

Protecting and improving the nation's health

SARS-CoV-2 variant data update, England

Version 7

25 June 2021

This briefing provides an update on previous data located in technical and variant data update briefings and updates up to 18 June 2021.

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Surveillance data overview

This document includes routine data on variants of concern and under investigation. Delta (VOC-21APR-02, B.1.617.2) and Lambda (VUI-21JUN-01, C.37) is detailed in technical briefing 17.

There are 4 variants of concern and 9 variants under investigation (Table 1).

Table 1. Variant lineage and designation as of 21 June 2021 (provisionally extinct variants removed)

World Health Organization nomenclature as of 21 June 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
Карра	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.1.1.7 with E484K	VOC-21FEB-02	*Monitoring
Epsilon	B.1.427/B.1.429		Monitoring
	B.1.1.7 with S494P		Monitoring
	A.27		Monitoring
lota	B.1.526		Monitoring
	B.1.1.7 with Q677H		Monitoring
	B.1.620		Monitoring

World Health Organization nomenclature as of 21 June 2021	Lineage	Designation	Status
	B.1.214.2		Monitoring
	R.1		Monitoring
	B.1.621		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

^{*} 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.

Note: 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.

[^] Designated as Variant of Interest by WHO on 14 June 2021 and as a variant under investigation by Public Health England on 23 June 2021.

Data on individual variants

Alpha

This variant was designated VUI 202012/01 (B.1.1.7) on detection and on review redesignated as VOC-20DEC-01 (202012/01, B.1.1.7) on 18 December 2020. This was named Alpha by the World Health Organization (WHO) on 31 May 2021.

International Epidemiology

As of 22 June 2021, 632,944 sequences of Alpha, excluding the UK, are listed from 145 countries or territories on GISAID.

Table 2. Number of confirmed (sequencing) and probable (genotyping) Alpha cases, by region of residence as of 21 Jun 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number	Total case number	Proportion of all cases ¹
East Midlands	16,045	473	16,518	7.3%
East of England	19,658	176	19,834	8.8%
London	39,956	763	40,719	18.1%
North East	14,736	114	14,850	6.6%
North West	41,908	1,684	43,592	19.4%
South East	23,849	118	23,967	10.6%
South West	8,032	48	8,080	3.6%
West Midlands	18,267	1,259	19,526	8.7%
Yorkshire and Humber	35,833	858	36,691	16.3%
Unknown region	1,286	22	1,308	0.6%
Total	219,570	5,515	225,085	-

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 1. Confirmed (sequencing) and probable (genotyping) Alpha cases by specimen date and region of residence as of 21 June 2021

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

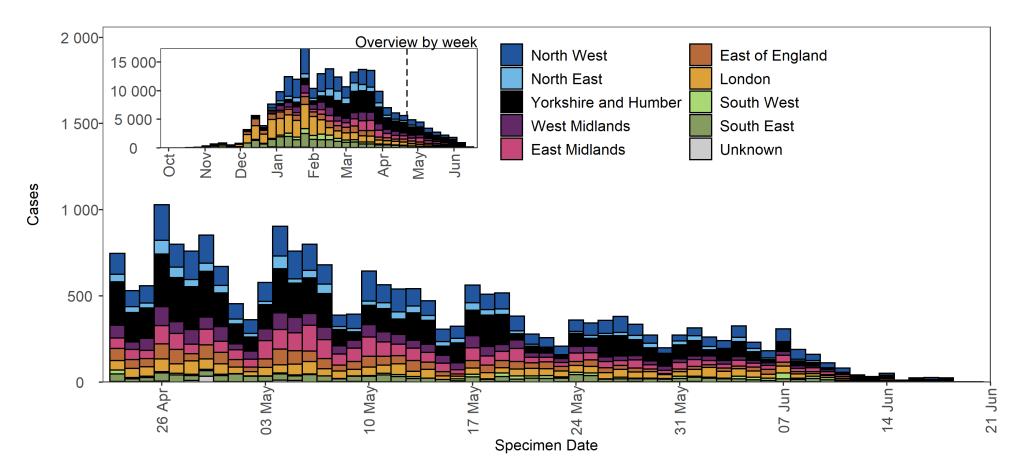


Figure 2. Confirmed (sequencing) and probable (genotyping) Alpha cases by specimen date and detection method as of 21 June 2021 (Find accessible data used in this graph in underlying data.)

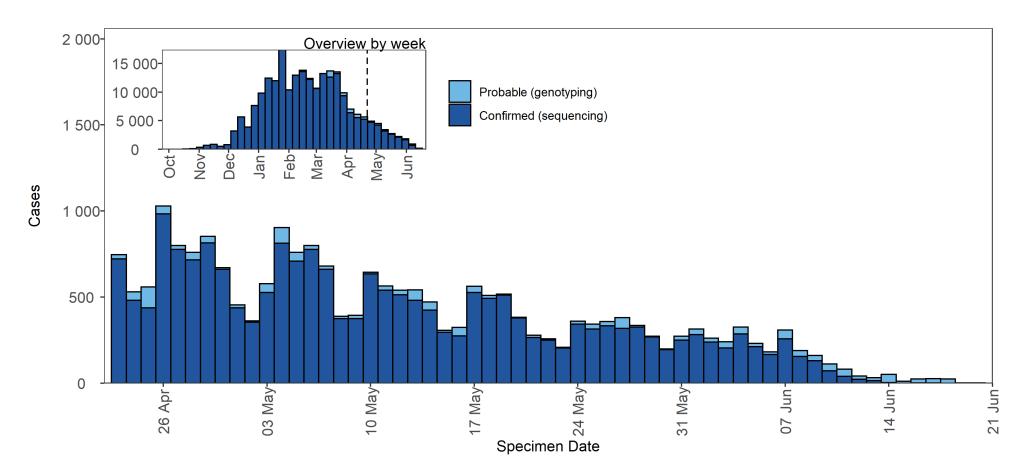
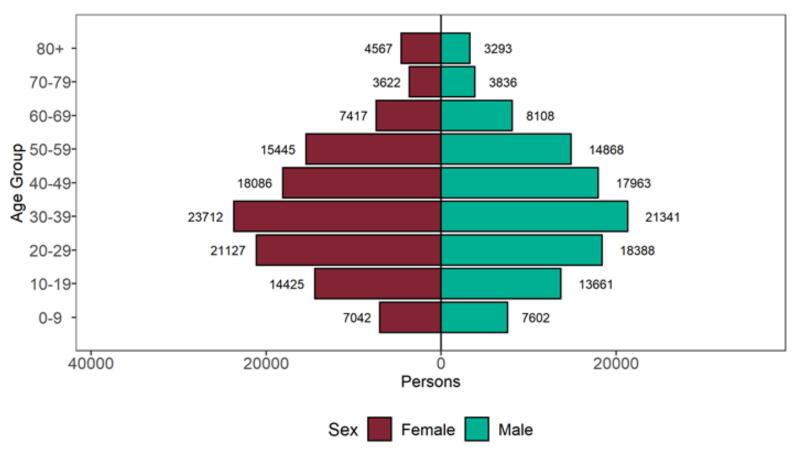


Figure 3. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Alpha cases as of June 21 2021 (Find accessible data used in this graph in underlying data.)



