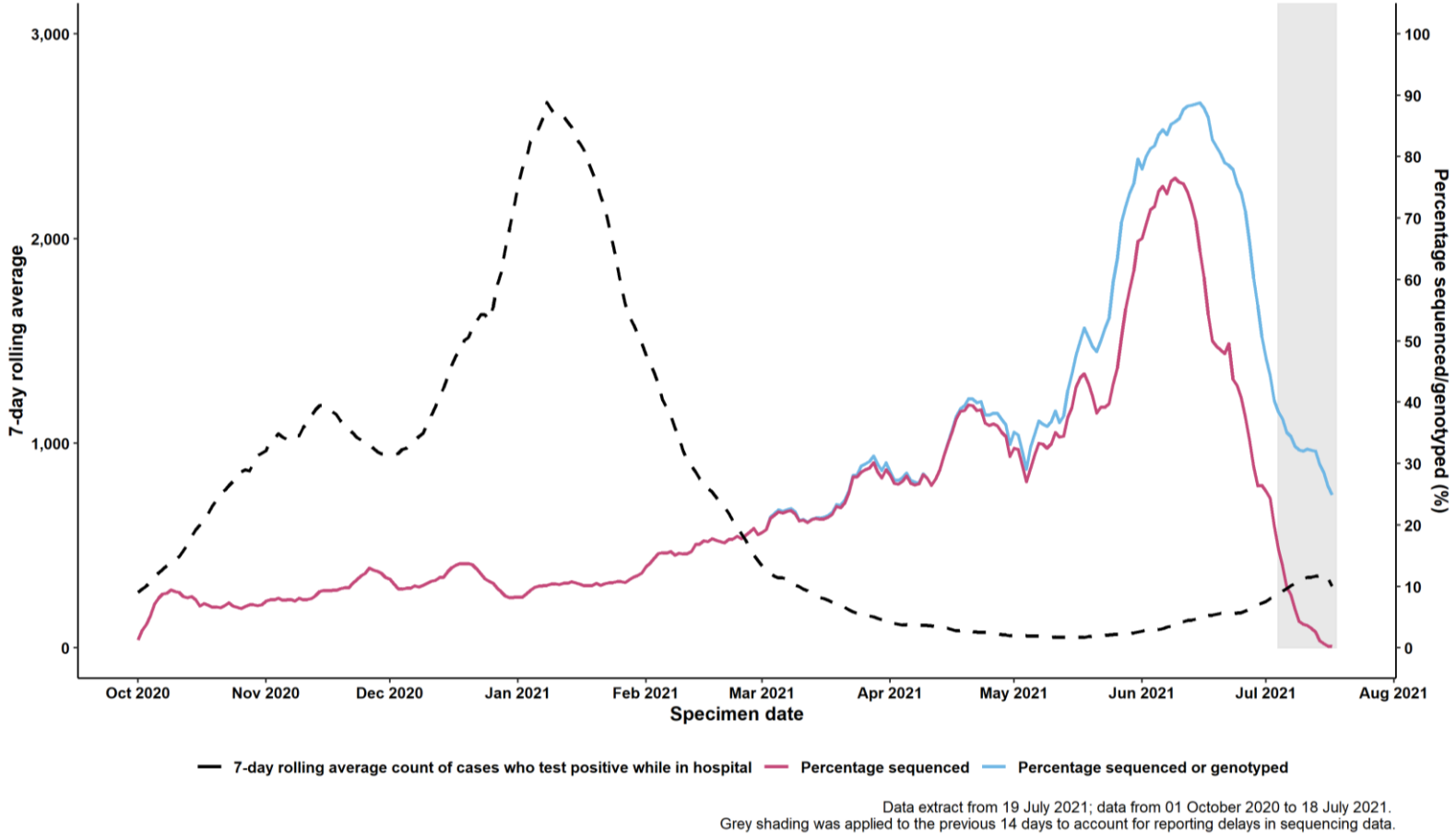
[1] From 14 to 18 June 2021 an operational issue at a sequencing site resulted in a reduction in the number of samples with sequencing data of sufficient quality for variant assignment. There were 19,502 samples reported to PHE as impacted by the incident. PHE has received approximately 10,000 sample 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. Approximately 9,000 samples are pending analysis and 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.

Figure 2. Coverage of sequencing and genotyping : percentage of SARS -CoV-2 cases sequenced over time by region as of 19 July 2021 (Find accessible data used in this graph in underlying data)



Date extract from 19 July 2021, data from 01 October 2020 to 18 July 2021.
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.
There were 5095 cases missing PHEC that were excluded.

Figure 3. Coverage of sequencing and genotyping : percentage of SARS -CoV-2 cases sequenced among cases who test positive while in hospital as of 19 July 2021 (Find accessible data used in this graph in underlying data)



[1] 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

Table 3 shows the number of cases and deaths associated with each VOC and VUI, and the proportion of total sequenced cases accounted for by each variant. Note case fatality rates are not comparable across variants (see Table 3 footnote). Tables 4 and 5 show the number of cases known to be infected with a VOC or VUI who visited an NHS Emergency Department, the number who were admitted, and the number who died in any setting (note data is shown from 1 February 2021 onwards to enable comparison). Figure 4 shows the cumulative number of cases per variant indexed by days since first report.

Hospitalisation data are subject to reporting delays as hospitals typically submit data once a month, although some may provide daily updates. The data show only cases who have been hospitalised and not those who are currently in hospital with COVID-19. As such, it is not appropriate for use for surveillance of those currently hospitalised with COVID-19. In addition, the data will not show cases who were directly admitted as inpatients without presenting to emergency care.

Attended emergency care are those cases with a record in the Emergency Care Data Set showing that they presented to emergency care one to 28 days after the specimen date. The Emergency Care Data Set is updated weekly, and sequence data are linked to the data daily.

Figure 4 shows cumulative case numbers per variant indexed by days since the fifth reported case.

Table 2. Number of confirmed and provisional Delta cases by region of residence as of 19 July 2021

Region	Confirmed case number	Provisional case number	Total case number	Proportion of total cases
East Midlands	8,192	4,936	13,128	5.7%
East of England	9,218	4,515	13,733	6.0%
London	18,248	15,099	33,347	14.5%
North East	8,765	10,264	19,029	8.3%
North West	35,996	30,425	66,421	29.0%
South East	13,903	10,868	24,771	10.8%
South West	12,875	3,139	16,014	7.0%
West Midlands	8,702	8,801	17,503	7.6%
Yorkshire and Humber	10,864	13,325	24,189	10.5%
Unknown region	573	594	1,167	0.5%
Total	127,336	101,966	229,302	n/a

Table 3. Number of confirmed (sequencing) and probable (genotyping) cases by variant as of 19 July 2021

Variant	Confirmed (sequencing) case number	Probable (genotyping) case number [1]	Total case number	Proportion of total cases	Deaths
Alpha	220,500	5,677	226,177	49.3%	4,265
Beta	898	71	969	0.2%	13
Delta	127,336	101,966	229,302	50.0%	461
Eta	443	0	443	0.1%	12
Gamma	189	42	231	0.1%	0
Kappa	446	0	446	0.1%	1
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	292	0	292	0.1%	1
VUI-21MAR-01	2	0	2	0.0%	0
VUI-21MAY-01	184	0	184	0.0%	1
VUI-21MAY-02	140	0	140	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 among all sequenced and genotyped COVID-19 cases in England, 1 February 2021 to 19 July 2021

Variant	Age Group (years)	Cases Since 1 Feb	Cases with specimen date in past 28 days		Cases with an A&E visit§ H [F O X V L R		Cases with an A&E visit§ (inclusion#)		Cases where presentation to A&E resulted in overnight inpatient admission§ H [F O X V L I		Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#)		Deaths^	
			n	%	n	%	n	%	n	%	n	%	n	%
Alpha (VOC-20DEC-01)	<50	118,082	331	0.3	4,963	4.2	5,808	4.9	1,230	1.0	1,680	1.4	66	0.1
	•	32,265	29	0.1	3,125	9.7	4,586	14.2	1,713	5.3	2,779	8.6	1,548	4.8
	All cases	150,436	361	0.2	8,088	5.4	10,394	6.9	2,943	2.0	4,459	3.0	1,614	1.1
Beta (VOC-20DEC-02)	<50	595	15	2.5	24	4.0	26	4.4	5	0.8	8	1.3	1	0.2
	•	161	2	1.2	17	10.6	25	15.5	7	4.3	15	9.3	7	4.3
	All cases	763	18	2.4	41	5.4	51	6.7	12	1.6	23	3.0	8	1.0
Gamma (VOC-21JAN-02)	<50	209	3	1.4	9	4.3	9	4.3	1	0.5	1	0.5	-	0.0
	•	21	3	14.3	1	4.8	1	4.8	-	0.0	-	0.0	-	0.0
	All cases	230	6	2.6	10	4.3	10	4.3	1	0.4	1	0.4	-	0.0
Delta (VOC-21APR-02)	<50	205,549	94,294	45.9	6,471	3.1	8,325	4.1	1,529	0.7	2,327	1.1	45	0.0
	•	23,379	10,933	46.8	1,319	5.6	2,263	9.7	687	2.9	1,365	5.8	415	1.8

Variant	Age Group (years)	Cases Since 1 Feb	Cases with specimen date in past 28 days		Cases with an A&E visit§ H [F O X V L R		Cases with an A&E visit§ (inclusion#)		Cases where presentation to A&E resulted in overnight inpatient admission§ H [F O X V L I		Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#)		Deaths^	
			n	%	n	%	n	%	n	%	n	%	n	%
	All cases	229,218	105,298	45.9	7,790	3.4	10,588	4.6	2,216	1.0	3,692	1.6	460	0.2
Zeta (VUI-21JAN-01)	<50	16	-	0.0	0	0.0	-	0.0	0	0.0	0	0.0	0	0.0
	•	8	-	0.0	1	12.5	1	12.5	1	12.5	1	12.5	0	0.0
	All cases	24	-	0.0	1	4.2	1	4.2	1	4.2	1	4.2	0	0.0
Eta (VUI-21FEB-03)	<50	273	-	0.0	11	4.0	13	4.8	5	1.8	6	2.2	0	0.0
	•	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	230	1	0.4	6	2.6	9	3.9	1	0.4	2	0.9	0	0.0
	•	54	-	0.0	1	1.9	2	3.7	0	0.0	1	1.9	1	1.9
	All cases	285	1	0.4	7	2.5	11	3.9	1	0.4	3	1.1	1	0.4
Theta (VUI-21MAR-02)	<50	4	0	0.0	1	25.0	1	25.0	0	0.0	0	0.0	0	0.0
	•	3	0	0.0	0	0.0	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§ H [F O X V L R		Cases with an A&E visit§ (inclusion#)		Cases where presentation to A&E resulted in overnight inpatient admission§ H [F O X V L I		Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#)		Deaths^	
			n	%	n	%	n	%	n	%	n	%	n	%
	All cases	7	0	0.0	1	14.3	1	14.3	0	0.0	0	0.0	0	0.0
Kappa (VUI-21APR-01)	<50	382	0	0.0	10	2.6	11	2.9	1	0.3	2	0.5	0	0.0
	•	64	0	0.0	5	7.8	5	7.8	2	3.1	2	3.1	1	1.6
	All cases	446	0	0.0	15	3.4	16	3.6	3	0.7	4	0.9	1	0.2
VUI-21APR-03	<50	11	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
	•	2	0	0.0	0	0.0	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	0	0.0	0	0.0
VUI-21MAY-01	<50	161	0	0.0	1	0.6	2	1.2	0	0.0	1	0.6	0	0.0
	•	23	-	0.0	0	0.0	0	0.0	0	0.0	0	0.0	1	4.3
	All cases	184	-	0.0	1	0.5	2	1.1	0	0.0	1	0.5	1	0.5
VUI-21MAY-02	<50	109	4	3.7	8	7.3	9	8.3	2	1.8	3	2.8	0	0.0
	•	30	-	0.0	0	0.0	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§ H [F O X V L R		Cases with an A&E visit§ (inclusion#)		Cases where presentation to A&E resulted in overnight inpatient admission§ H [F O X V L I		Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#)		Deaths^	
			n	%	n	%	n	%	n	%	n	%	n	%
	All cases	140	4	2.9	8	5.7	9	6.4	2	1.4	3	2.1	0	0.0
Lambda (VUI-21JUN-01)	<50	8	0	0.0	1	12.5	1	12.5	1	12.5	1	12.5	0	0.0
	•	-	-	-	-	-	-	-	-	-	-	-	-	-
	All cases	8	0	0.0	1	12.5	1	12.5	1	12.5	1	12.5	0	0.0

Data sources: Emergency care attendance and admissions from Emergency Care Dataset (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
ÁExclusion: 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.

