UK Health Security Agency

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

Technical briefing 43

24 June 2022

This report provides an update on previous briefings up to 20 May 2022

Contents

Summary

This report has been published to share the detailed variant surveillance analyses which contribute to the variant risk assessments and designation of new SARS-CoV-2 variants. This specialist technical briefing contains early data and analysis on emerging variants and findings have a high level of uncertainty.

Unless stated otherwise, this technical briefing uses a data cut-off of 21 June 2022 to allow time for analyses.

Interpreting variant data

The current testing policy needs to be considered when interpreting all variant data; the targeting of testing at specific groups is likely to delay the detection and characterisation of variants.

BA.4 and BA.5

Growth

BA.4 and BA.5 were designated Variants of Concern (VOC) on 18 May 2022 based on a growth advantage which could plausibly lead to increased community transmission.

BA.4 and BA.5 are now dominant and COVID-19 incidence is increasing. Updated modelling shows that BA.4 and BA.5 continue to demonstrate a growth advantage over BA.2 with a relatively high degree of certainty. The relative growth advantage for BA.5 is larger than BA.4 and it is therefore most likely that BA.5 will become the dominant variant in the UK. We estimate that 22.28% (CI: 16.25 to 28.77) and 39.46% (CI: 32.19 to 51.31) of cases are currently BA.4 and BA.5, respectively.

Severity

The real time infection hospitalisation risk has been growing since April 2022. This is still a relatively small effect at present. The reason is unclear, and if confirmed may have both variant (antigenic +/- fitness) and population immunity contributors.

Reports from Variant Technical Group members

Laboratory data from Genotype2Phenotype (G2P) Consortium (unpublished) and others suggest that there is a minimal change in fusogenicity of the spike of BA.4 and BA.5 (compared to other Omicron variants), and that the entry route is similar to that of BA.1 and BA.2. Other data from G2P (which will be cited when available) shows some changes in the interaction with the human host cell by BA.4 and BA.5 virus compared with earlier Omicron variants that could

be associated with increased fitness. Neutralisation data has been described previously. Taken together the laboratory data suggest small changes in antigenicity and potentially small increases in fitness may both contribute to the observed growth advantage.

Published information on variants

On 1 April 2022 UK Health Security Agency (UKHSA) amended its variant classification system. Further details are available in Technical Briefing 39.

SARS-CoV-2 Routine variant data update covers surveillance data and sequencing coverage data on all other VOCs and VUIs up to 25 March 2022.

The collection page gives content on variants, including prior technical briefings. Technical briefings are published periodically. From technical briefing 15, briefings include variant diagnoses identified by whole-genome sequencing and a genotyping polymerase chain reaction (PCR) test, including the categorisation of sequenced and genotyped variant results and a rules-based decision algorithm to identify variant and mutation profiles from genotype assay mutation profiles.

The Public Health England repository from 5 March 2021 contains the previous genomic definitions for VOCs and variants under investigation (VUIs).

Part 1. Surveillance overview

World Health Organization (WHO) nomenclature from 24 January 2022 is incorporated. Tables 1a and 1b show the current VOCs, variants (V-date-number), and signals in monitoring detected and not detected in the United Kingdom (UK) incorporating WHO designations with Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin lineages).

Table 1a. Variants detected in the UK in the past 12 weeks

Variants of concern	Variants (Vs)	Signals in monitoring
Omicron (B.1.1.529) sub-lineage BA.1 and descendant lineages VOC-21NOV-01	V-22MAY-01 (BA.2.12.1)	BA.3
Omicron (B.1.1.529) sub-lineage BA.2 and descendant lineages VOC-22JAN-01	Delta (B.1.617.2 and sub-lineages) V-21APR-02	Delta and Omicron recombinant lineages (UK) Including Omicron-like variant with additional spike mutations: M153I, T299I, R346K, L368I, E484K, G1219C
Omicron (B.1.1.529) sub-lineage BA.4 VOC-22APR-03	XE Recombinant (BA.1 x BA.2) V-22APR-02	BA.1/BA.2 Recombinant (with unique mutation C3583T)
Omicron (B.1.1.529) sub-lineage BA.5 VOC-22APR-04		XF Recombinant
		BA.2.12.1

Table 1b. Variants detected in GISAID, but not in the UK, in the past 12 weeks

Variants of concern	Variants (Vs)	Signals in monitoring
	Alpha (V-20DEC-01/B.1.1.7)	AY.119.2/BA.1.1 Recombinant
	V-21OCT-01 (AY.4.2) †	BA.3
		XF Recombinant

† AY.4.2 is a sub-lineage within Delta that has been assigned as a distinct V-date-number

VOCs and other Variants (V-date-number) 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 Variants has not been observed in the UK or international data sets within the preceding 12 weeks, it is designated as provisionally extinct, but monitoring remains in place. Variants and signals in monitoring may also be removed from the grid if they show consistently low growth rates.