Beta

B.1.351 was initially detected in South Africa. This variant was designated variant under investigation on detection and on review re-designated as VOC-20DEC-02 (B.1.351) on 24 December 2020. It was named Beta by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of the 22 June 2021, 22,978 sequences of Beta, are listed from 95 countries or territories excluding the UK.

Table 3. Number of confirmed (sequencing) and probable (genotyping) Beta cases, by region of residence as of 21 June 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number	Total case number	Proportion of all cases ¹
East Midlands	46	1	47	5.0%
East of England	81	2	83	8.8%
London	409	24	433	45.8%
North East	17	6	23	2.4%
North West	80	9	89	9.4%
South East	110	4	114	12.1%
South West	31	1	32	3.4%
West Midlands	64	0	64	6.8%
Yorkshire and Humber	32	7	39	4.1%
Unknown region	22	0	22	2.3%
Total	892	54	946	-

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 4. Confirmed (sequencing) and probable (genotyping) Beta cases by specimen date and region of residence as of 21 June 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

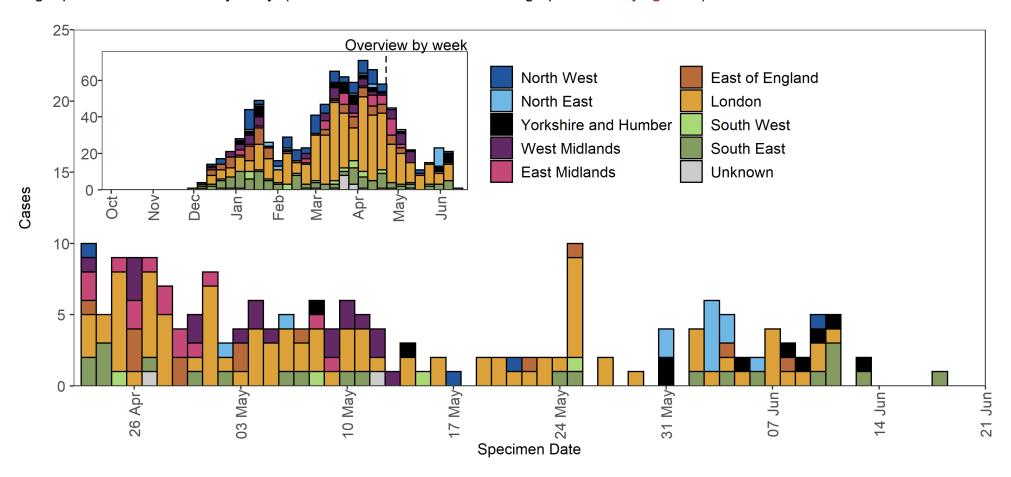


Figure 5. Confirmed (sequencing) and probable (genotyping) Beta cases by specimen date and detection method as of 21 June 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

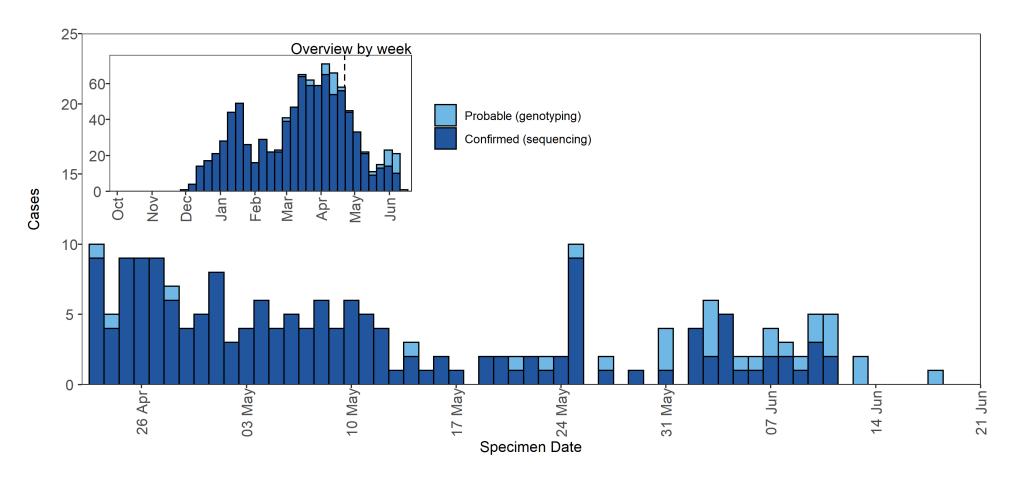
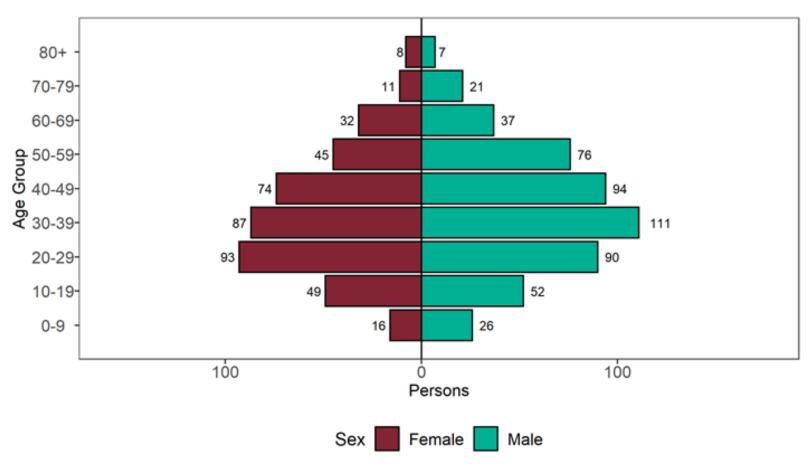


Figure 6. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Beta cases as of June 21 2021 (Find accessible data used in this graph in underlying data.)