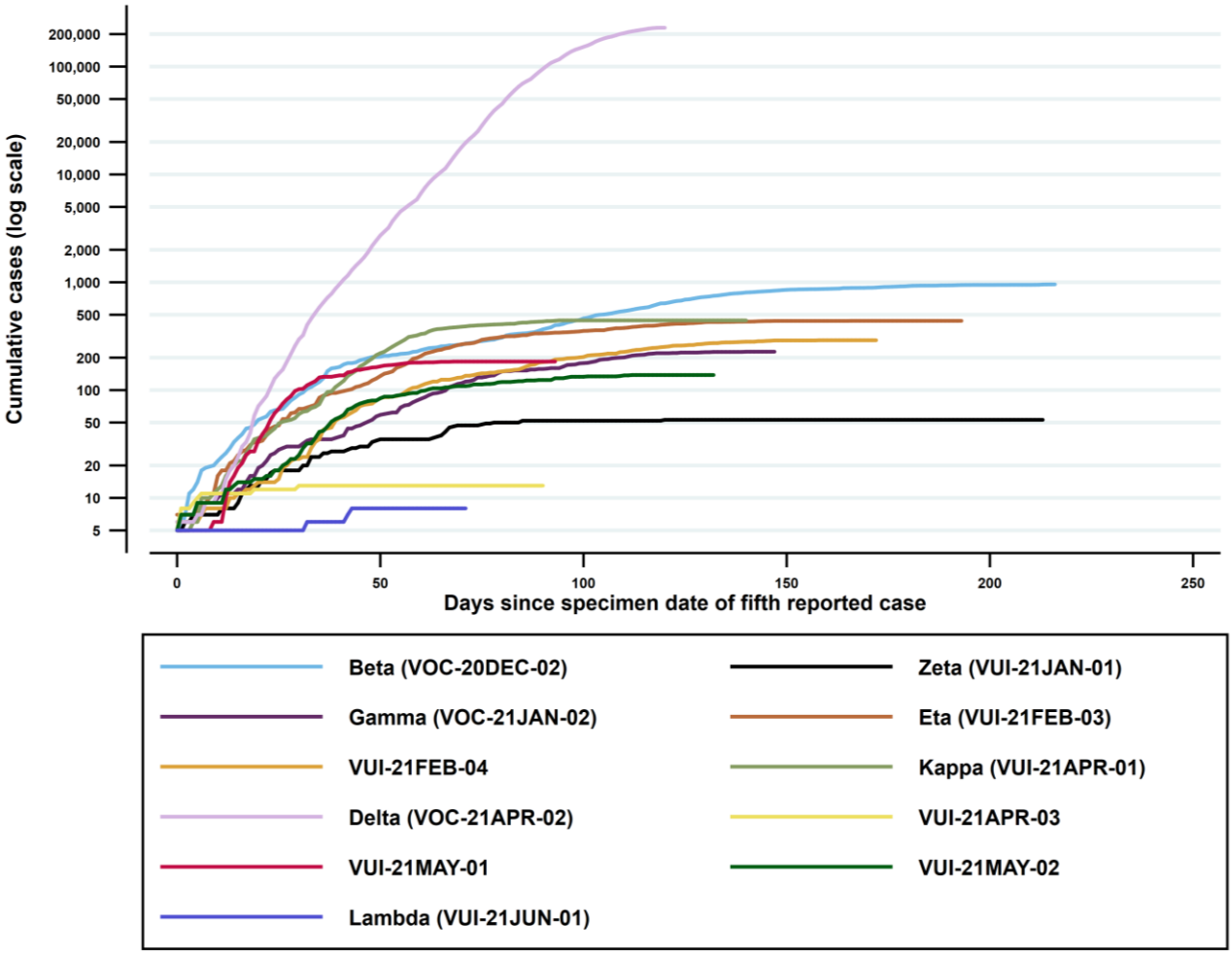
Table 5. Attendance to emergency care and deaths by vaccination status among all sequenced and genotyped Delta cases in England from 1 February 2021 to 19 July 2021

Variant	Age group (years)**	Total	Cases with specimen date in past 28 days	Unlinked	<21 days post dose 1	• G D \ V post dose 1	Received 2 doses	Unvaccinated
Delta cases	<50	205,549	94,294	22,496	20,930	27,714	15,346	119,063
	•	23,379	10,933	2,169	157	5,289	13,427	2,337
	All cases	229,218	105,298	24,952	21,088	33,003	28,773	121,402
Cases with an emergency care Y L V L W † H [F O X V L R Q	<50	6,471	N/A	73	597	851	429	4,521
	•	1,319	N/A	7	11	297	672	332
	All cases	7,790	N/A	80	608	1,148	1,101	4,853
Cases with an emergency care visit§ (inclusion#)	<50	8,325	N/A	110	756	1,025	531	5,903
	•	2,263	N/A	18	22	435	1,125	663
	All cases	10,588	N/A	128	778	1,460	1,656	6,566
Cases where presentation to emergency care resulted in overnight inpatient admission§ H [F O X V L R Q Á	<50	1,529	N/A	36	127	158	103	1,105
	•	687	N/A	4	9	107	371	196
	All cases	2,216	N/A	40	136	265	474	1,301
Cases where presentation to emergency care resulted in	<50	2,327	N/A	51	185	239	140	1,712

overnight inpatient admission§ (inclusion#)	•	1,365	N/A	13	18	191	703	440
	All cases	3,692	N/A	64	203	430	843	2,152
Deaths within 28 days of positive specimen date	<50	45	N/A	1	3	3	4	34
	•	415	N/A	5	2	57	220	131
	All cases	460	N/A	6	5	60	224	165

Data sources: Emergency care attendance and admissions from Emergency Care Dataset (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
ÁExclusion: 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 µ D O O pe Dateg or y 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 19 July 2021
(Find accessible data used in this graph in underlying data)



1.4 Variant prevalence

The prevalence of different variants amongst all genotyped and sequenced cases is presented in Figures 5 and 6 and split by region in Figures 7 and 8. Genotyping allows a shorter turnaround time of 12 to 24 hours (after initial confirmation of COVID-19) for a probable variant result. 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 5 to 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 96% genotyped cases from 4 July to 10 July 2021.

Figure 5. Variant prevalence for all England available genotyped cases from 1 February 2021 to 19 July 2021
(Find accessible data used in this graph in underlying data)

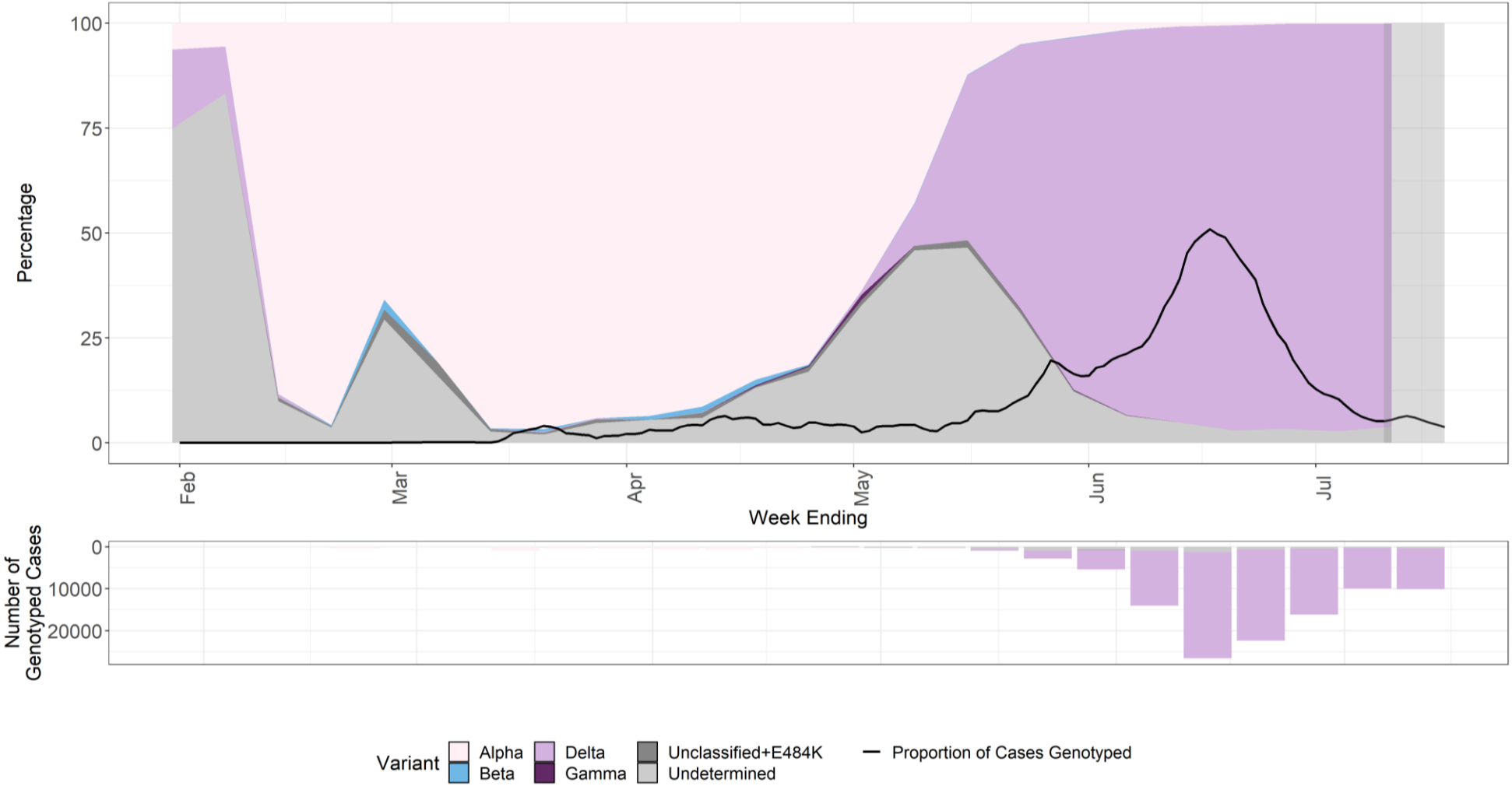


Figure 6. Variant prevalence for all England available sequenced cases from 1 February 2021 as of 19 July 2021
Dashed lines indicate period incorporating issue at a sequencing site. (Find accessible data used in this graph in underlying data).