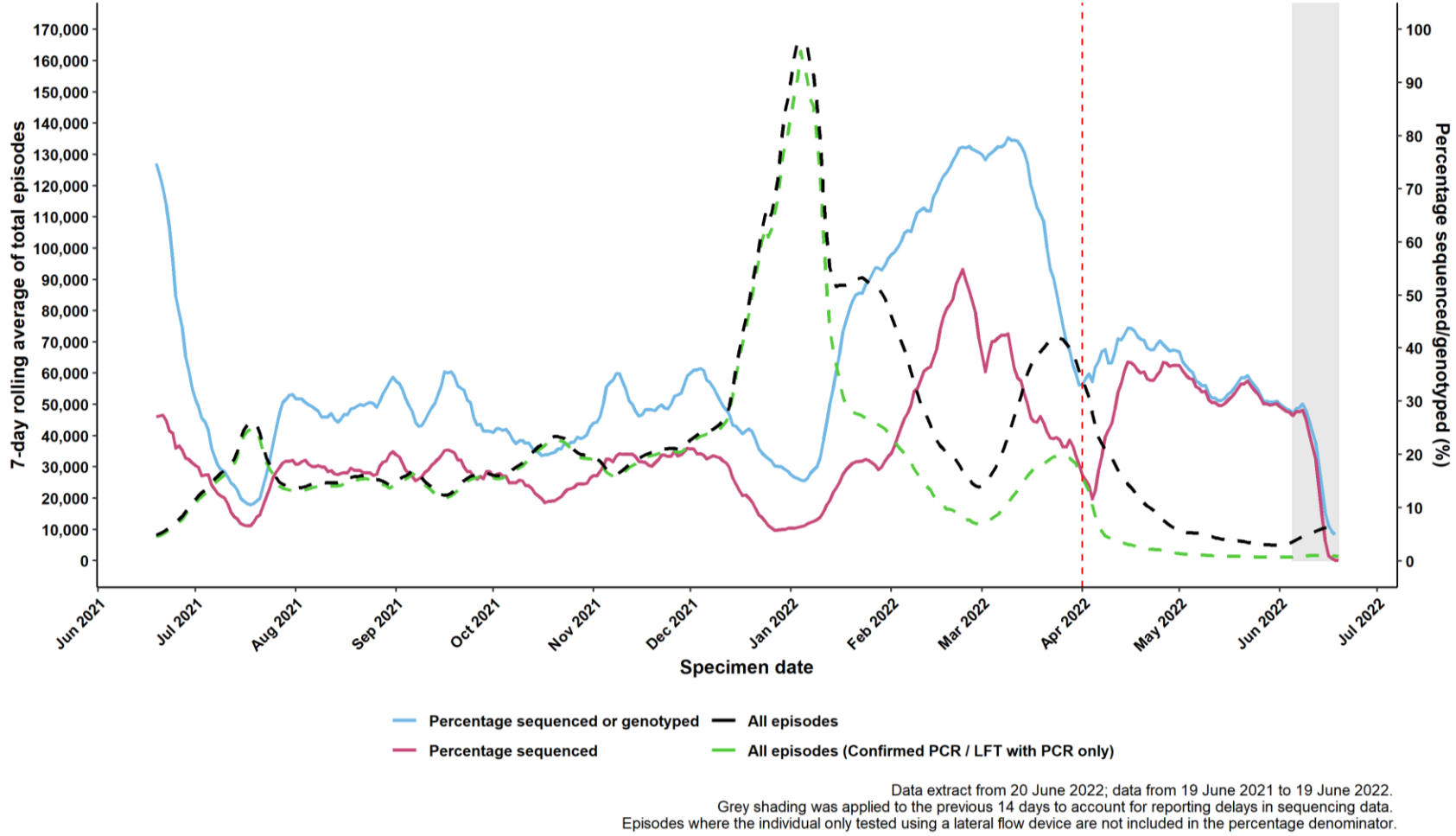
1.1 Sequencing coverage

Figure 1 shows the proportion of coronavirus (COVID-19) episodes as detected by PCR that have linked to a valid sequencing result (sequences included have 50% of the genome with sufficient read coverage) or genotyping PCR result over time. Figure 2 shows the proportion of episodes sequenced and genotyped over time by regions. Figure 3 shows the proportion of episodes sequenced and genotyped amongst individuals who tested positive whilst in hospital. The vertical dashed red line indicates the 1 April 2022 when free testing for the general public ended.

Sequencing coverage of PCR confirmed episodes were high during March 2022 (Figure 1) However, this needs to be interpreted with care as PCR tests have declined substantially since mid-February 2022 and case ascertainment is reduced.