Gamma

First identified in Japan amongst travellers from Brazil, the P.1 lineage is a descendant of B.1.1.28. This variant was designated variant under investigation on detection and on review re-designated as VOC-21JAN-02 (P.1) on 13 January 2021. This was named Gamma by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 22 June 2021, 37,969 sequences (excluding the UK) of Gamma from 60 countries.

Table 4. Number of confirmed (genotyping) and probable (genotyping) Gamma cases, by region of residence as of 21 June 2021

Region	Confirmed (sequencing) number	Probable (genotyping) number	Total case number	Proportion of all cases ¹
East Midlands	3	0	3	1.3%
East of England	13	0	13	5.8%
London	103	29	132	58.7%
North East	0	3	3	1.3%
North West	9	1	10	4.4%
South East	27	3	30	13.3%
South West	10	2	12	5.3%
West Midlands	7	1	8	3.6%
Yorkshire and Humber	2	6	8	3.6%
Unknown region	6	0	6	2.7%
Total	180	45	225	-

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 7. Confirmed (sequencing) and probable (genotyping) Gamma cases by region of residence and specimen date as of 21 June 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

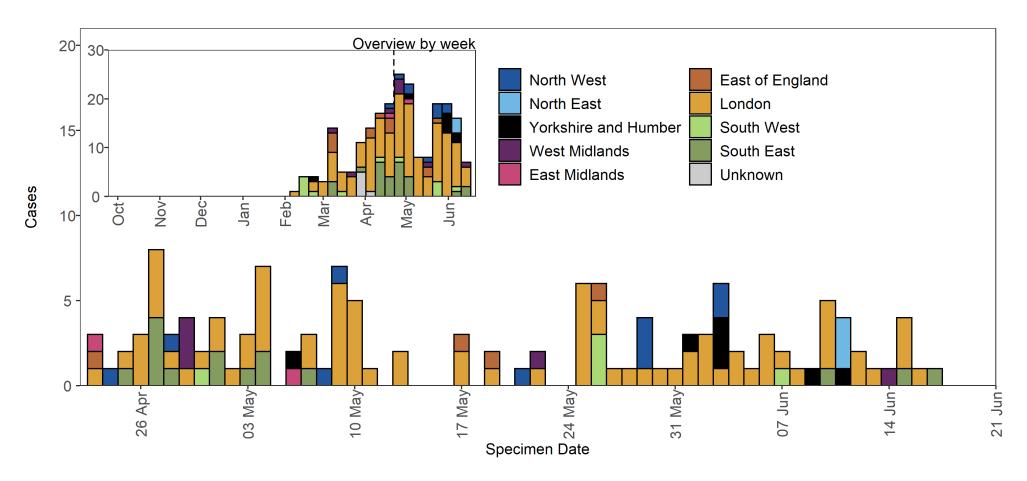


Figure 8. Confirmed (sequencing) and probable (genotyping) Gamma cases by specimen date and detection method as of 21 June 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

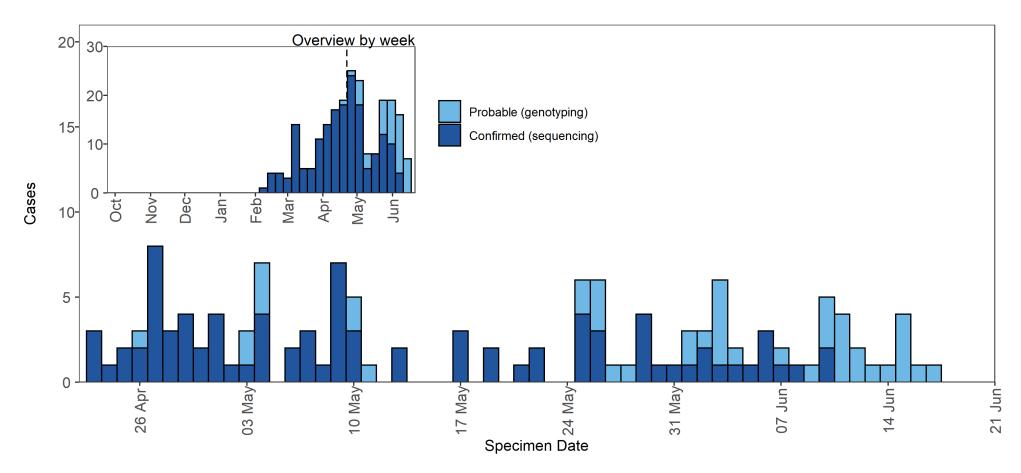
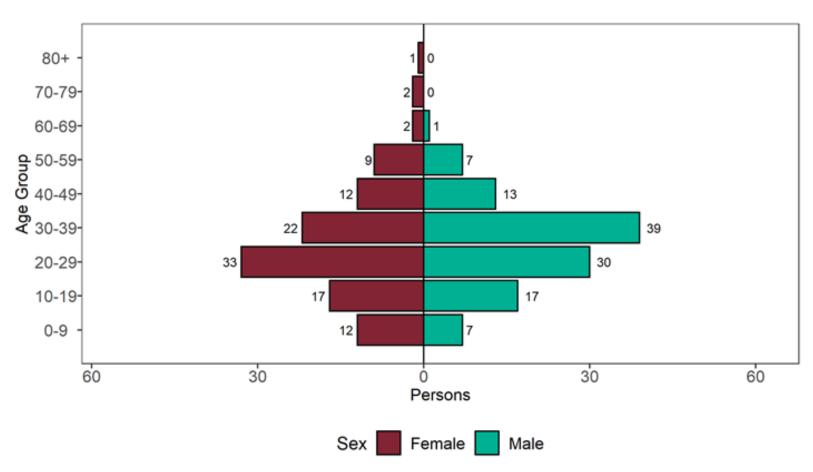


Figure 9. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Gamma cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



Zeta

First identified in Brazil, the P.2 lineage is a descendant of B.1.1.28. This variant was designated VUI-21JAN-01 (P.2) on 13 January 2021. It was first sequenced in the UK in November 2020. This was named Zeta by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 22 June 2021, 3,798 sequences (excluding the UK) of Zeta from 39 countries.