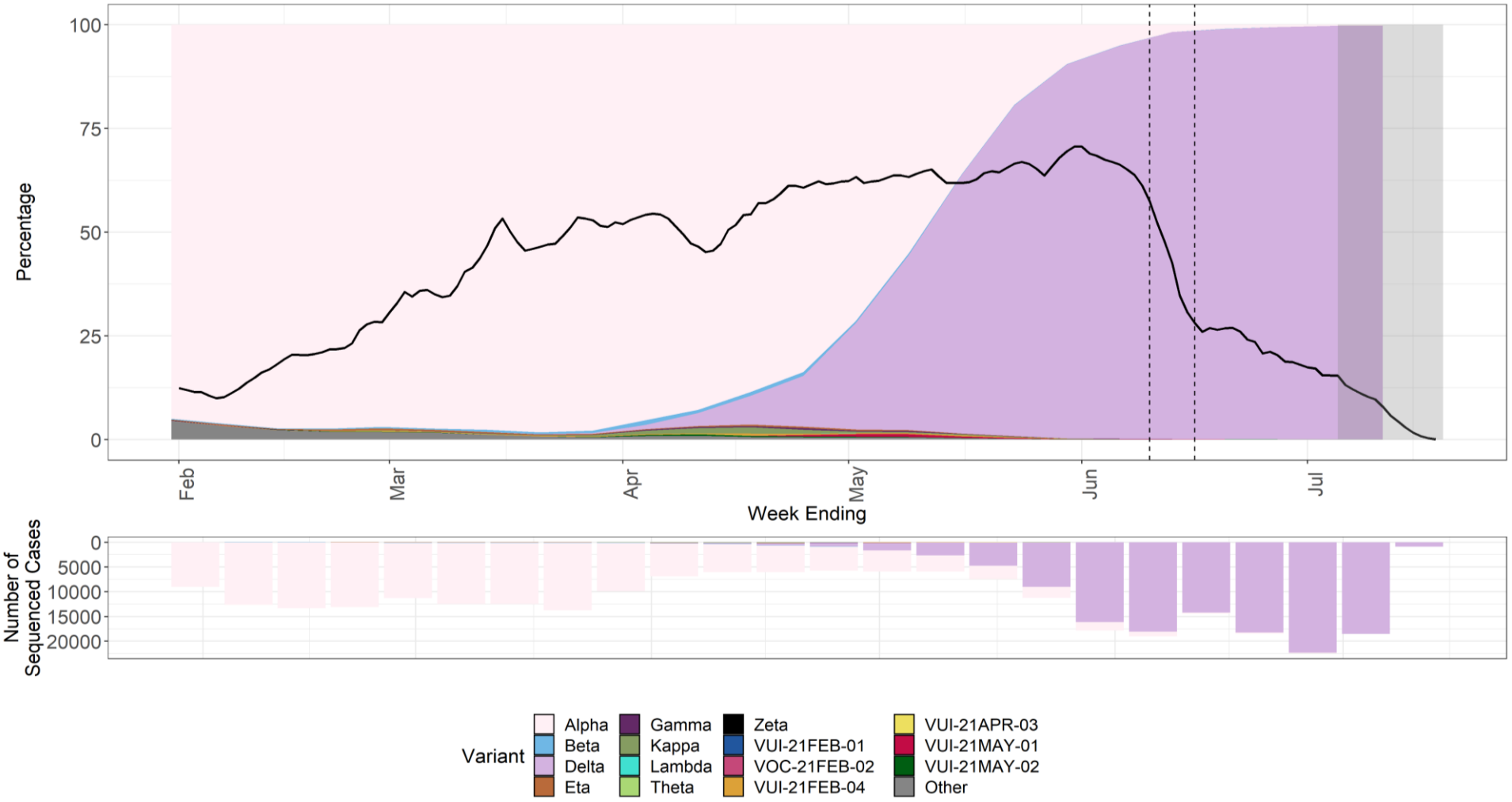
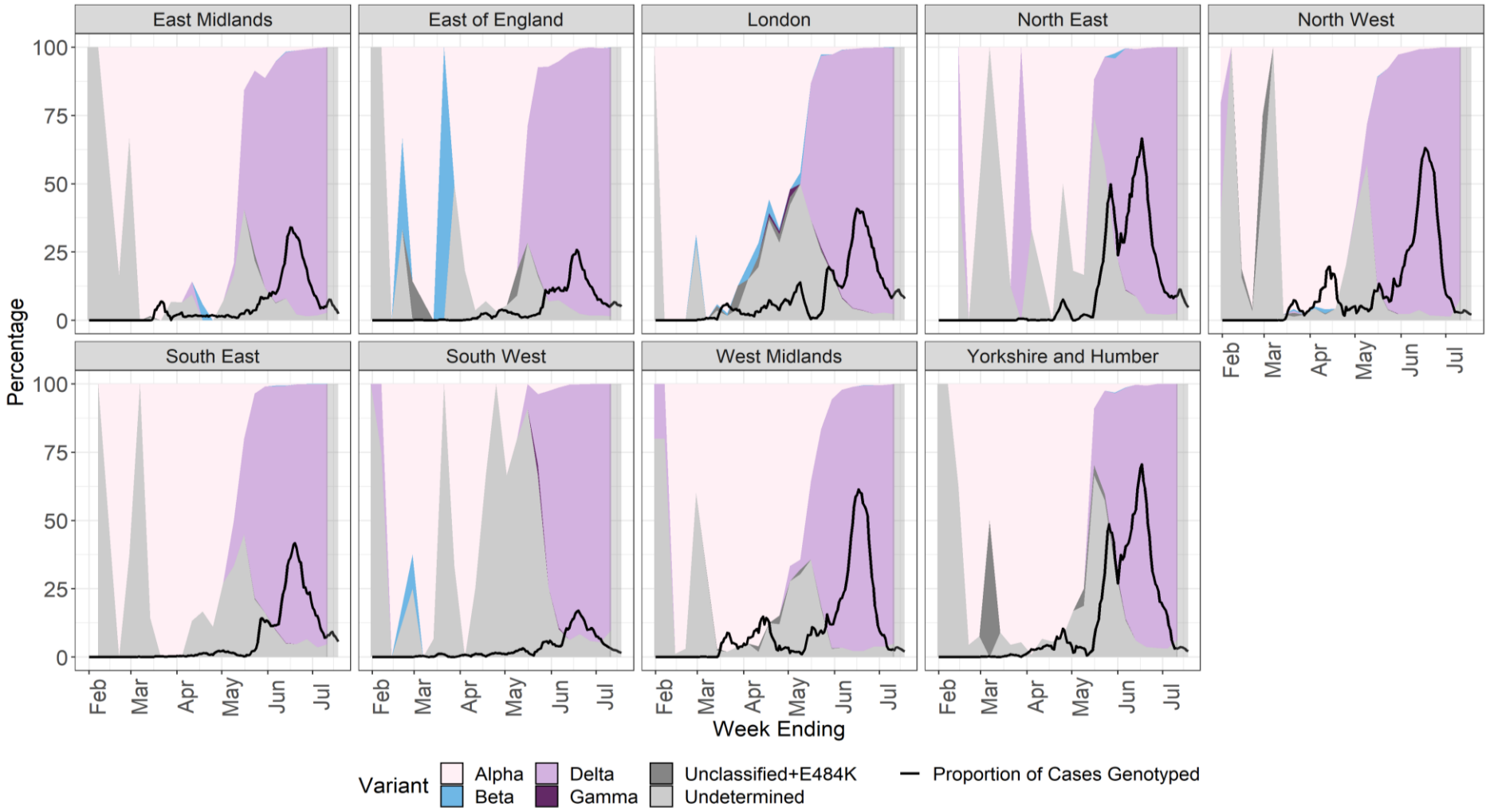
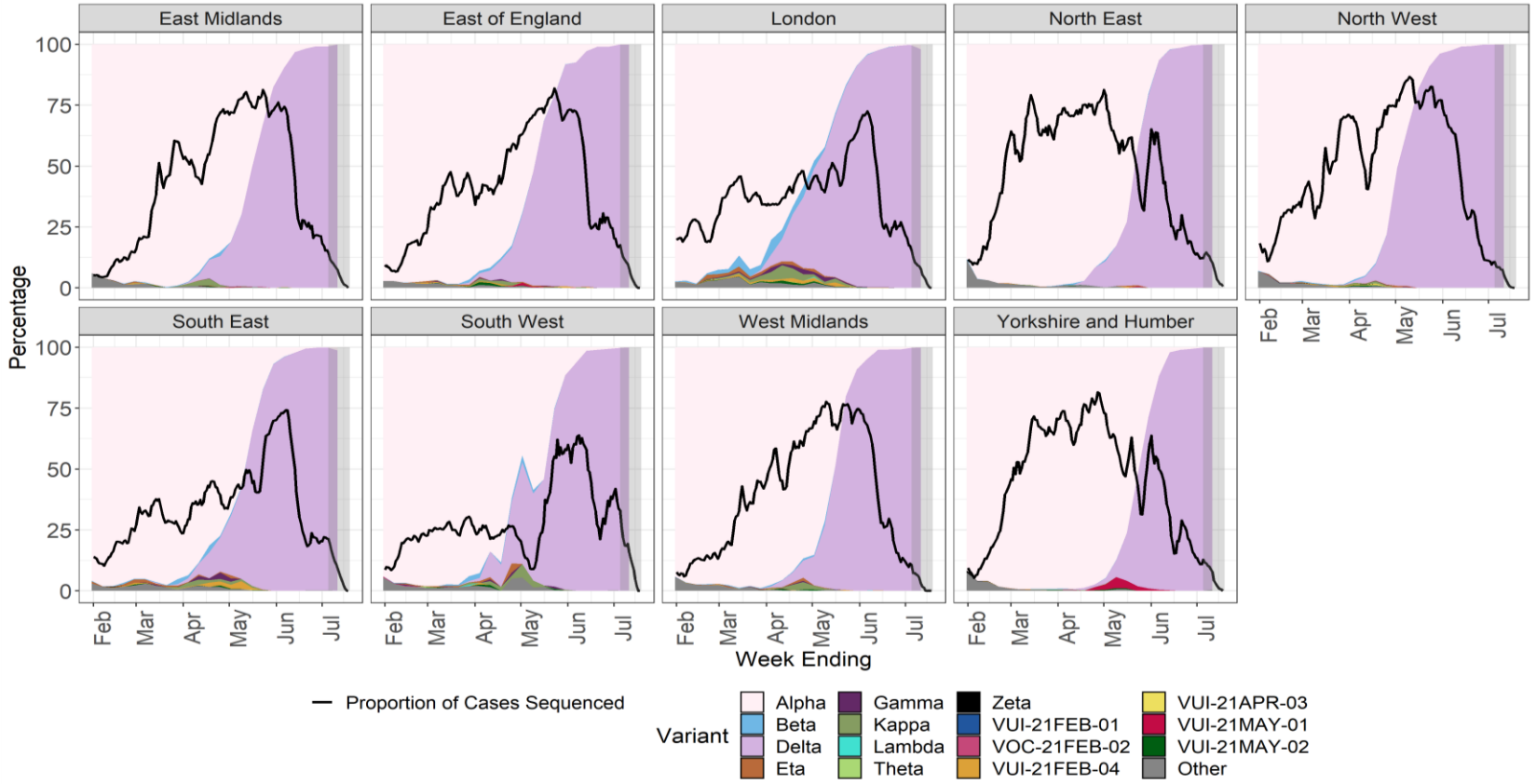


Figure 7. Variant prevalence from 1 February 2021 as of 19 July 2021 by region for all genotyped cases in England
(Find accessible data used in this graph in underlying data)



Note that 717 cases were excluded due to missing region or specimen date information.

Figure 8. Variant prevalence from 1 February 2021 as of 19 July 2021 by region for all sequenced cases in England
(Find accessible data used in this graph in underlying data)



Note that 1166 cases were excluded due to missing region or specimen date information. 7 U D Y H O VWDWXV LV DVVLJQHG EDVHG RQ DQ LQWHUY
arrival and positive specimen date. Travel information is derived from Passenger Locator Forms (PLF), contact tracing and international arrivals. Where people indicate that they have not travelled in response to contact tracing and do not have associated PLF data, they are categorised as not-travel associated. Cases for which there is no matching PLFs or information about travel status from other sources are marked as awaiting information. Travel status was assigned based on the LQGLYLGXDO¶V KLVWRU\ RI WUDYHO LQFOXGLQJ WUDQVLW UDWKHU WKDQ VHTXHQFLQJ FDVH GDWH Therefore, the proportions are less likely to reflect prevalence accurately. The total number of sequencing cases in each week is shown in the bars below, split by travel status.

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 16 July 2021 (excluding UK data). The increase in the number of antigenic mutations over time is illustrated for all variants in Figure 9 and for all 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 16 June 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.