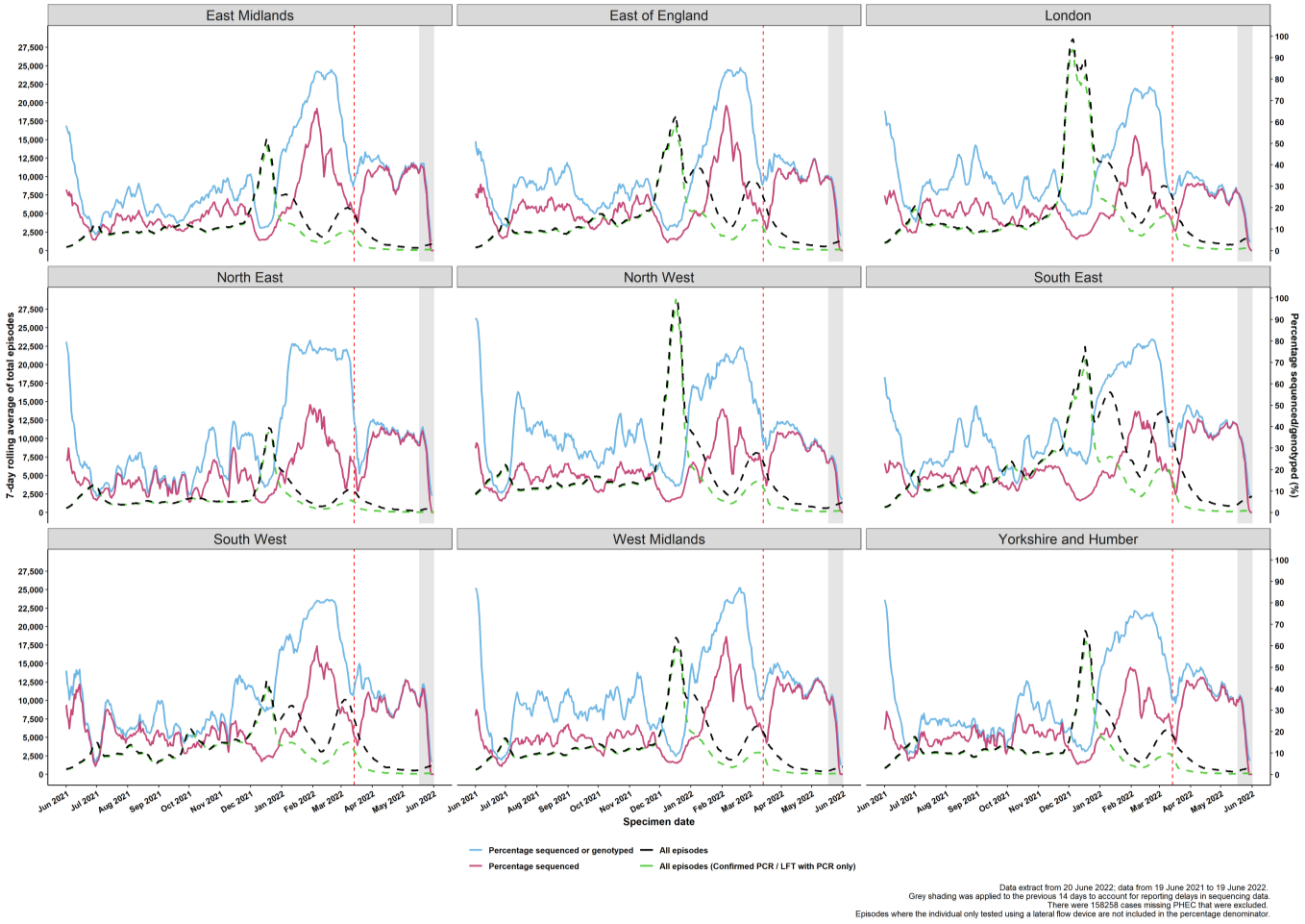
Currently, the sequencing strategy prioritises hospitalised cases, patients who are receiving specific antiviral therapy, and national core priority studies.

Figure 1. Coverage of sequencing with a valid result and genotyping over time (19 June 2021 to 20 June 2022)



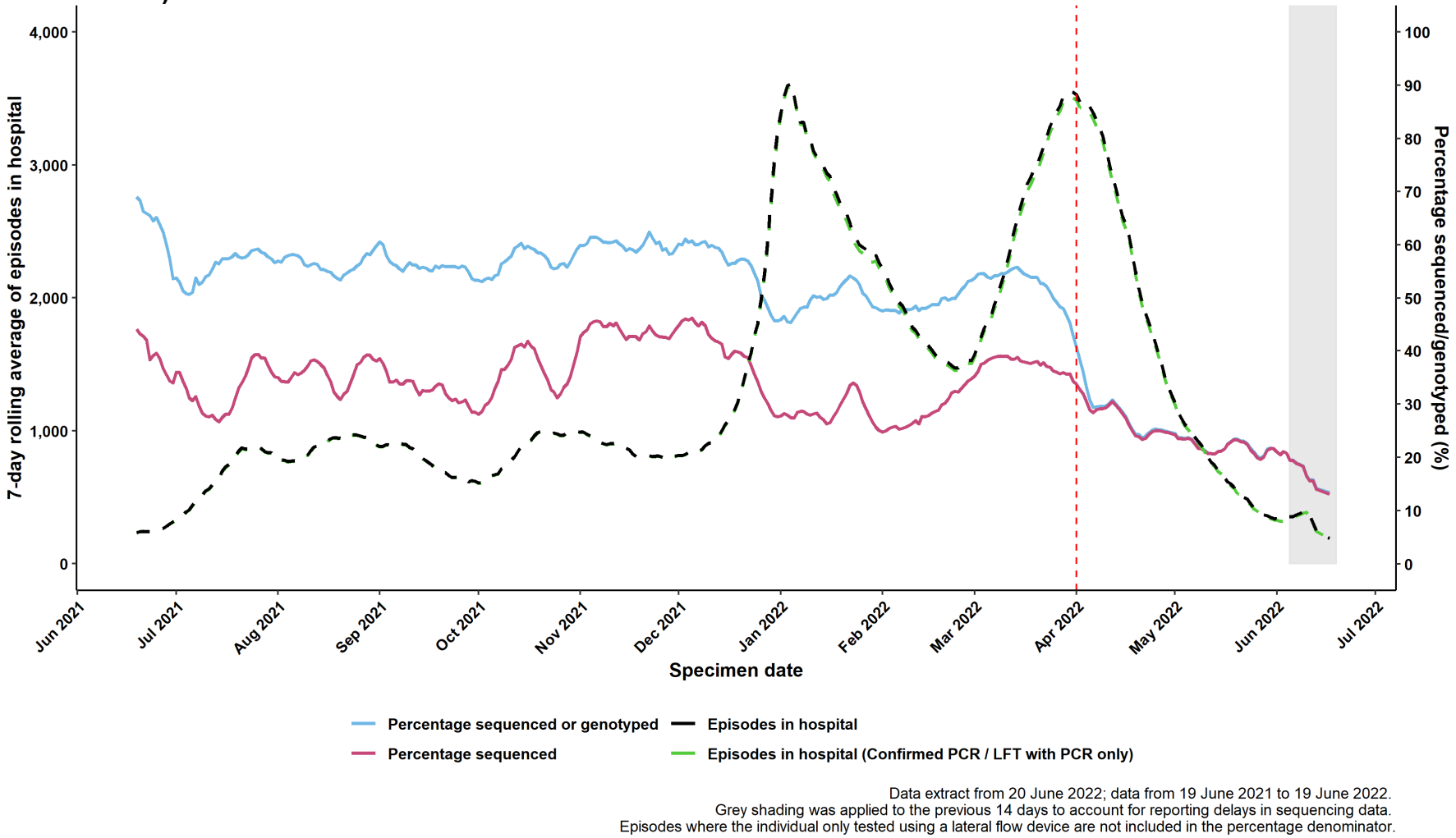
Episodes where the individual only tested using a lateral flow device are excluded. Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the accompanying spreadsheet.)