Table 5. Number of confirmed (sequencing) Zeta cases, by region of residence as of 21 June 2021

Region	Total case number	Proportion of all cases
East Midlands	1	1.9%
East of England	2	3.7%
London	14	25.9%
North East	0	0.0%
North West	12	22.2%
South East	6	11.1%
South West	7	13.0%
West Midlands	1	1.9%
Yorkshire and Humber	11	20.4%
Total	54	-

Figure 10. Confirmed (sequencing) Zeta cases by specimen date and region of residence as of 21 June 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

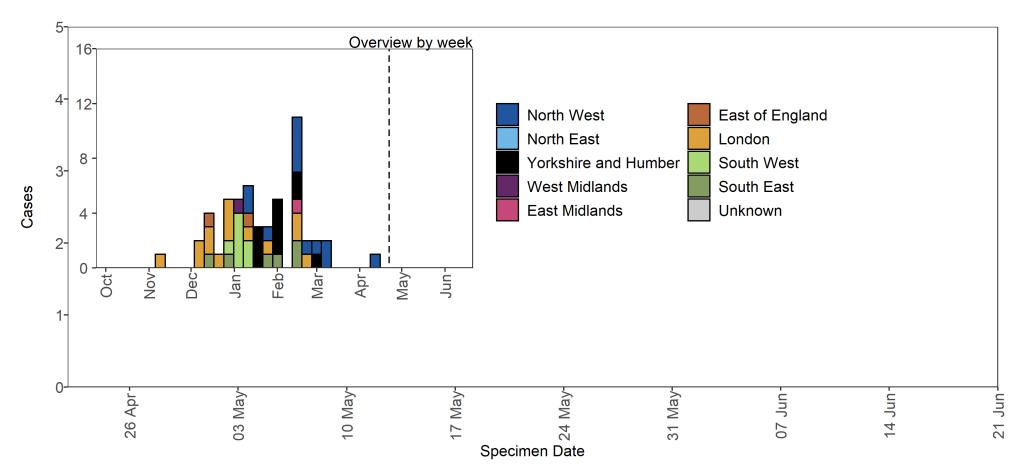
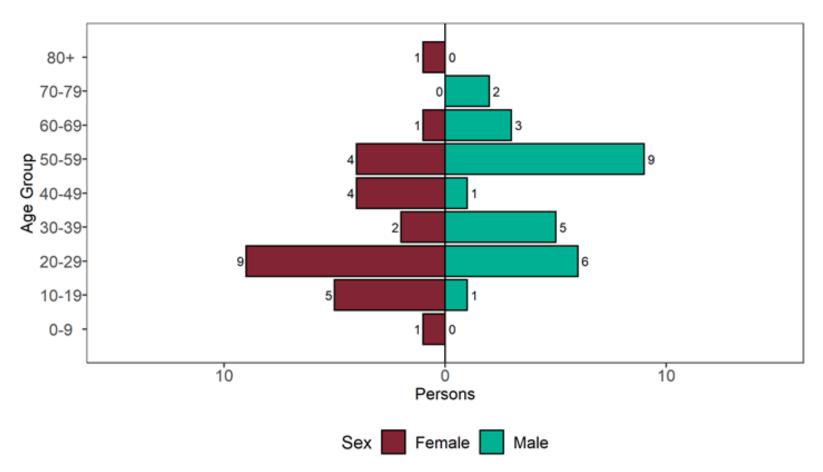


Figure 11. Age-sex pyramid of confirmed (sequencing) Zeta cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



Eta

B.1.525 was identified as a geographically dispersed cluster in UK on the 2 February 2021. This variant was designated VUI-21FEB-03 (B.1.525) on 12 February 2021. The earliest sample date for VUI-21FEB-03 (B.1.525) in England was 15 December 2020. This was named Eta by WHO on 31 May 2021. Genotyping data is not collected for this variant.

International Epidemiology

GISAID includes data on sequences available internationally. As of 22 June 2021, 5,780 sequences of Eta are listed, from 65 countries or territories, excluding the UK.

Table 6. Number of confirmed (sequencing) Eta cases, by region of residence as of 21 June 2021

Region	Total case number	Proportion of all cases
East Midlands	10	2.3%
East of England	29	6.6%
London	157	35.5%
North East	5	1.1%
North West	77	17.4%
South East	80	18.1%
South West	18	4.1%
West Midlands	35	7.9%
Yorkshire and Humber	20	4.5%
Unknown region	11	2.5%
Total	442	-

Figure 12. Confirmed (sequencing) Eta cases by specimen date and region of residence as of 21 June 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

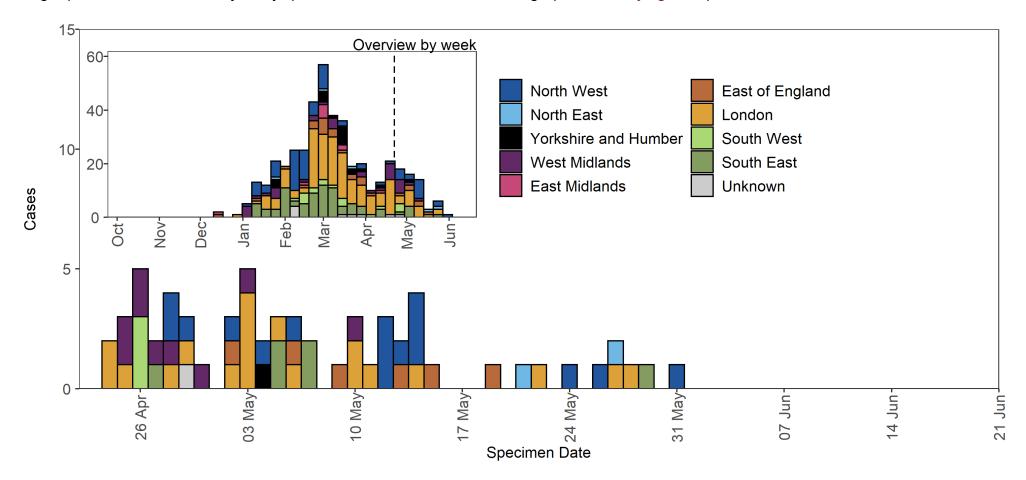
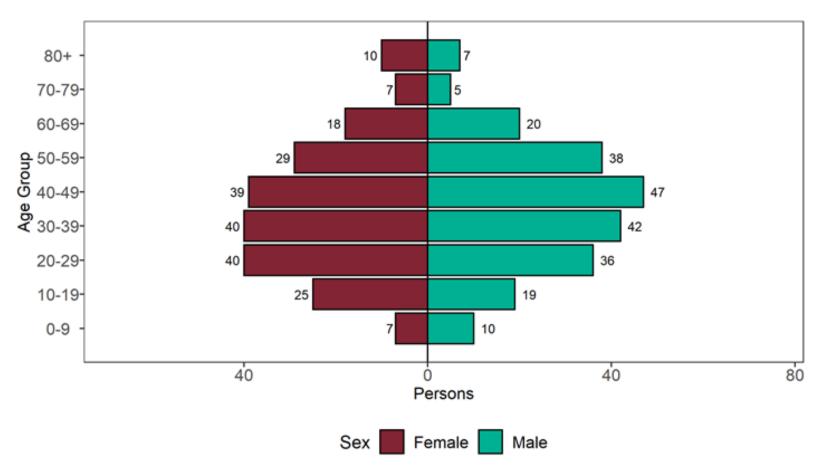