Figure 9. Prevalence of antigenic mutations over time for all genomes in GISAID (excluding UK data), as of 16 July 2021
(Find accessible data used in this graph in underlying data)

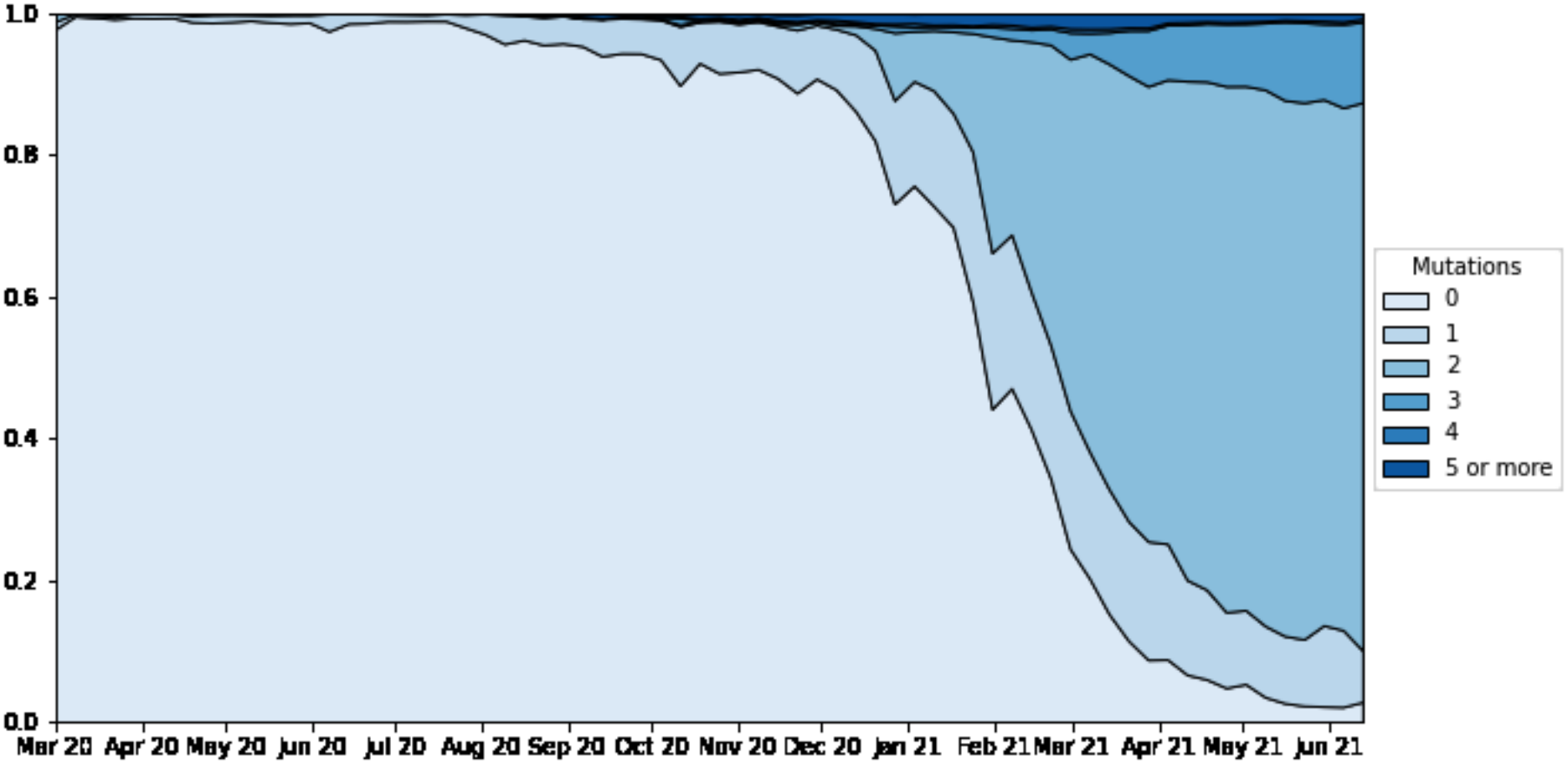
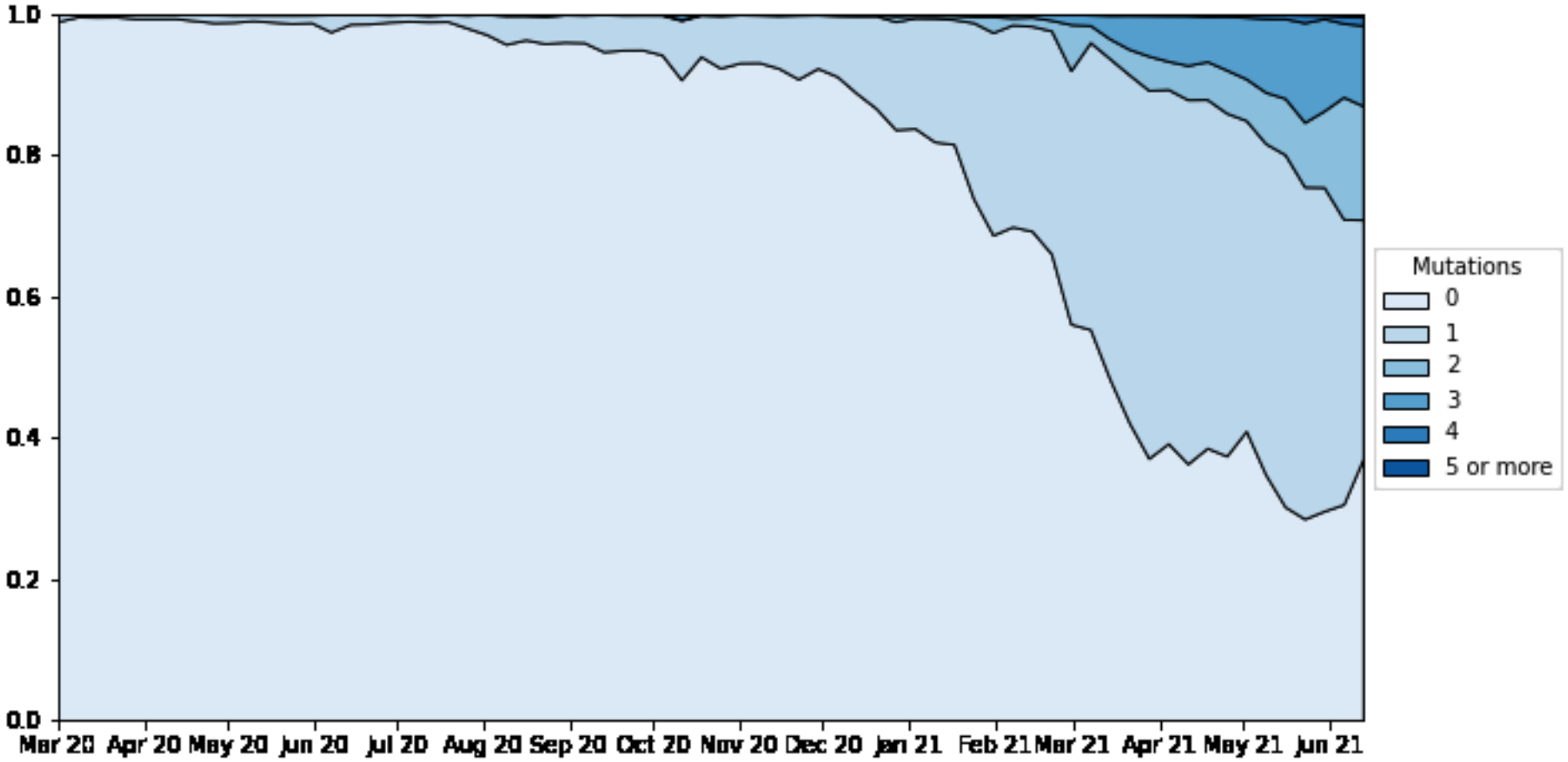


Figure 10. Prevalence of antigenic mutations over time for all genomes in GISAID (excluding UK data), excluding VOCs and VUIs, as of 16 July 2021
(Find accessible data used in this graph in underlying data)



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 confirmed or probable VOC or VUI. Variant cases are identified using confirmed (sequencing) results supplemented with probable (genotyping) results as of 19 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 6 shows secondary attack rates for all variants. The time period of study for secondary attack rates is between 5 January 2021 and 30 June 2021 to capture data for all variants. Vaccination levels and social restrictions in England have varied over this period, so comparisons between variants prevalent during different periods are not valid. Estimates of secondary attack rates for contacts of those that have travelled with variants of concern or variants under investigation were all considerably lower than those that have not travelled, due to the difference in contact definition.

Figure 11 shows the secondary attack rates amongst household and non-household contacts of non-travel cases with Delta and Alpha over time for the period 29 March 2021 to 27 June 2021, with 95% confidence intervals. A modest increase in secondary attack rate amongst household contacts of cases with Delta in the most recent 2 weeks of reporting is observed, with an estimate of 11.1% (10.9% to 11.4%) for exposure events in week commencing 21 June 2021 compared to 10.3% (10.1% to 10.6%) in the week commencing 7 June 2021. Over the period presented, secondary attack rates for household contacts of cases with Delta remain higher than for Alpha.

Table 6. Secondary attack rates for all variants
(5 January 2021 to 30 June 2021, variant data as of 19 July 2021, contact tracing data as of 21 July 2021)

Variant	Cases in those that have travelled (with contacts)	Cases in those that have not travelled or unknown (with contacts)	Case proportion that have travelled	Secondary attack rate among contacts of cases that have travelled (95% CI) [secondary cases/contacts]	Secondary Attack Rate among household contacts of cases that have not travelled or unknown (95% CI) [secondary cases/contacts]	Secondary Attack Rate among non-household contacts of cases that have not travelled or unknown (95% CI) [secondary cases/contacts]
Alpha (VOC-20DEC-01)	4388 (76.6% with contacts)	184,980 (73.0% with household, 14.0% with non-household contacts)	2.3%	1.5% (1.4% to 1.6%) [1,249/81,942]	10.2% (10.1% to 10.3%) [34596/338352]	5.6% (5.5% to 5.8%) [3303/58625]
Beta (VOC-20DEC-02)	341 (69.8% with contacts)	420 (64.5% with household, 14.5% with non-household contacts)	44.8%	1.8% (1.5% to 2.2%) [110/6,027]	10.0% (8.0% to 12.4%) [74/741]	3.0% (1.4% to 6.3%) [6/202]
Zeta (VUI-21JAN-01)	4 (75.0% with contacts)	27 (70.4% with household, 3.7% with non-household contacts)	12.9%	Unavailable [0/159]	Unavailable [4/51]	Unavailable [0/1]

Gamma (VOC-21JAN-02)	72 (63.9% with contacts)	146 (71.9% with household, 15.8% with non-household contacts)	33.0%	1.0% (0.5% to 1.9%) [9/889]	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 (57.1% with household, 12.7% with non-household contacts)	0.0%	Unavailable [0/0]	9.9% (5.1% to 18.3%) [8/81]	Unavailable [1/12]
Eta (VUI-21FEB-03)	196 (70.4% with contacts)	198 (70.7% with household, 12.6% with non-household contacts)	49.7%	1.1% (0.8% to 1.5%) [47/4,281]	9.8% (7.1% to 13.4%) [33/337]	Unavailable [1/43]
VUI-21FEB-04	113 (69.0% with contacts)	159 (76.7% with household, 20.1% with non-household contacts)	41.5%	0.5% (0.3% to 0.8%) [16/3,106]	8.5% (5.8% to 12.1%) [26/307]	6.5% (3.0% to 13.4%) [6/93]
VUI-21MAR-01	1 (100.0% with contacts)	0 (0 with household, 0 with non-household contacts)	100.0%	Unavailable [0/7]	Unavailable [0/0]	Unavailable [0/0]
Theta (VUI-21MAR-02)	5 (40.0% with contacts)	1 (100.0% with household, 0.0% with	83.3%	Unavailable [0/4]	Unavailable [0/3]	Unavailable [0/0]

		non-household contacts)				
Kappa (VUI-21APR-01)	233 (77.3% with contacts)	173 (74.6% with household, 13.3% with non-household contacts)	57.4%	1.9% (1.5% to 2.3%) [83/4,449]	9.7% (7.1% to 13.0%) [38/392]	Unavailable [3/45]
Delta (VOC-21APR-02)	1387 (69.9% with contacts)	174632 (76.8% with household, 22.9% with non-household contacts)	0.8%	1.7% (1.5% to1.9%) [429/25,424]	11.0% (10.9% to 11.1%) [37440/341069]	5.8% (5.6% to 5.9%) [7119/123393]
VUI-21APR-03	7 (14.3% with contacts)	5 (100.0% with household, 0.0% with non-household contacts)	58.3%	Unavailable [1/201]	Unavailable [1/12]	Unavailable [0/0]
VUI-21MAY-01	2 (0.0% with contacts)	176 (83.0% with household, 17.6% with non-household 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	68 (73.5% with contacts)	54 (81.5% with household, 9.3% with non-household contacts)	55.7%	0.8% (0.5% to1.5%) [11/1,298]	8.2% (4.4% to14.8%) [9/110]	Unavailable [0/13]
Lambda (VUI-21JUN-01)	8	0	100.0%	Unavailable [1/193]	Unavailable [0/0]	Unavailable [0/0]