Figure 2. Coverage of sequencing with a valid result and genotyping over time by region (19 June 2021 to 20 June 2022)



Episodes where the individual only tested positive using a lateral flow device are excluded. Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the accompanying spreadsheet.)

Figure 3. Coverage of sequencing with valid result and genotyping for cases who test positive in hospital (19 June 2021 to 20 June 2022)

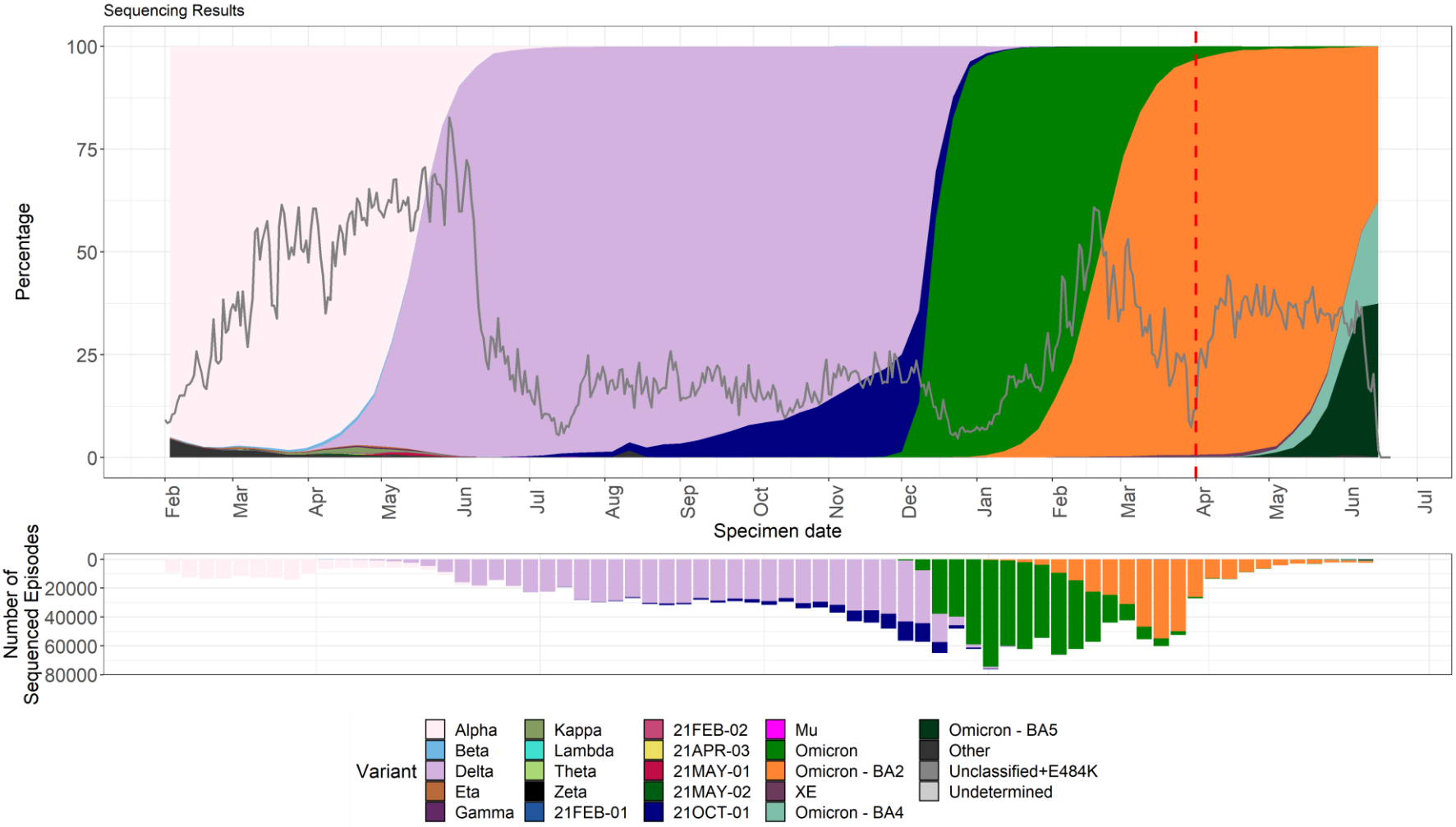


Episodes where the individual only tested positive using a lateral flow device are excluded. Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the accompanying spreadsheet.)