Figure 13. Age-sex pyramid of confirmed (sequencing) Eta cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



VUI-21FEB-04 (B.1.1.318)

B.1.1.318 was identified in England in mid-February 2021 through routine horizon scanning for the development of new clusters of genomes containing E484K. This analysis identified an initial cluster of 6 cases containing E484K and other spike mutations, designated VUI-21FEB-04 (B.1.1.318) on 23 February 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 22 June 2021, 173 international VUI-21FEB-04 (B.1.1.318) sequences, excluding the UK: Austria (1), Bangladesh (1), Belgium (2), Brazil (1), Cameroon (3), Canada (27), Denmark (1), France (10), Germany (16), Ghana (2), Greece (20), India (2), Italy (16), Nigeria (10), Senegal (1), Spain (2), Sweden (4), Switzerland (16), Turkey (1), USA (37).

Table 7. Number of confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases, by region of residence as of 21 June 2021

Region	Total case number	Proportion of all cases
East Midlands	11	3.9%
East of England	34	12.2%
London	106	38.0%
North East	2	0.7%
North West	48	17.2%
South East	48	17.2%
South West	1	0.4%
West Midlands	11	3.9%
Yorkshire and Humber	11	3.9%
Unknown region	7	2.5%
Total	279	-

Figure 14. Confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 21 June 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

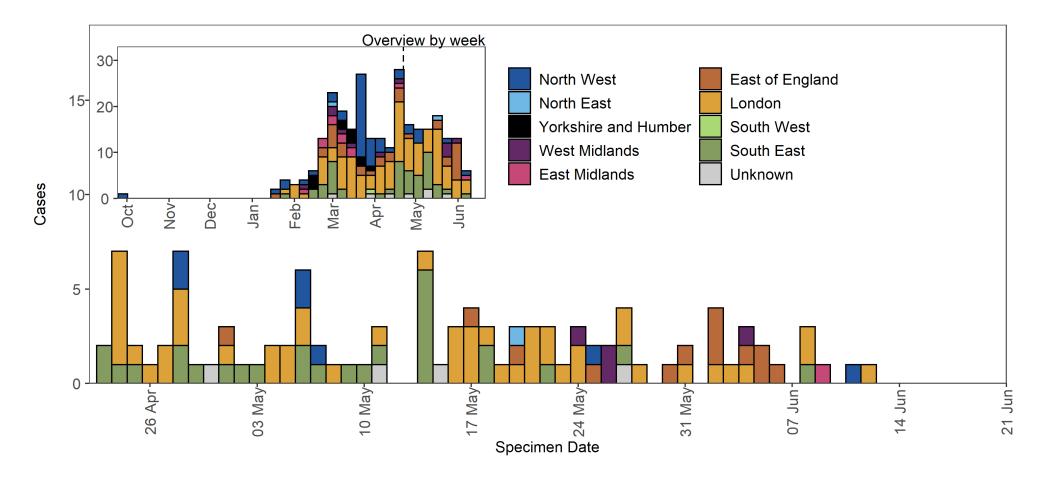
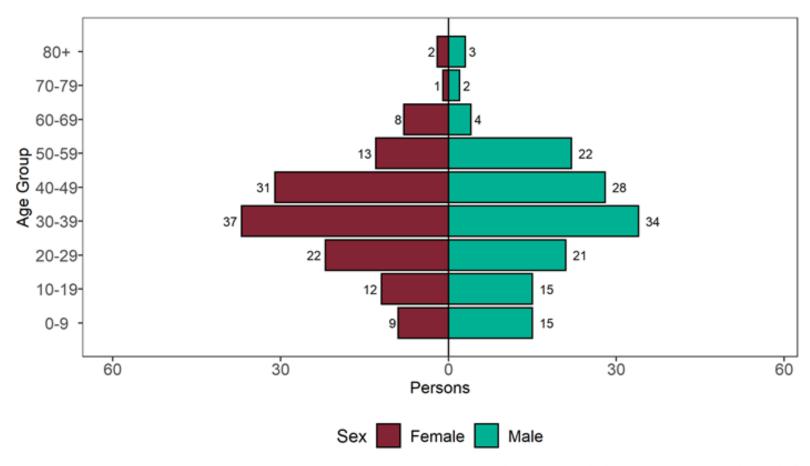


Figure 15. Age-sex pyramid of confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases, as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



Theta

P.3 was identified on 9 March 2021 in a report of 33 genomes from the Philippines with 13 lineage defining mutations. This variant shares important mutations with Variants of Concern including E484K, N501Y and P681H. Based on genomic profile, PHE has designated P.3 as VUI-21MAR-02 on 11 March 2021. This variant arises from B.1.1.28, the same parent lineage that gave rise to P.1 and P.2 in Brazil. Phylogenetic analysis of P.3 shows diversity indicating circulation prior to detection. This variant was named Theta by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 22 June 2021, 246 sequences are listed internationally of Theta excluding the UK: Angola (1), Australia (3), China (2), Germany (8), Hong Kong (10), Japan (4), Malaysia (9), Netherlands (7), New Zealand (3), Norway (2), Philippines (179), Singapore (3), South Korea (1), USA (14).