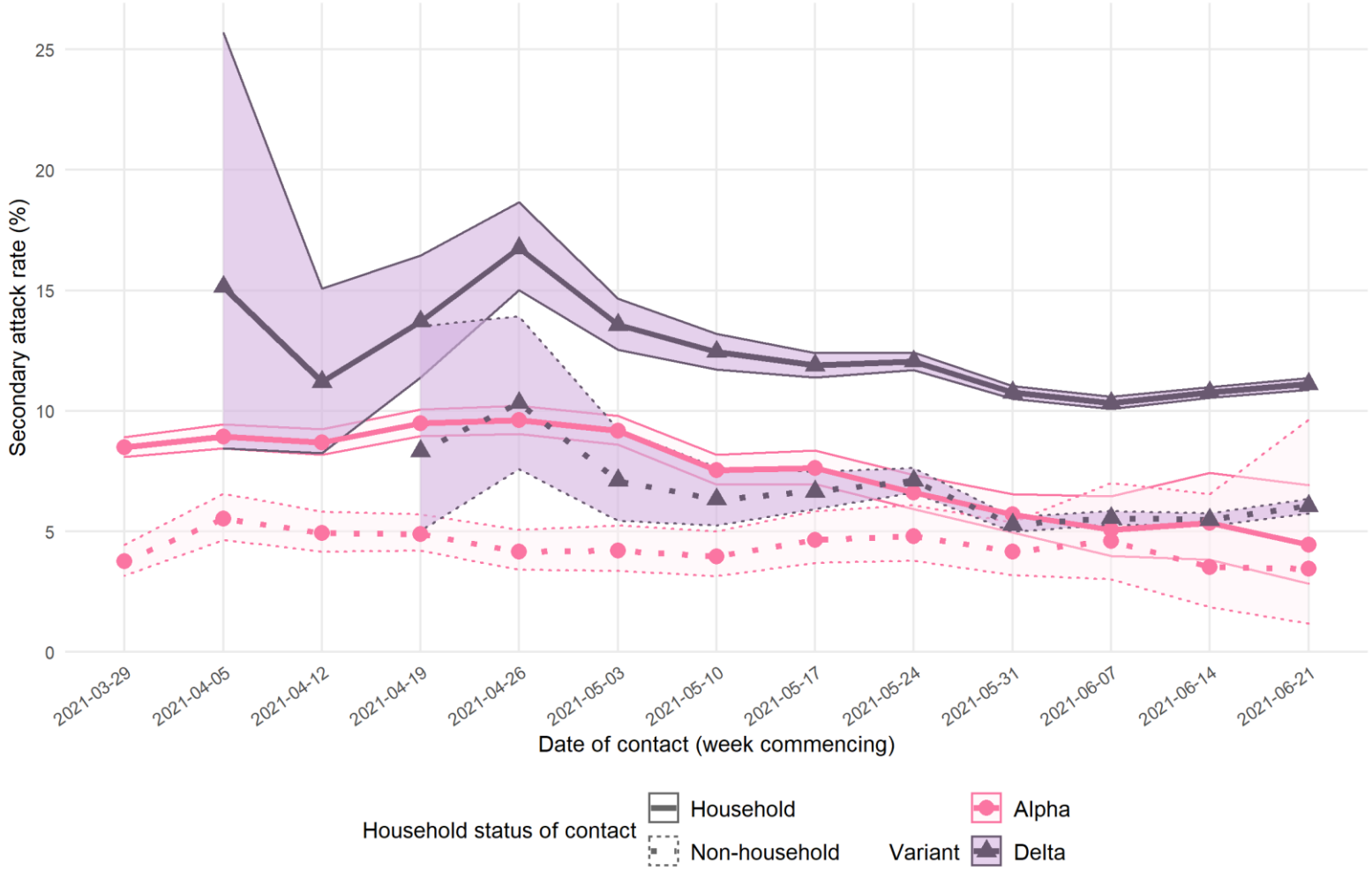
	(62.5% with contacts)	(0 with household, 0 with non-household contacts)				

Footnote to table 6: 6 H F R Q G D U \ D W W D F N U D W H V D U H P D U N H G D V 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 30 June 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. Probable (genotyping) results are included, but low-quality genomic results are excluded.
Secondary attack rates are suppressed when count of contacts is less than 50 or count of cases is less than 20. Data provided is for period until 27 June 2021 in order to allow time for contacts to become cases and complete weeks to be shown. Probable (genotyping) results are included, low quality genomic results are not.

Figure 11. Secondary attack rates amongst household and non-household contacts of non-travel cases of Alpha and Delta, with 95% confidence intervals (29 March 2021 to 27 June 2021, variant data as of 19 July 2021, contact tracing data as of 21 July 2021)

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



1.7 Reinfections

1.7.1 National Surveillance of Reinfections

Symptomatic SARS-CoV- FDVHV LQ SHUVRQV DJHG • \HDUV LGHQWL through the Pillar 2 route between 12 April and 27 June 2021 were compiled. Cases were identified as having an Alpha or Delta variant through sequencing or inferred through s-gene target data. All previous SARS-CoV2 positive PCR and/or LFD test results for these cases were scrutinised for possible reinfections, where a previous positive result had occurred at least 90 days earlier. Multivariable logistic regression models in Stata were used to assess the risk of reinfection with the Alpha and Delta variants. The models were adMXVWHG IRU DJH RU • \HDUV VH[UH vaccination status (any vaccine at least 14 days earlier or no vaccine), ethnicity, and week of test. The model was also run separately for cases of reinfection with shorter (90 to 179 days) and ORQJHU • GD\V LQWHUYDOV EHWZHHQ HSLVRG people who tested positive in the 11-week period, of whom 980 (1.2%) were possible reinfections.

The adjusted odds ratio of reinfection with the Delta variant was 1.46 (95% CI 1.03 to 2.05) compared to the Alpha variant. The risk of reinfection was not elevated for Delta if the primary infection was <180 days (adjusted odds ratio = 0.79, 95% CI 0.49 to1.28) but ZDV KLJKHU IRU WKRVH ZLWK D SULRU ed odds ratio = 2.37, • GD\V 95%CI 1.43 to 3.93). Further work to examine the risk of reinfection is being undertaken.

Table 7: Multivariable logistic regression model of the risk of reinfection with alpha and delta variants during a period of emergent delta infection in England

			Risk of reinfection -week 2021-15 to 2021-25		
		Totals	Crude OR	aOR (95% CI)*	aP-Value
Definition of reinfection applied	All possible reinfections	980 (1.2%)			
	All first infections	82,217 (98.8%)			
All possible reinfections arising at least 90 days after prior infection	Alpha variant	83/14,509 (0.6%)	1	1	
	Delta variant	897/68,688 (1.3%)	2.30 (1.84 to 2.88)	1.46 (1.03 to 2.05)	0.031
Possible reinfections arising between 90-179 days after prior infection	Alpha variant	54/14,480 (0.4%)	1	1	
	Delta variant	243/68,034 (0.4%)	0.96 (0.71to 1.29)	0.79 (0.49 to1.28)	0.342
Possible reinfections arising at least 180 days after prior infection	Alpha variant	29/14,455 (0.2%)	1	1	
	Delta variant	654/68,445 (1.0%)	4.80 (3.31 to 6.96)	2.37 (1.43 to 3.93)	0.001

*adjusted for age group (<30 years, 30+years), sex, Region, vaccination status (any vaccine at least 14 days earlier vs no vaccine), ethnicity and week

1.7.2 SARS-CoV-2 Immunity and Reinfection Evaluation (the SIREN study) cohort monitoring

The SIREN study is a cohort of National Health Service healthcare workers, including 135 sites and 44,546 participants across the UK, 35,684* in England, who remain under active follow-up with PCR testing every 2 weeks for COVID-19 by PCR. This cohort had high seropositivity on recruitment (30% before the second wave) and is now highly vaccinated (95%). The incidence of new infections and potential reinfections in SIREN is monitored and would be expected to rise if a new variant became highly prevalent and was able to escape predominantly vaccine-derived immunity.

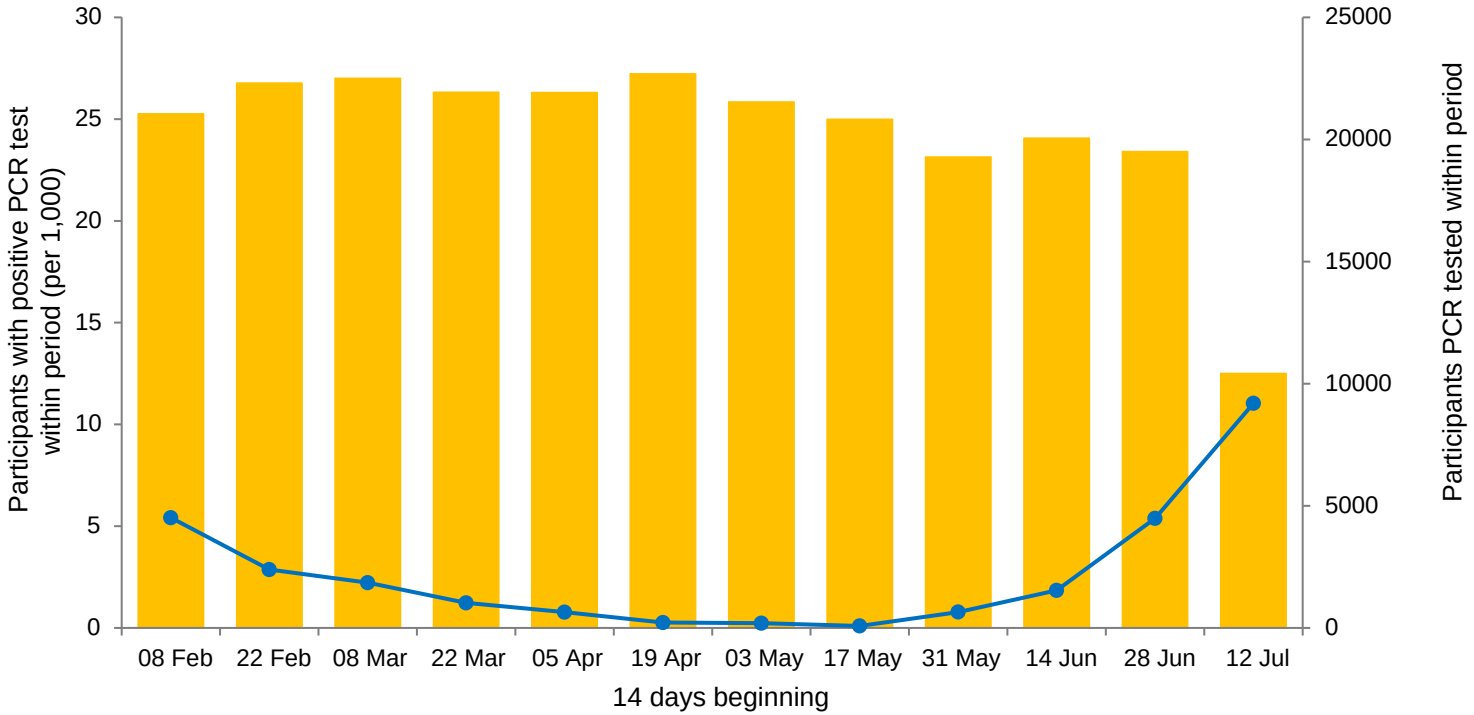
The frequency of PCR positivity in the SIREN cohort overall has increased in June 2021, with 5.4 PCR positives per 1000 tested between 28 June 2021 and 11 July 2021 after low levels in April and May (0.1 PCR positives per 1000 tested between 17 May 2021 and 30 May 2021) (Figure 12). Of the 263 participants with a PCR positive sample since April 2021 in the SIREN cohort overall, 221 (84%) occurred 14 days or more following their

second vaccine dose. Please note that historical infections and reinfections have increased since the last Technical Briefing due to improvements in data linkage.