1.2 Variant prevalence

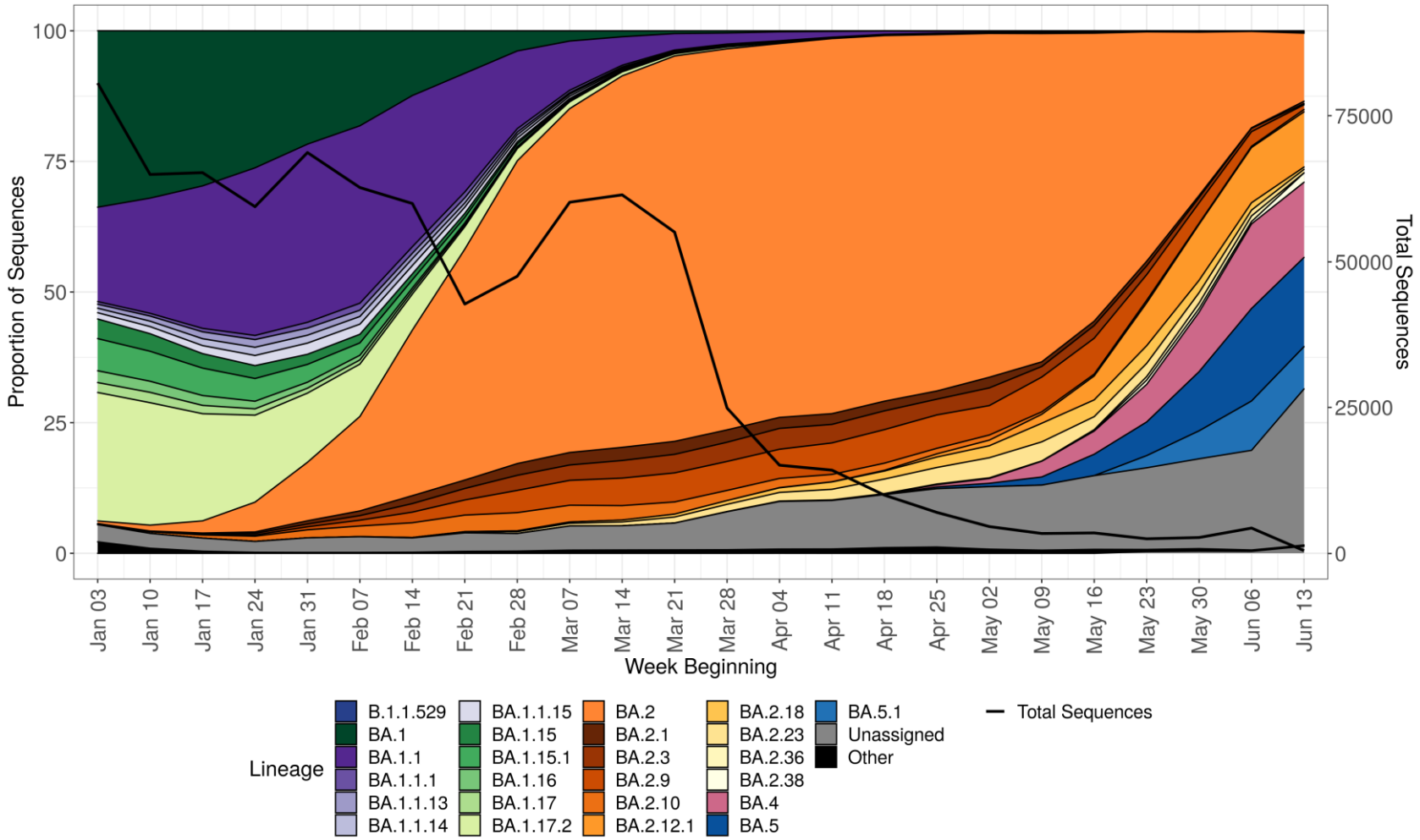
The prevalence of different UKHSA-designated variants amongst sequenced episodes is presented in Figure 4 and by Pangolin designation in Figure 5. Of the sequenced episodes from 5 June 2022 to 12 June 2022, 45.0% were Omicron lineage BA.2 (VOC-22JAN-01) and 0.04% were Omicron lineage BA.1 (VOC-21NOV-01). A further 54.5% were made up of Omicron lineage BA.4 (VOC-22APR-03), Omicron lineage BA.5 (VOC-22APR-04) and Omicron recombinant XE (V-22APR-02).

Figure 4. Variant prevalence of available sequenced episodes for England from 1 February 2021 as of 20 June 2022



Find accessible data used in this graph in underlying data. Dashed lines indicate period incorporating issue at a sequencing site. Grey line indicates proportion of cases sequenced. The red dash line denotes the start of England's 'Living with COVID' Plan. Note recombinants, such as XD, are not specified but are largely within the 'other' group currently as numbers are too small.

Figure 5. Prevalence of Pangolin lineages in the UK with sequence data from 3 January 2022 to 19 June 2022



The ‘Other’ category in this plot contains all lineages that do not meet the relevant criteria after combining smaller lineages. ‘Unassigned’ are sequences that could not be assigned a lineage by Pangolin. Due to the increasing similarities across BA lineages, it is difficult to assign lineages to sequences with lower genome coverage.

Of the 1402 sequences that are Unassigned since 30 May 2022, 792 are called as VOC-22APR-04, 311 VOC-22JAN-01, 160 VOC-22APR-03, and 139 are an unknown Omicron lineage using the UKHSA variant definitions. The total number of valid sequence results per week is shown by the black line. Lineages are shown if there are >= 5000 sequences since 3 January 2022 or if they are >=1% of sequences within a single week over the last 6 weeks. Lineages that do not met these criteria are combined with their parent lineage (for example, BA.2.4 is combine with BA.2). Find accessible data used in this graph in underlying data.