Table 8. Number of confirmed (sequencing) Theta cases, by region of residence as of 21 June 2021

Region	Total case number	Proportion of all cases
East Midlands	0	0.0%
East of England	1	14.3%
London	2	28.6%
North East	0	0.0%
North West	1	14.3%
South East	0	0.0%
South West	2	28.6%
West Midlands	0	0.0%
Yorkshire and Humber	1	14.3%
Total	7	-

Figure 16. Confirmed (sequencing) Theta cases by specimen date as of 21 June 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

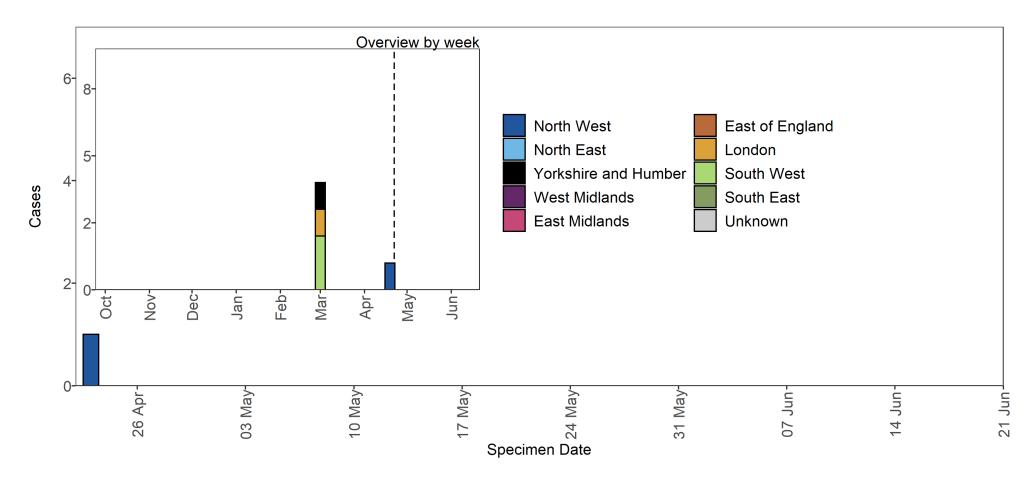
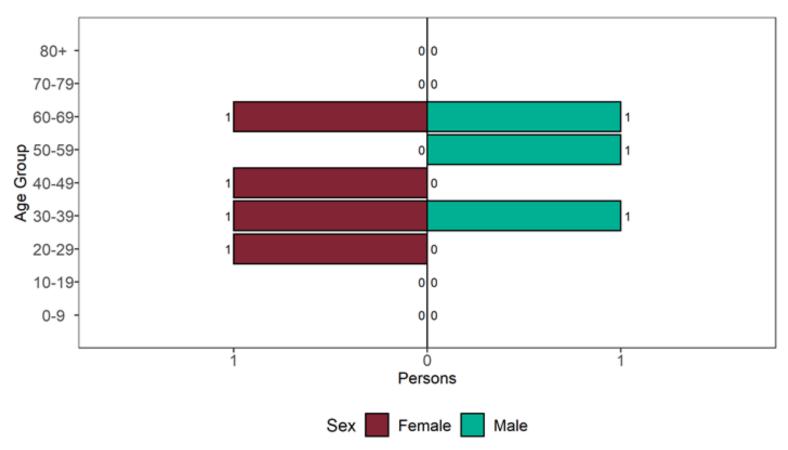


Figure 17. Age-sex pyramid of confirmed (sequencing) Theta cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



Kappa

B.1.617 lineage was escalated to a variant under investigation on 1 April 2021 (B.1.617.1) was escalated to a separate variant under investigation on 27 April 2021 (VUI-21APR-01). This variant was named Kappa by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 22 June 2021, 4,217 Kappa sequences from the following countries (excluding the UK) have been identified in GISAID: Angola (2), Australia (108), Austria (1), Bahrain (8), Belgium (10), Canada (241), China (1), Curacao (1), Czech Republic (4), Denmark (27), Finland (5), France (14), Germany (101), Ghana (5), Greece (1), Guadeloupe (2), Hong Kong (9), India (3083), Ireland (148), Italy (6), Japan (25), Jordan (4), Kenya (5), Luxembourg (6), Malaysia (1), Mexico (5), Nepal (3), Netherlands (11), New Zealand (4), Portugal (9), Qatar (3), Saint Martin (2), Singapore (61), Slovakia (1), Slovenia (1), South Africa (1), South Korea (12), Spain (4), Sweden (5), Switzerland (9), Thailand (1), USA (266), Uganda (1).

Table 9. Number of confirmed (sequencing) Kappa cases, by region of residence as of 21 June 2021

Region	Total case number	Proportion of all cases
East Midlands	48	10.9%
East of England	31	7.1%
London	193	44.0%
North East	5	1.1%
North West	32	7.3%
South East	42	9.6%
South West	13	3.0%
West Midlands	48	10.9%
Yorkshire and Humber	18	4.1%
Unknown region	9	2.1%
Total	439	-

Figure 18. Confirmed (sequencing) Kappa cases by specimen date as of 21 June 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

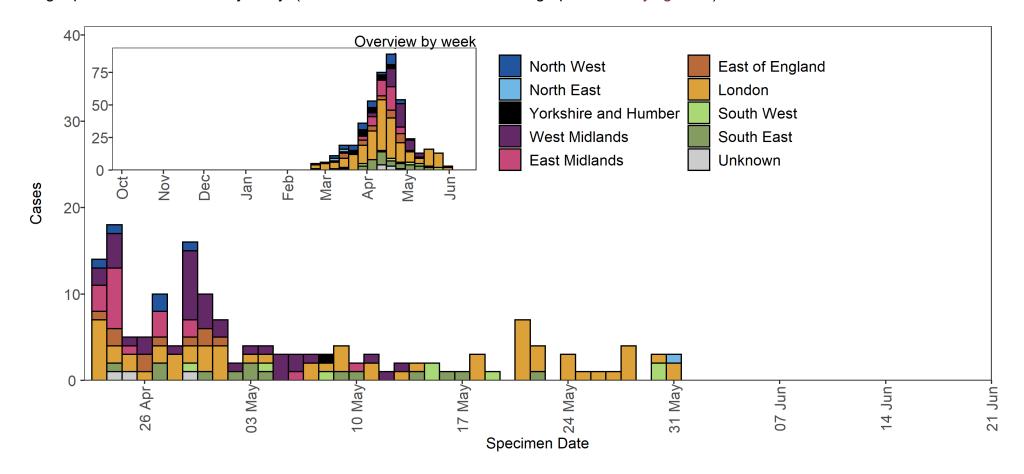
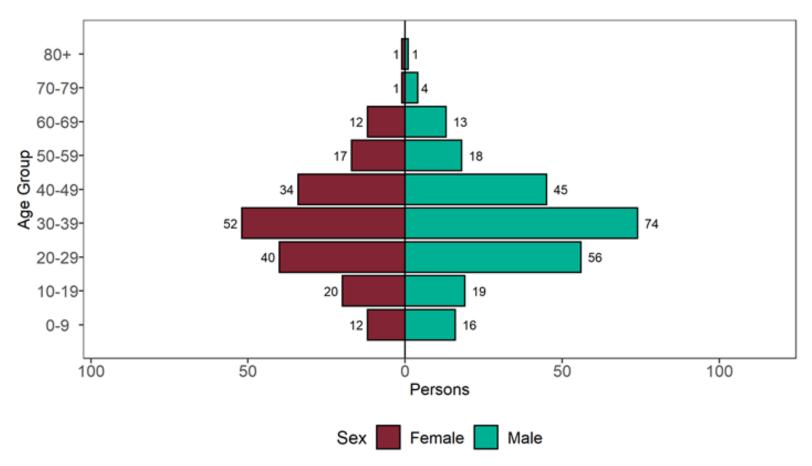