Of the SIREN cohort, 9,813 (31%) had evidence of prior infection (previous PCR positive or antibody positive) at enrolment. This number has increased during follow-up as participants move from the negative to positive cohort after a primary infection. Up to the 11 July 2021, there were 301 potential reinfections (blue line) identified in England (Figure 13). This is provisional data as potential reinfection cases flagged are undergoing further investigation, and some may subsequently be excluded. Reinfections in the SIREN cohort have been increasing since June 2021 (20 cases in June and 24 cases in July), after low levels in April 2021 (3 cases) and May 2021 (4 cases). Of the 51 potential reinfection events since April 2021, 3 were at least 21 days after the 1st vaccine dose and 42 (82%) were at least 14 days after the 2nd vaccine dose.

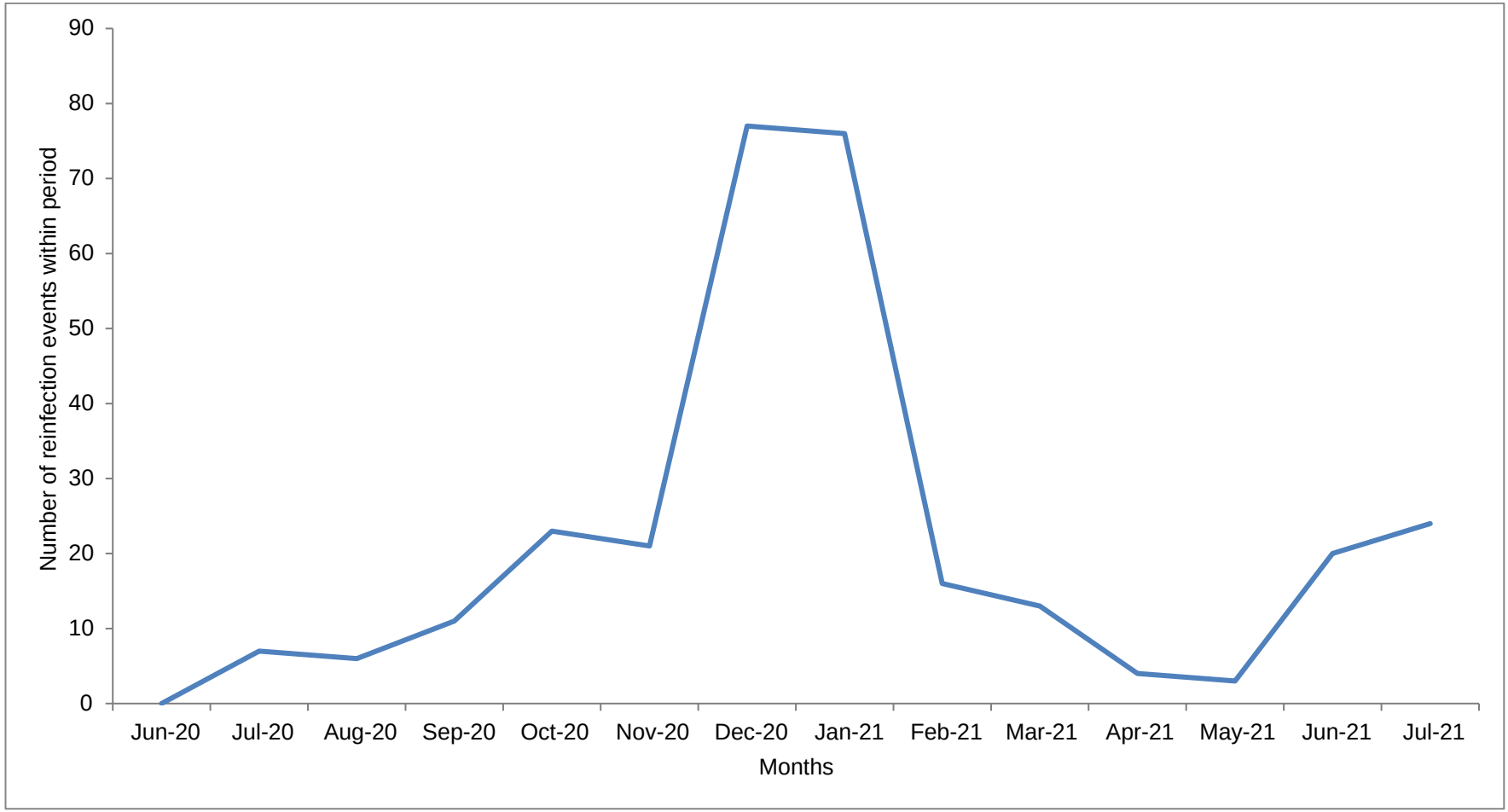
*Number excludes participants who have withdrawn from the study and requested their data to be removed and participants recruited in hospitals in the devolved administrations.

Figure 12. PCR positivity within the SIREN study for all regions, England (fortnightly testing interval) data up to 18 July 2021
(Find accessible data used in this graph in underlying data)



*Incomplete week commencing 28 June 2021
Yellow bars indicate participants PCR-tested within period (right axis), Blue line indicates participants with positive PCR within period (per 1,000) (left axis). Please note that Figure 15 only contains data from participants with at least one PCR test within the given period. Participants are counted as positive if at least one PCR test within the given period is positive. The data has not been restricted by antibody status or vaccination status, and only includes participants from trusts in England.

Figure 13. Monthly frequency of potential reinfection events within SIREN data up to 11 July 2021
(Find accessible data used in this graph in underlying data)



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

The G2P consortium reports experimental data (growth in airway epithelium, and animal to animal transmission) suggesting that Beta is not highly fit and is likely to be less transmissible than Alpha.

1.8.2 University of Oxford

The University of Oxford reports preliminary findings that convalescent sera from individuals with Delta infection neutralises Beta and Gamma less effectively than convalescent sera from individuals with Alpha infection (all cases were unvaccinated). This is data from a single laboratory with limited numbers of samples tested at present.

1.8.3 MRC Biostatistics Unit, University of Cambridge

The MRC Biostatistics Unit reported preliminary findings from analysis of deaths data. Analysis of deaths in England is limited by low numbers, but suggests that Delta has at least an equivalent case fatality rate to Alpha. There is currently a high level of uncertainty and further analyses will be undertaken.

Part 2: Surveillance of individual variants

2.1 Delta (B.1.617.2) surveillance

The lineage B.1.617.2 was escalated to a VOC in the UK on 6 May 2021 (VOC-21APR-02). This variant was named Delta by WHO on 31 May 2021.

2.1.1 Diversity in Delta

Table 8 shows additional spike mutations with a potential impact on antigenicity, avidity or the furin cleavage site significance that have been 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 (for example, through published literature) are presented. The number of unlinked sequences represents 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.

Figure 14 shows the phylogeny of Delta in the UK, which is dominated by a large distinct clade. The clade has distinguishing mutations outside spike with uncertain biological significance, including NSP3: A488S, P1228L, P1469S; NSP4: D144D, V167L, T492I; NSP6: T77A, V120V; NSP14:A394V; ORF7b: T40I; N: G215C. The dominance of this clade in the UK may relate to epidemiological or biological effects or both. Further investigations are being undertaken. Figure 15 shows the percentage of sequences in each clade over time.

Table 8. Additional spike mutations of interest detected in Delta genomes in the UK as of 20 July 2021

Amino acid change	Nucleotide change	Total number of sequences (UK)	Number of unlinked sequences	Number of sequences 21April to 20 May 2021	Number o f sequences 21 May to 20 June 2021	Number of sequences 21 June to 20 July 2021
P251L	C22314T	1,159	968	1	36	154
G446V	G22899T	490	277	5	105	103
L18F	C21614T	271	89	0	31	151
D253G	A22320G	193	13	0	31	149
R683Q	G23610A	162	5	1	55	101
S255F	C22326T	151	18	6	14	113
N148S	A22005G	87	12	0	4	71
R158G	A22034G	77	3	4	70	0
T716I	C23709T	73	24	0	12	37
P479S	C22997T	57	7	1	13	36
Q677H	G23593T	55	10	4	25	16
K417N	G22813T	52	8	33	11	0
P479L	C22998T	41	2	0	15	24
V483F	G23009T	40	5	0	6	29
S477I	G22992T	40	7	1	14	18
S494L	C23043T	24	9	3	6	6
S477G	A22991G	20	1	0	5	14
K458N	G22936T	20	0	0	2	18
P681L	C23604T	20	1	0	12	7
Total Sequences	C23604G	165,981	165,981	9,266	64,316	57,865

Note that G142D is in a part of the genome with consistently reduced coverage in the Delta variant due to the lineage-defining deletion from position 22029 to 22035, which affects one of the PCR primer sites in the ARTIC v3 protocol. While it is only reported as detected in ~60% of sequences, the remaining 40% of sequences are almost all "N" at that position [illegible] (the reference allele). As the mutation occurred early in the history of the lineage the majority of sequences (>99%) in this lineage can be assumed to harbour the mutation.

Figure 14. Maximum likelihood tree of all UK Delt a sequences
Phylogenetic tree showing clades are defined using the clusterfunk method. Clades defined by the clusterfunk method are shown in separate colours (N.B. these do not relate to Pangolin lineage names). The clade in green is predominant in the UK. (There is no underlying data for this figure)