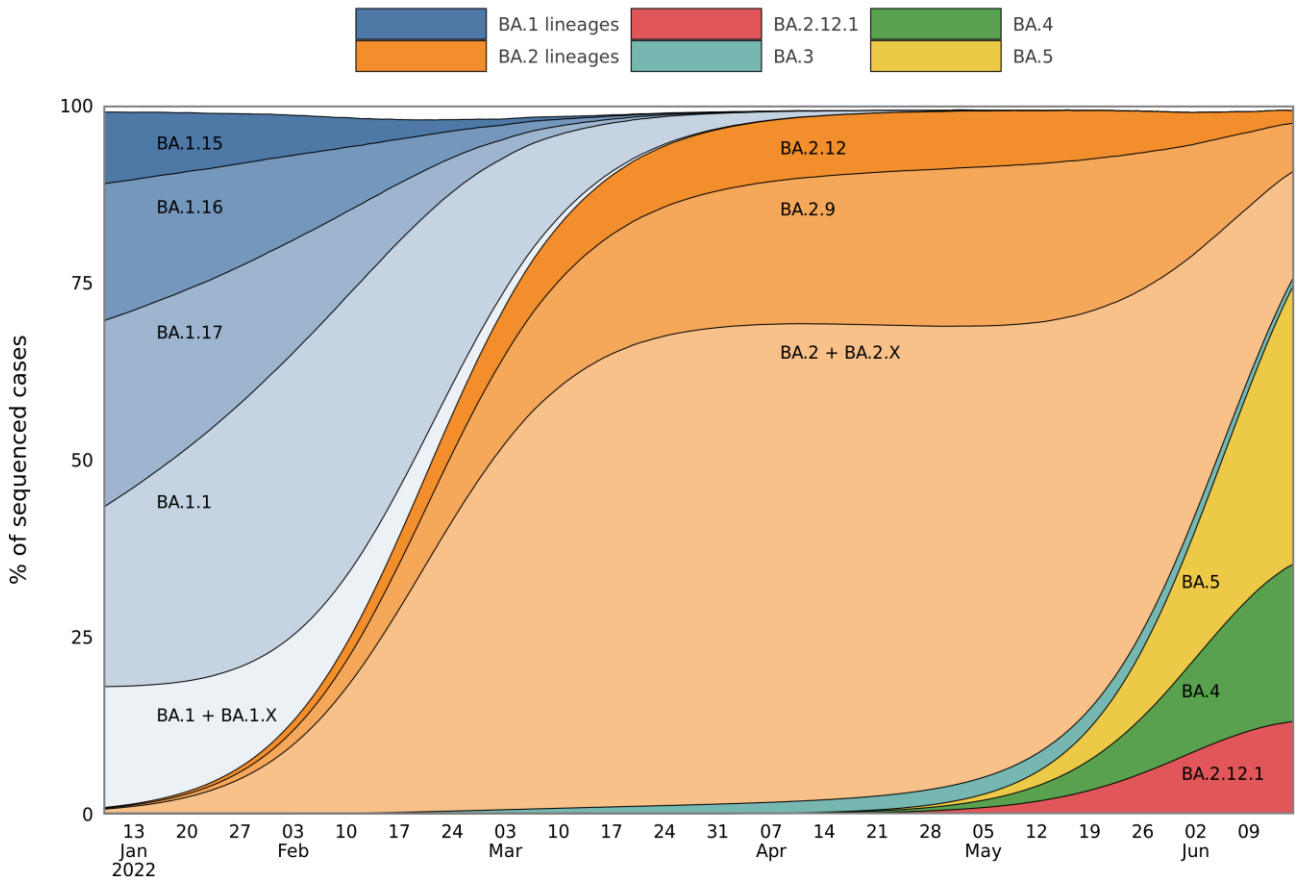
1.3 Variant modelling

Multinomial model

A Bayesian hierarchical multinomial model was used to describe the dynamics of Omicron lineages in England since the first full week of 2022 (beginning 9 January 2022), with the objective of determining which of BA.2.12.1, BA.4 and BA.5 had the largest relative fitness advantage. The model accounts for heterogeneity in the regional arrival times of each lineage. The data is sourced from the Sanger Mart which are more timely but not corrected retrospectively for changes to the Pangolin.