Figure 19. Age-sex pyramid of confirmed (sequencing) Kappa cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



VUI-21APR-03 (B.1.617.3)

B.1.617 lineage was escalated to a variant under investigation on 1 April 2021. VUI-21APR-03 (B.1.617.3) was escalated to a variant under investigation on 28 April 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 22 June 2021, 161 sequences from the following countries (excluding the UK) have been identified in GISAID of VUI-21APR-03 (B.1.617.3): India (148), Japan (1), Malawi (7), Russia (2), Singapore (1), USA (2).

Table 10. Number of confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases, by region of residence as of 21 June 2021

Region	Total case number	Proportion of all cases
East Midlands	0	0.0%
East of England	0	0.0%
London	5	38.5%
North East	0	0.0%
North West	6	46.2%
South East	2	15.4%
South West	0	0.0%
West Midlands	0	0.0%
Yorkshire and Humber	0	0.0%
Total	13	-

Figure 20. Confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases by region of residence and specimen date as of 21 June 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

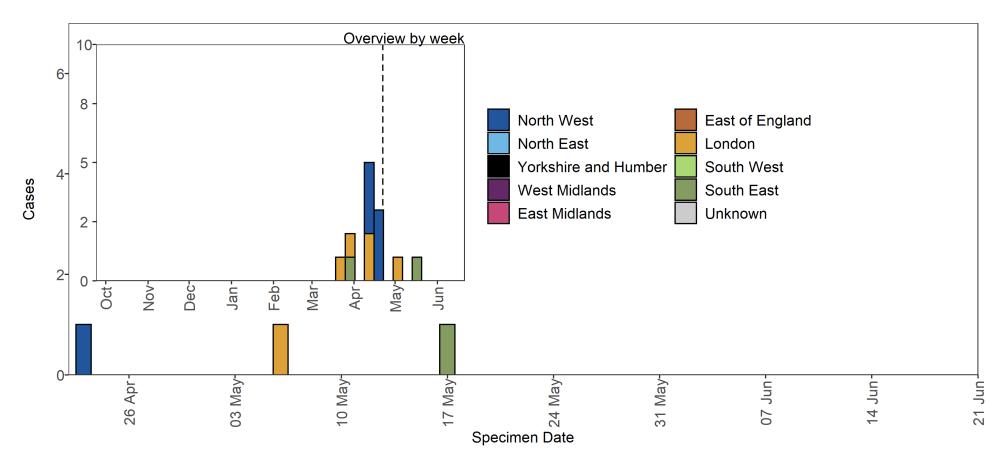
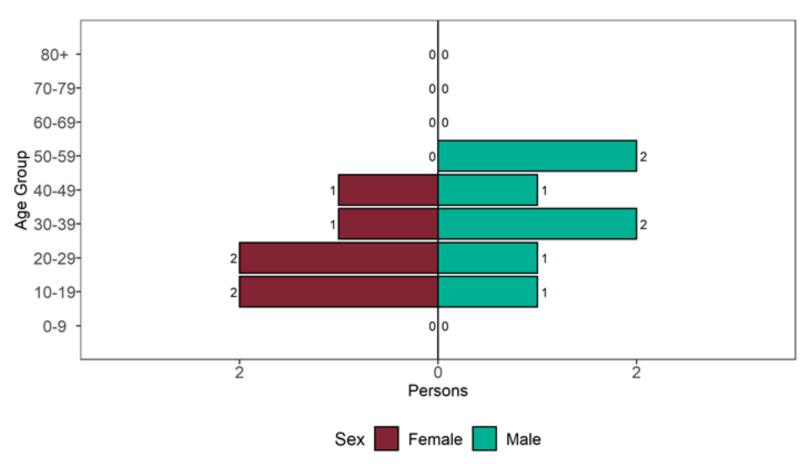


Figure 21. Age-sex pyramid of confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



VUI-21MAY-01 (AV.1)

AV.1 was first detected in UK sequences and was designated under investigation on 14 May 2021 as VUI-21MAY-01 on the basis of the mutation profile and apparent localised cluster in Yorkshire and Humber region.

International Epidemiology

GISAID includes data on sequences available internationally excluding the UK. As of 22 June 2021, 5 sequences of VUI-21MAY-01 (AV.1) from France have been identified on GISAID.

Table 11. Number of confirmed (sequencing) VUI-21MAY-01 (AV.1) cases, by region of residence as of 21 June 2021

Region	Total case number	Proportion of all cases
East Midlands	7	4.0%
East of England	11	6.2%
London	1	0.6%
North East	1	0.6%
North West	7	4.0%
South East	0	0.0%
South West	0	0.0%
West Midlands	4	2.3%
Yorkshire and Humber	145	81.9%
Unknown region	1	0.6%
Total	177	-

Figure 22. Confirmed (sequencing) VUI-21MAY-01 (AV.1) cases by specimen date as of 21 June 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