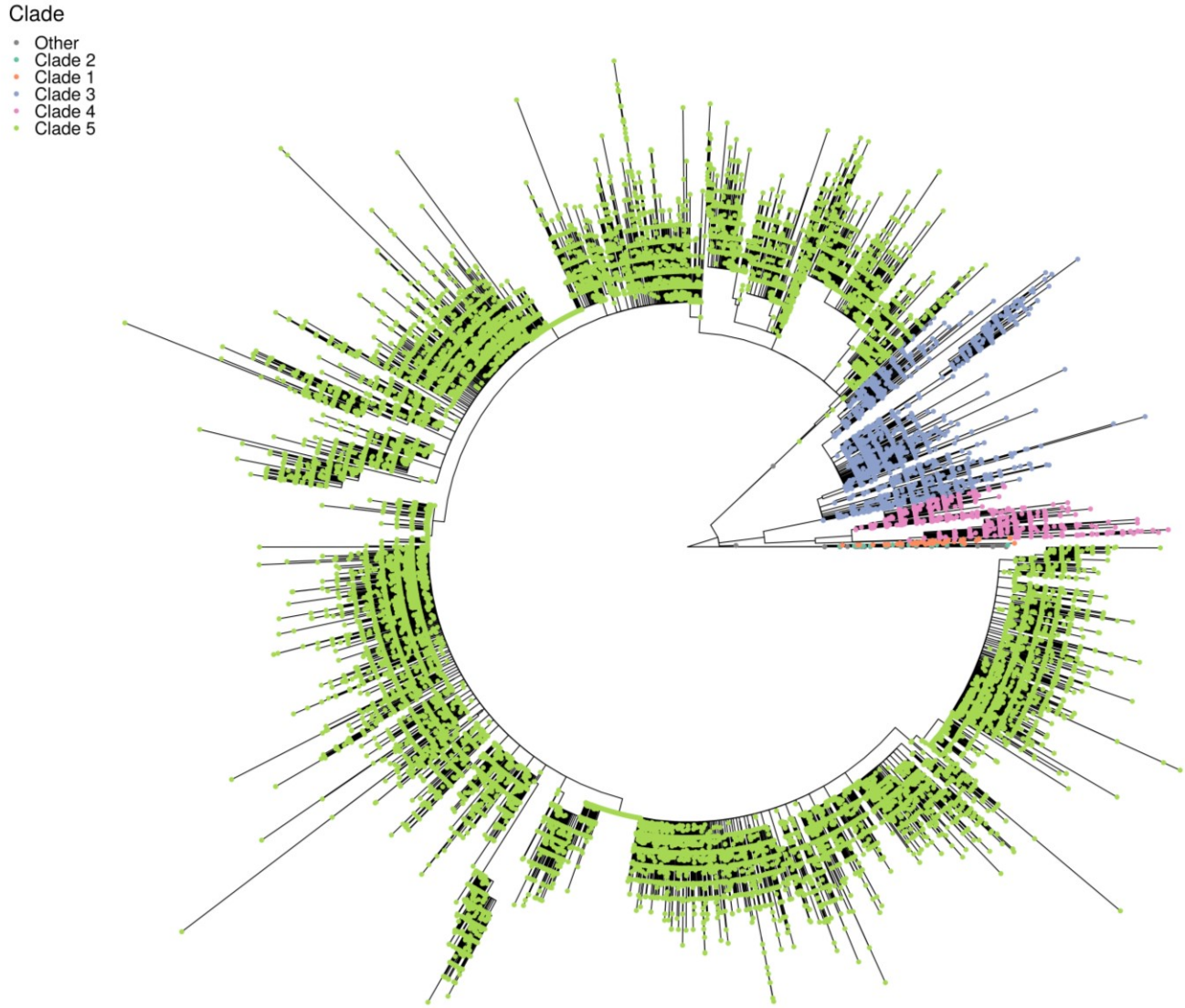
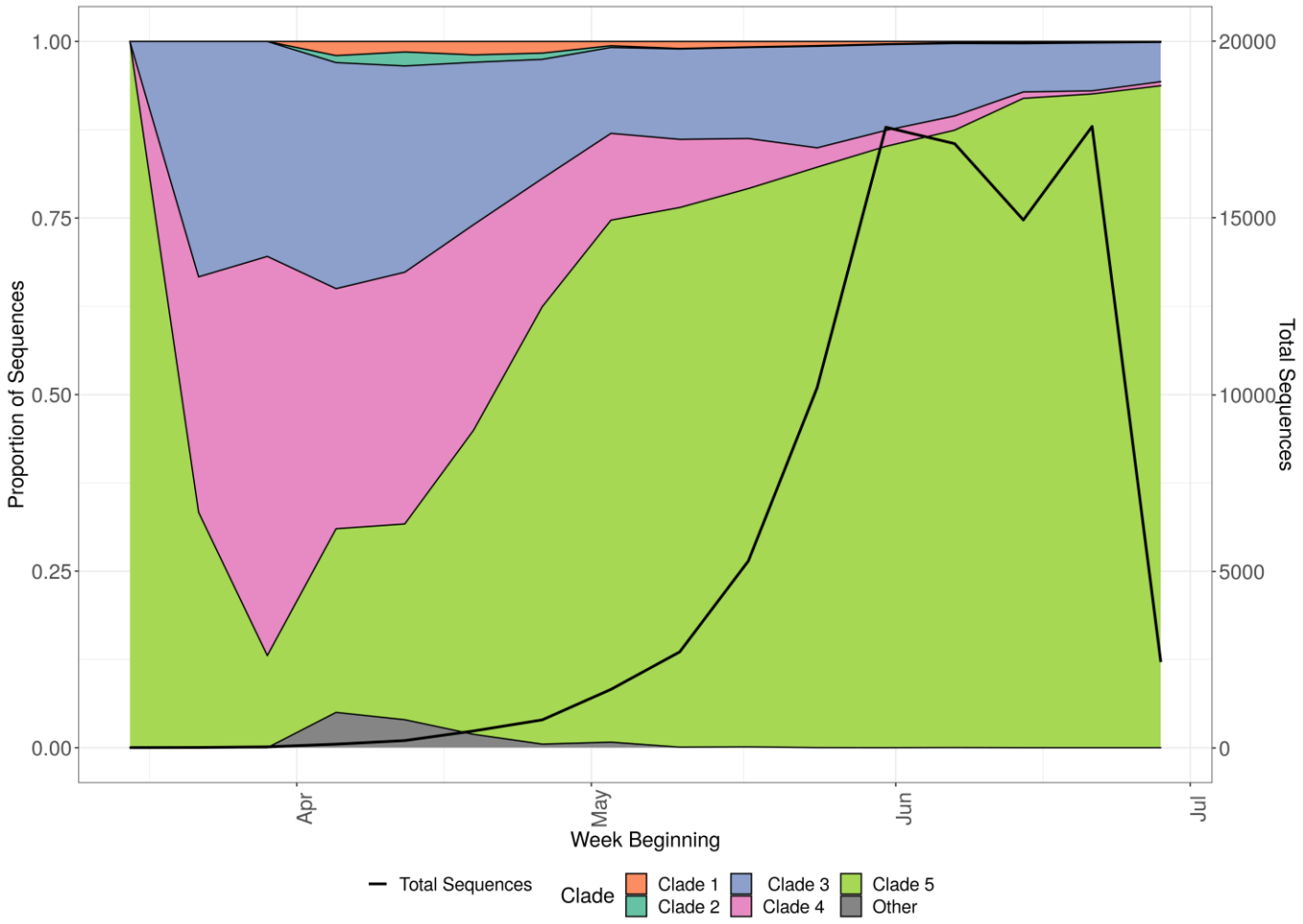


Figure 15. Proportion of Delta sequences in each clade over time
Sequences are grouped by week and any clades with fewer than 100 sequences are J U R X S H G L Q W K H L U Z H H N V I R U H D F K Z H H N D U H L Q G L F D W H G E \ W K H E O D F N O L Q H .



2.1.2 Delta with K417N

Through routine scanning of variation in Delta a small number of sequences were detected with the K417N spike protein mutation.

Data suggest that there are at least 2 separate clades of Delta with K417N. One clade is large and internationally distributed with the PANGO lineage designation AY.1. A second clade found in sequences uploaded to GISAID from the US, which is now designated AY.2.

Preliminary results for live virus neutralisation of AY.1 with a small number of sera from vaccine recipients are reassuring, however further testing is required (data provided by G2P consortium).

2.1.2.1 International epidemiology

GISAID includes data on sequences available internationally. As of 16 July 2021, 828 genomes of Delta-with K417N have been identified in GISAID internationally, excluding the UK: US (592), Portugal (56), Japan (47), Switzerland (41), Poland (27), India (23), France (11), Nepal (11), Germany (3), Netherlands (2), Spain (2), Qatar (2), Australia (2), Mexico (2), Canada (1), Kuwait (1), Ecuador (1), Romania (1), Russia (1), Denmark (1), and Czech Republic (1).

2.1.2.2 Epidemiology

There are currently 45 cases of Delta with K417N in England (39 confirmed sequencing and 6 probable genotyping). Cases have been detected in 7 different regions in England (Table 9, Figure 16).

Delta with K417N can be detected by genotyping assay, which means that rapid case identification and response activities can be undertaken. Until laboratory characterisation has been undertaken, Health Protection Teams will respond with high priority to case finding and control measures for cases of Delta with K417N. Neutralisation assays are underway for Delta-AY.1

Table 9. Number of confirmed (sequencing) and probable (genotyping) Delta cases with K417N mutation, by region of residence as of 19 July 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number [1]	Total case number	Case Proportion
East Midlands	1	0	1	2.2%
East of England	0	1	1	2.2%
London	7	1	8	17.8%
North East	0	2	2	4.4%
North West	3	0	3	6.7%
South East	15	1	16	35.6%
South West	2	1	3	6.7%
West Midlands	10	0	10	22.2%
Yorkshire and Humber	0		0	0.0%
Unknown region	1	0	1	2.2%
Total	39	6	45	-

[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

Figure 16. Confirmed (sequencing) and probable (genotyping) Delta cases with K417N cases by specimen date and region of residence as of 19 July 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

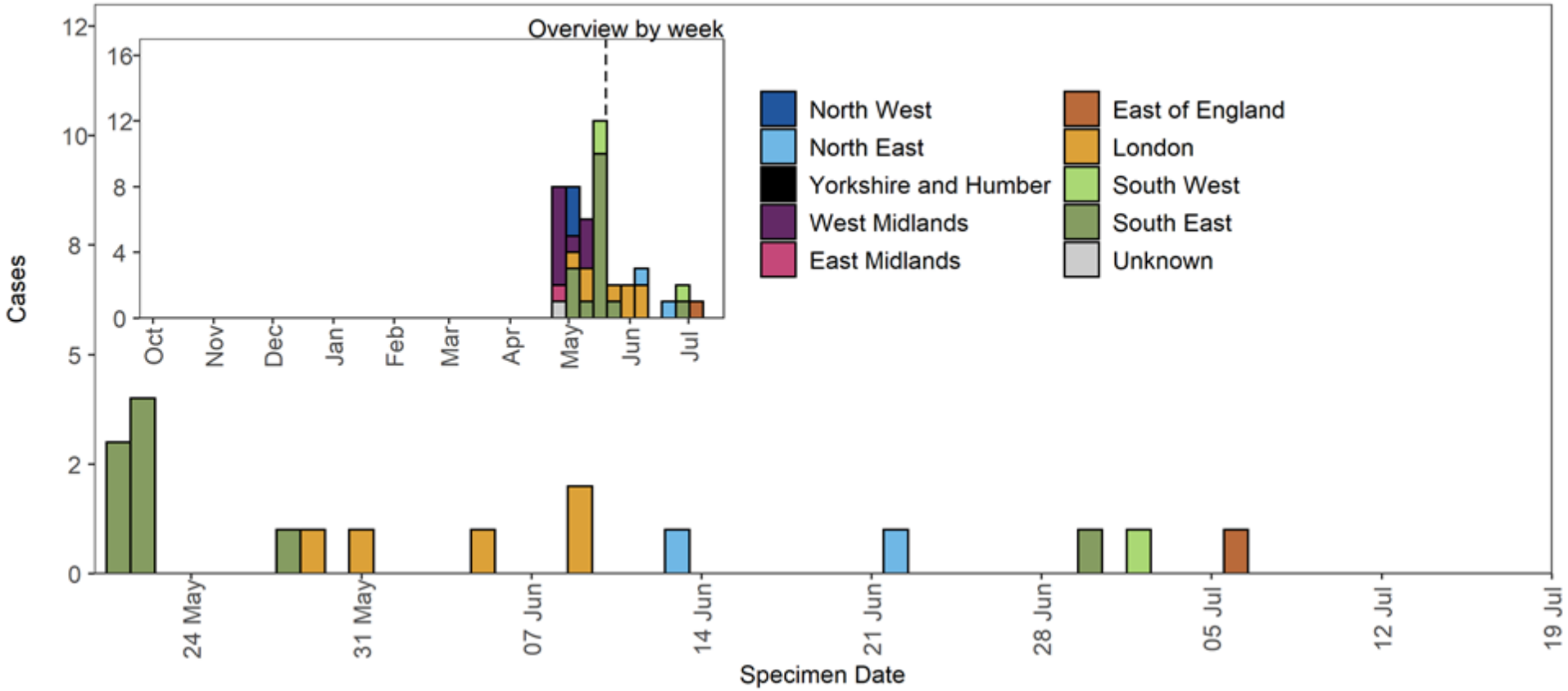


Figure 17. Confirmed (sequencing) and probable (genotyping) Delta cases with K417N cases by specimen date and detection method as of 19 July 2021 (Find accessible data used in this graph in underlying data)