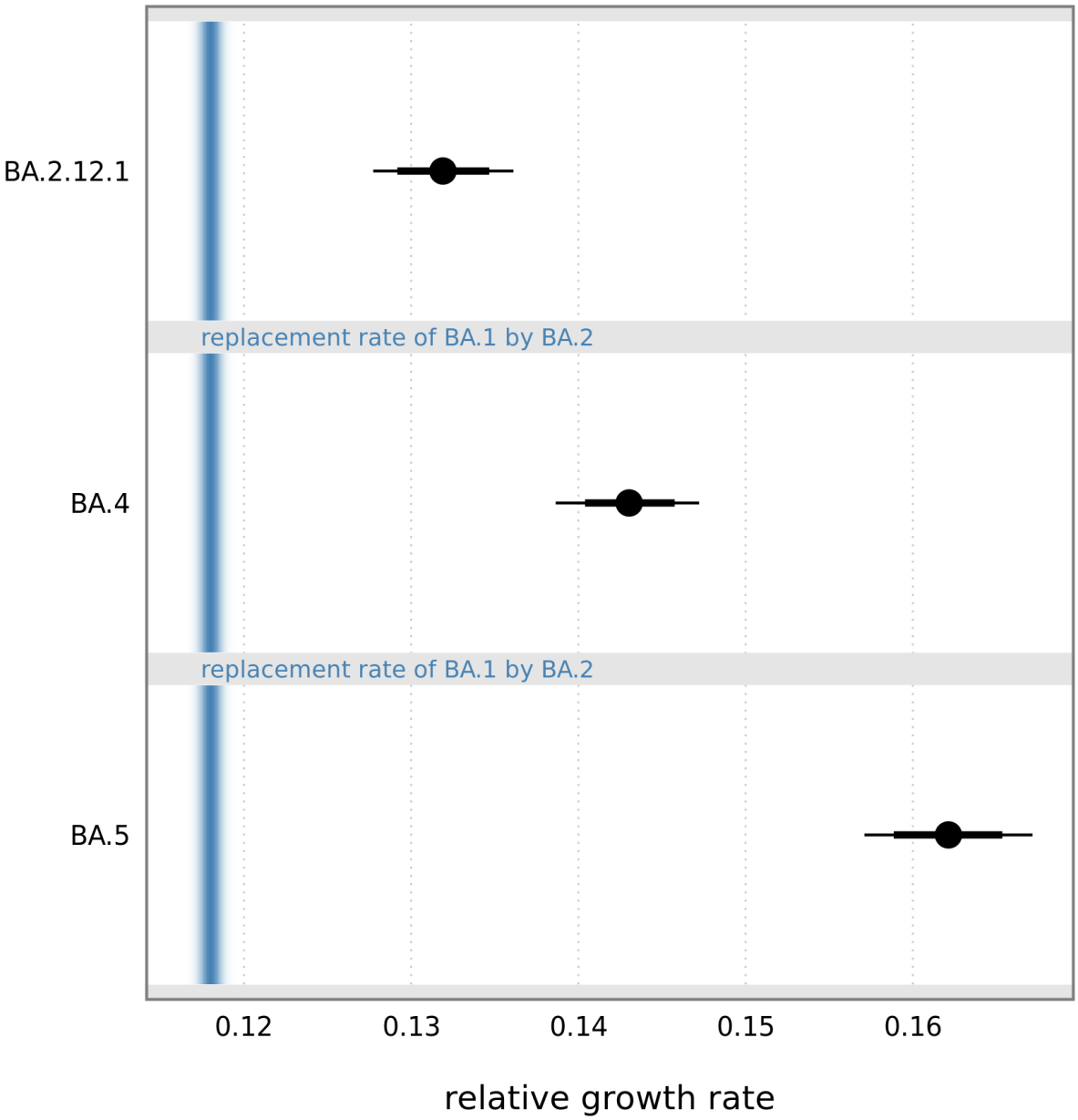
The model output is shown in Figure 6 and the estimated relative growth rates for each lineage of Omicron. This model suggests that BA.5 has the largest relative fitness advantage, followed by BA.4 then BA.2.12.1 (Figure 7). It is anticipated that BA.5 will be the dominant variant in all UK regions (Figure 8). Table 2 gives the estimated percentages for each lineage.

Figure 6. Area plot showing the predicted representation of each lineage of the multinomial model



This figure shows the predicted representation of different lineages from the multinomial model. The white region denotes other non-Omicron variants. Supplementary data is not available for this figure.

Figure 7. Estimated relative growth rates for BA.4, BA.5 and BA.2.12.1 from a multinomial model of sequenced cases in England



The relative growth rates are taken from a multinomial model of sequenced cases that accounts for regional differences in arrival time. Supplementary data is not available for this figure.

Table 2. Modelled percentage representation of BA.2.12.1, BA.4 and BA.5 from the multinomial model

Region name	BA.5	BA.4	BA.2.12.1
National	**39.46% (CI: 32.19 to 51.31)**	**22.28% (CI: 16.25 to 28.77)**	**13.11% (CI: 8.59 to 17.52)**
East Midlands	40.05% (CI: 35.21 to 44.88)	20.53% (CI: 17.03 to 24.43)	11.9% (CI: 9.43 to 14.85)
East of England	40.57% (CI: 36.45 to 44.78)	22.87% (CI: 19.6 to 26.37)	13.89% (CI: 11.48 to 16.5)
London	43.09% (CI: 39.54 to 46.67)	20.64% (CI: 17.98 to 23.59)	17.74% (CI: 15.28 to 20.37)
North East	39.44% (CI: 33.93 to 44.86)	17.52% (CI: 13.92 to 21.72)	11.65% (CI: 8.74 to 14.94)
North West	32.97% (CI: 29.16 to 36.83)	26.76% (CI: 23.39 to 30.07)	11.65% (CI: 9.48 to 14.05)
South East	43.6% (CI: 40.39 to 46.86)	22.91% (CI: 20.35 to 25.6)	13.87% (CI: 11.88 to 15.92)
South West	42.27% (CI: 38.27 to 46.41)	14.58% (CI: 11.96 to 17.56)	17.36% (CI: 14.7 to 20.46)
West Midlands	35.42% (CI: 30.84 to 39.91)	29.87% (CI: 25.96 to 34.06)	11.79% (CI: 9.39 to 14.69)
Yorkshire	31.5% (CI: 27.18 to 35.96)	28.62% (CI: 24.87 to 32.81)	10.35% (CI: 7.92 to 12.81)

Estimates are as of the 15 of June 2022. The national estimate is an unweighted percentage (that is, it is the average of regions, not weighted by the population size of the constituent regions).