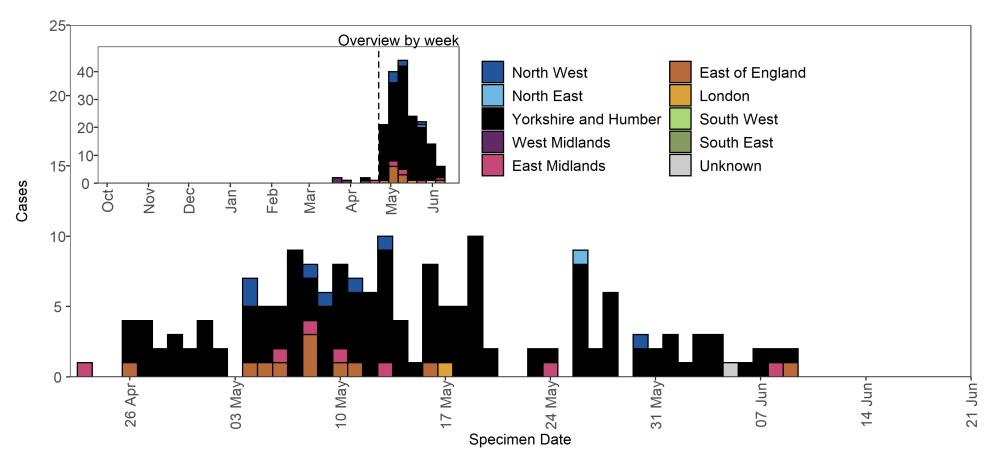
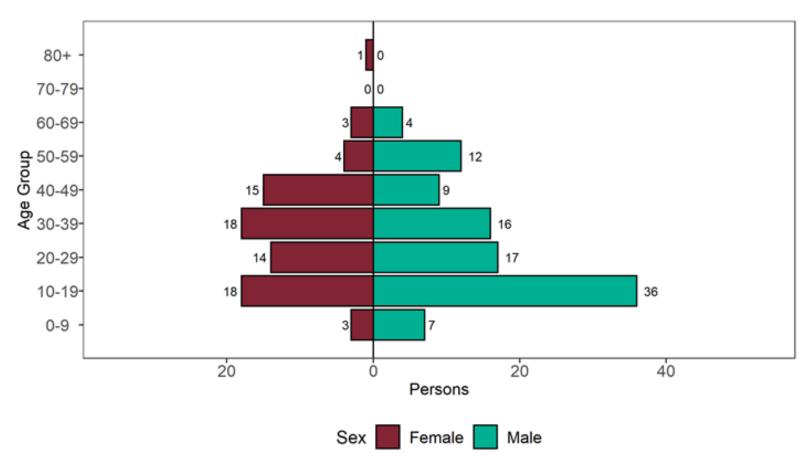


Figure 23. Age-sex pyramid of confirmed (sequencing) VUI-21MAY-01 (AV.1) cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



VUI-21MAY-02 (C.36.3)

C.36.3 was designated a Variant Under Investigation on 24 May 2021 (VUI-21MAY-02) on the basis of the mutation profile and increased importation from a widening international area.

International Epidemiology

GISAID includes data on sequences available internationally excluding the UK. As of 22 June 2021, 1,069 sequences of VUI-21MAY-02 (C.36.3) from 42 countries have been identified on GISAID.

Table 12. Number of confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases, by region of residence as of 21 June 2021

Region	Total case number	Proportion of all cases
East Midlands	8	6.0%
East of England	21	15.8%
London	39	29.3%
North East	1	0.8%
North West	13	9.8%
South East	10	7.5%
South West	4	3.0%
West Midlands	10	7.5%
Yorkshire and Humber	26	19.5%
Unknown region	1	0.8%
Total	133	-

Figure 24. Confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases by specimen date and region of residence as of 21 June 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

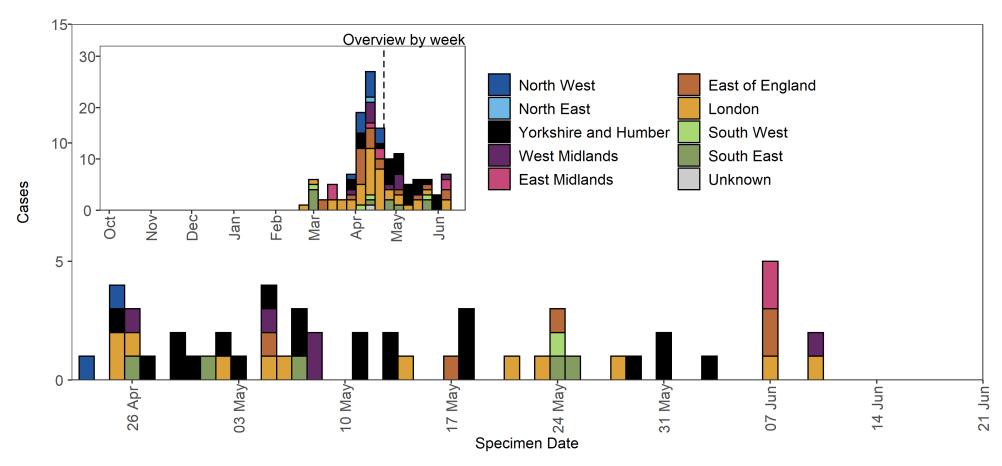
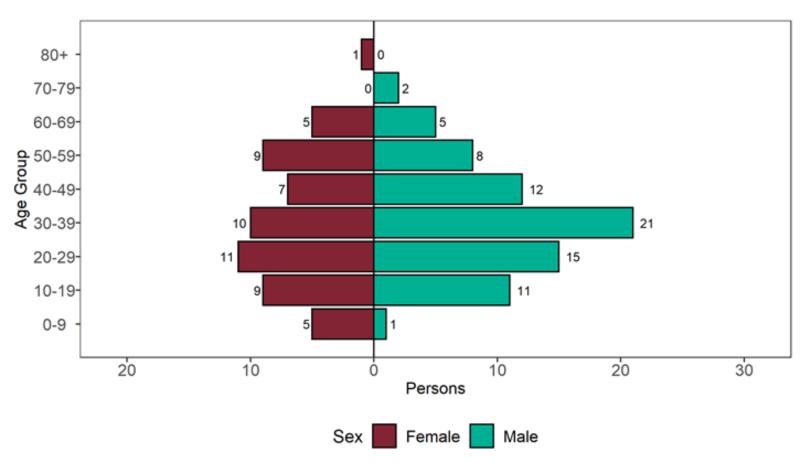


Figure 25. Age-sex pyramid of confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.)



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 and Emergency Care Data Set (ECDS). 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

A repository containing the up-to-date genomic definitions for all VOC and VUI as curated by Public Health England was created 5 March 2021. The repository can be accessed on GitHub. They 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 Public Health England. 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 Cell Data Team

PHE International Cell

Variant Technical Group Membership

The PHE Variant Technical Group includes representation from the following organisations: PHE, DHSC, BEIS, Public Health Wales, Public Health Scotland, Public Health Agency Northern Ireland, Imperial College London, London School of Hygiene and Tropical Medicine, University of Birmingham, University of Cambridge, University of Edinburgh, University of Liverpool, the Wellcome Sanger Institute.

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