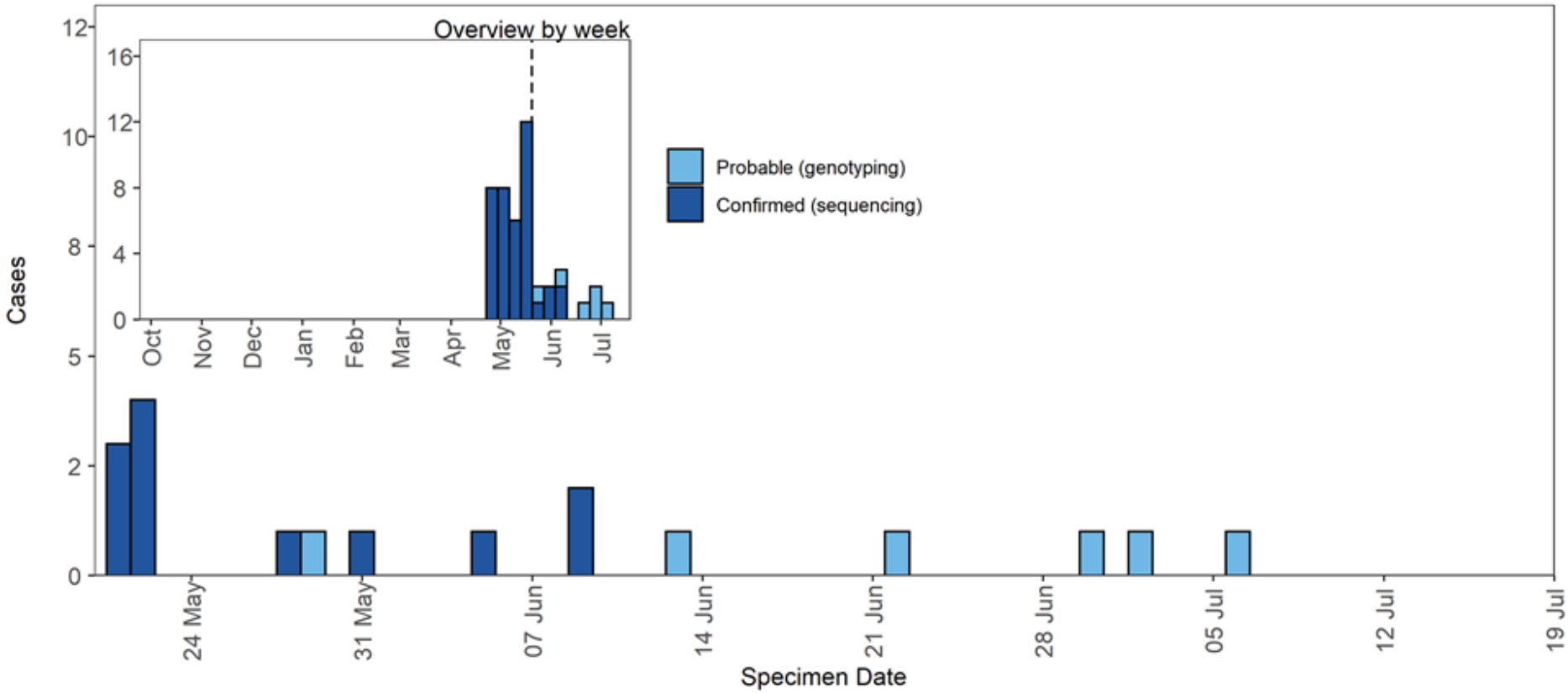
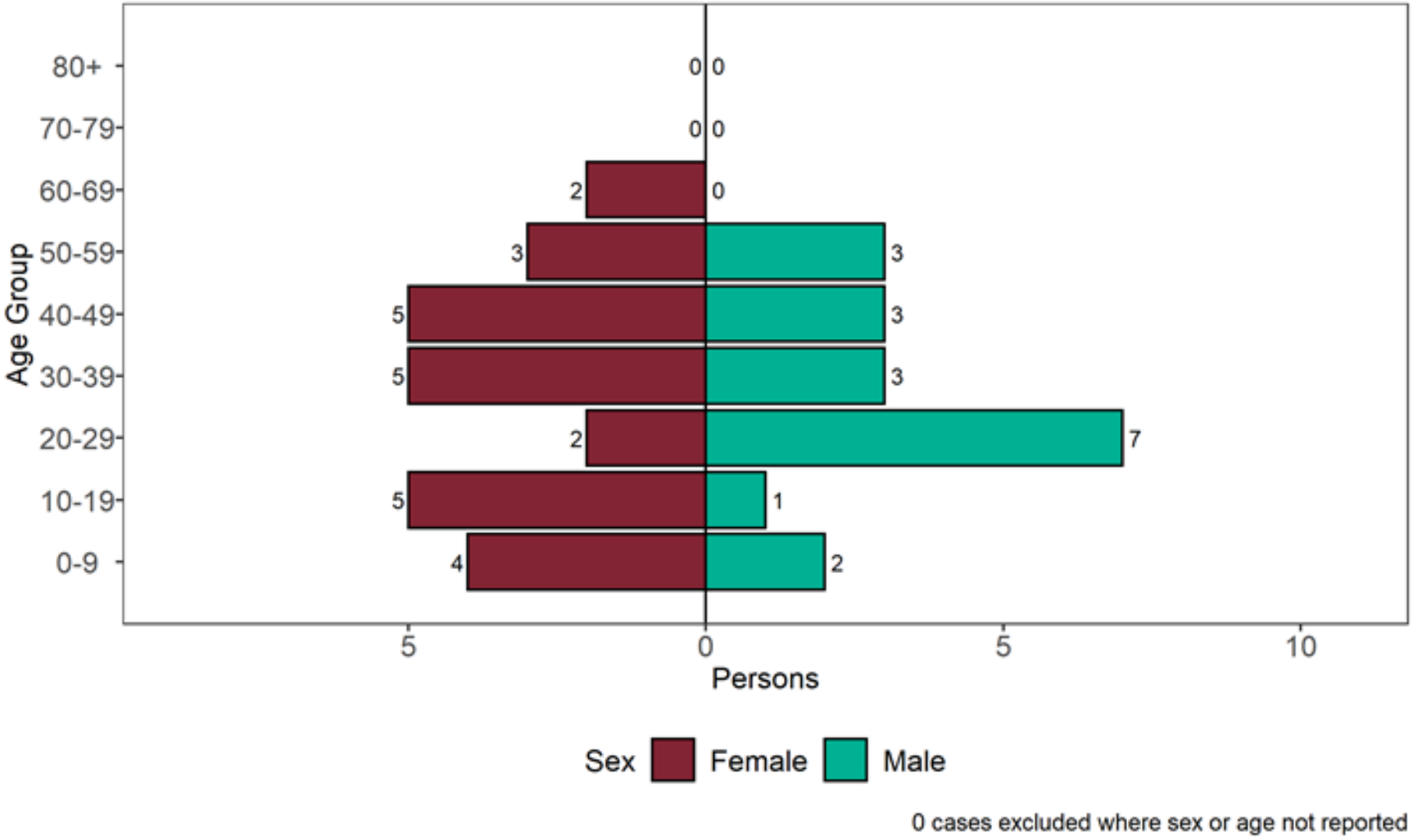


Figure 18. Age and sex pyramid of confirmed (sequencing) and probable (genotyping) Delta cases with K417N cases as of 19 July 2021 (Find accessible data used in this graph in underlying data)



2.2 VUI-21JUL-01 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 20 July 2021, PHE designated lineage B.1.621 as a new variant of interest, 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 K417N S gene mutation.

2.2.1. International epidemiology

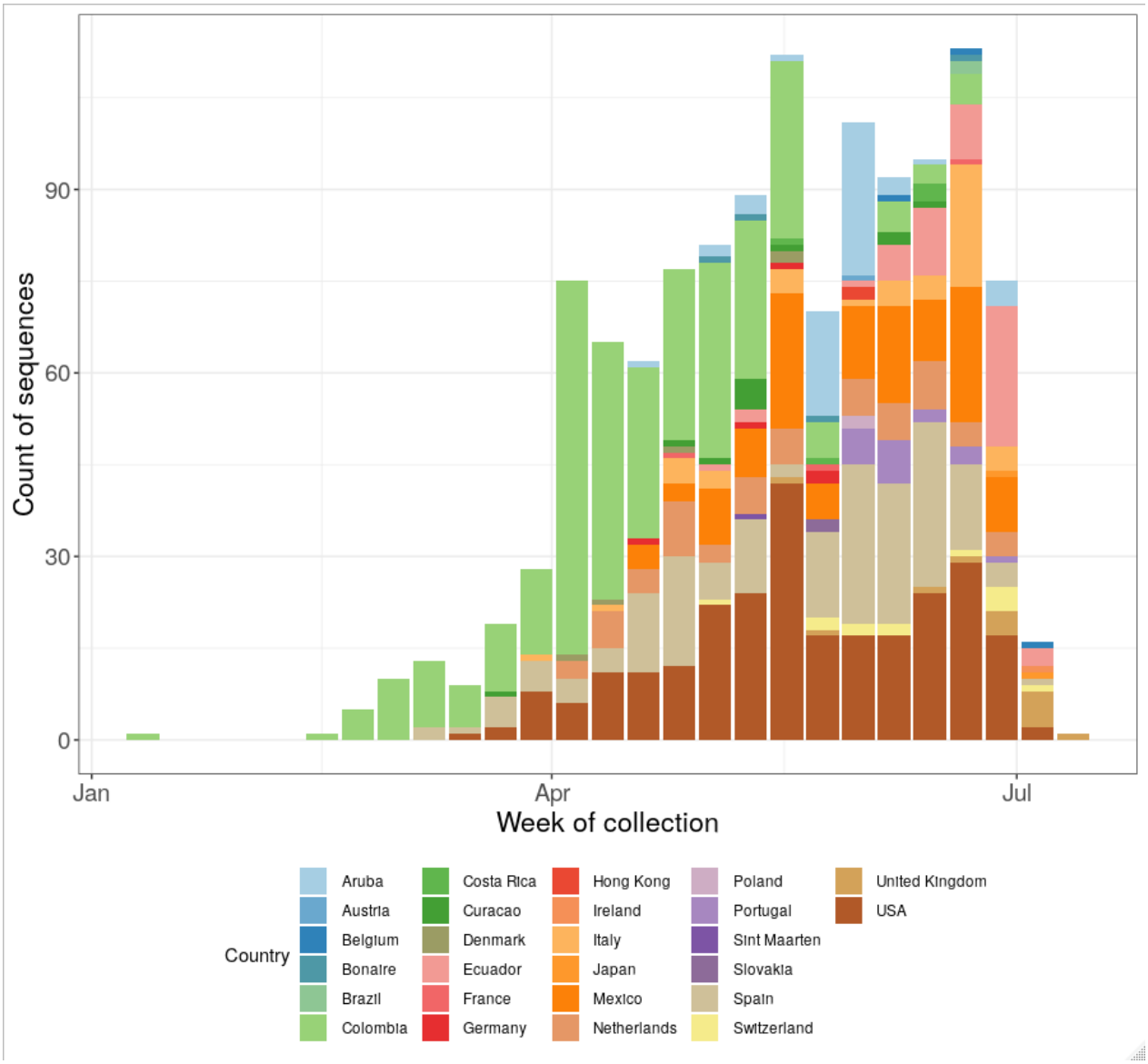
As of 20 July 2021, 1,230 sequences on GISAID have been assigned to the B.1.621 lineage. B.1.621 sequences have been uploaded from Colombia (325), US (264), Spain (196), Mexico (122), Netherlands (65), Aruba (57), Ecuador (56), Italy (47), Portugal (19) United Kingdom (16), Switzerland (13), Curacao (12), Costa Rica (5), Denmark (5),Germany (5) Bonaire (4), Belgium (3), France (3), Brazil (2), Hong Kong (2), Japan (2), Poland (2), Slovakia (2), Austria (1), Ireland (1), and Sint Maarten (1). Figure 19 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.

2.2.2 Epidemiology in England

As of 22 July 2021, there are 16 cases of VUI-21JUL-01 in England plus an additional 6 genomes for which case data is being sought. Cases have been detected in 3 different regions in England, with the majority of cases detected in London (10, 63%). The 20-to-29 years age group formed the largest age group (6 cases). Three of the 16 cases have history of travel which include travel from or transit through Mexico, Spain, Dominican Republic and Colombia.

Of the 16 cases, 10 cases were known to have a vaccination status within the National Immunisation Management System (NIMS), when linked on NHS number. Of these, 3 cases occurred in people who were not vaccinated, 3 cases in people who had received their first dose within 21 days at the time of testing positive, 2 cases in people who had received their first dose more than 21 days before testing positive, and 2 cases where there were more than 14 days after their second dose of vaccine at the time of testing positive. No deaths have been recorded amongst the 16 cases.

Figure 19. Count of B.1.621 classified s equences by week of collection uploaded to GISAID by week as of 20 July 2021



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 Health Protection Data Science Team
PHE International Cell
Contributions from the Variant Technical Group Members

Variant Technical Group members and contributors

The PHE Variant Technical Group includes members and contributors from the following organisations: PHE, 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

Acknowledgements

The authors are grateful to those teams and groups providing data for these analyses including: the Lighthouse Laboratories, NHS, COG-UK, the Wellcome Sanger Institute, Health Protection Data Science teams, the Joint Biosecurity Centre and the Genotype to Phenotype Consortium.

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.

Public Health England
Wellington House
133-155 Waterloo Road
London SE1 8UG
Tel: 020 7654 8000

Published: July 2021
PHE gateway number: GOV-9044

PHE supports the UN Sustainable Development Goals

SUSTAINABLE DEVELOPMENT GOALS