Relative growth rates

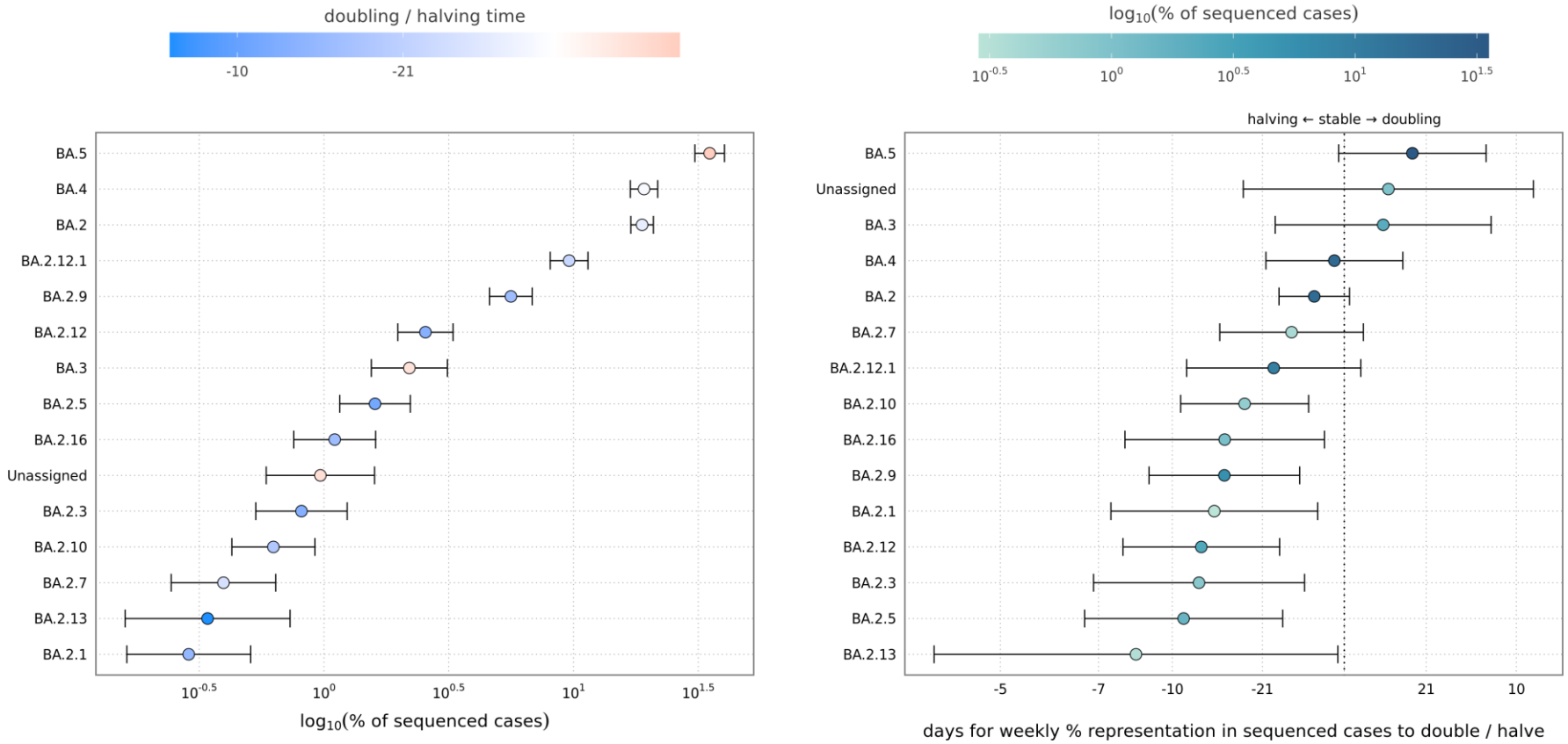
The representation of different variants among sequenced cases was modelled for the last 3 months in England. Generalised additive models are fit with a negative binomial error structure to weekly-aggregated counts of variants to determine growth rates. An offset term is used to control for sampling effort. Models are fit at the weekly timescale due to small daily sample sizes. Doubling times therefore refer for the time for the weekly representation of variants to double or halve. Only variants that were sequenced 10 or more times in the past 2 weeks are included (Figure 8). Estimates are for the week ending the 19 June 2022. The data is sourced from the Sanger Mart which are more timely but not corrected retrospectively for changes to the Pangolin.

The model suggests that the relative growth rate of BA.2.12.1 and BA.4 has slowed considerably and is likely stable or declining (both doubling and halving times are included in the confidence intervals (Table 3). The relative growth rate of BA.5 has slowed considerably, but its representation is likely still increasing.

Table 3. Modelled relative growth rates (as doubling times) and representation among sequenced cases for BA.2.12.1, BA.4 and BA.5

Date of estimate (week ending)	Variant	Total samples	Percentage	Relative doubling time
19 June 2022	BA.2.12.1	945	9.61% (CI: 8.07 to 11.43)	-24.38 days (CI: -10.91 to 104.03)
19 June 2022	BA.4	1301	19.17% (CI: 16.9 to 21.75)	-173.52 days (CI: -21.95 to 29.38)
19 June 2022	BA.5	1787	35.14% (CI: 30.65 to 40.28)	25.24 days (CI: -306.54 to 12.12)

Figure 8. Modelled representation and growth rate (as doubling times) of sequenced cases in England



Estimates are for the week ending 19 June 2022. Only variants with 10 or more detections in the last 2 weeks were analysed. Generalised additive models were fitted with a negative binomial error structure to counts of cases of a specific variant, using a log-offset term to correct for sampling effort. Data were analysed at the weekly time scale due to sample size constraints. Note that doubling times refer to the weekly representation of variants. Supplementary data are not available for this figure.

1.4 Hospital modelling

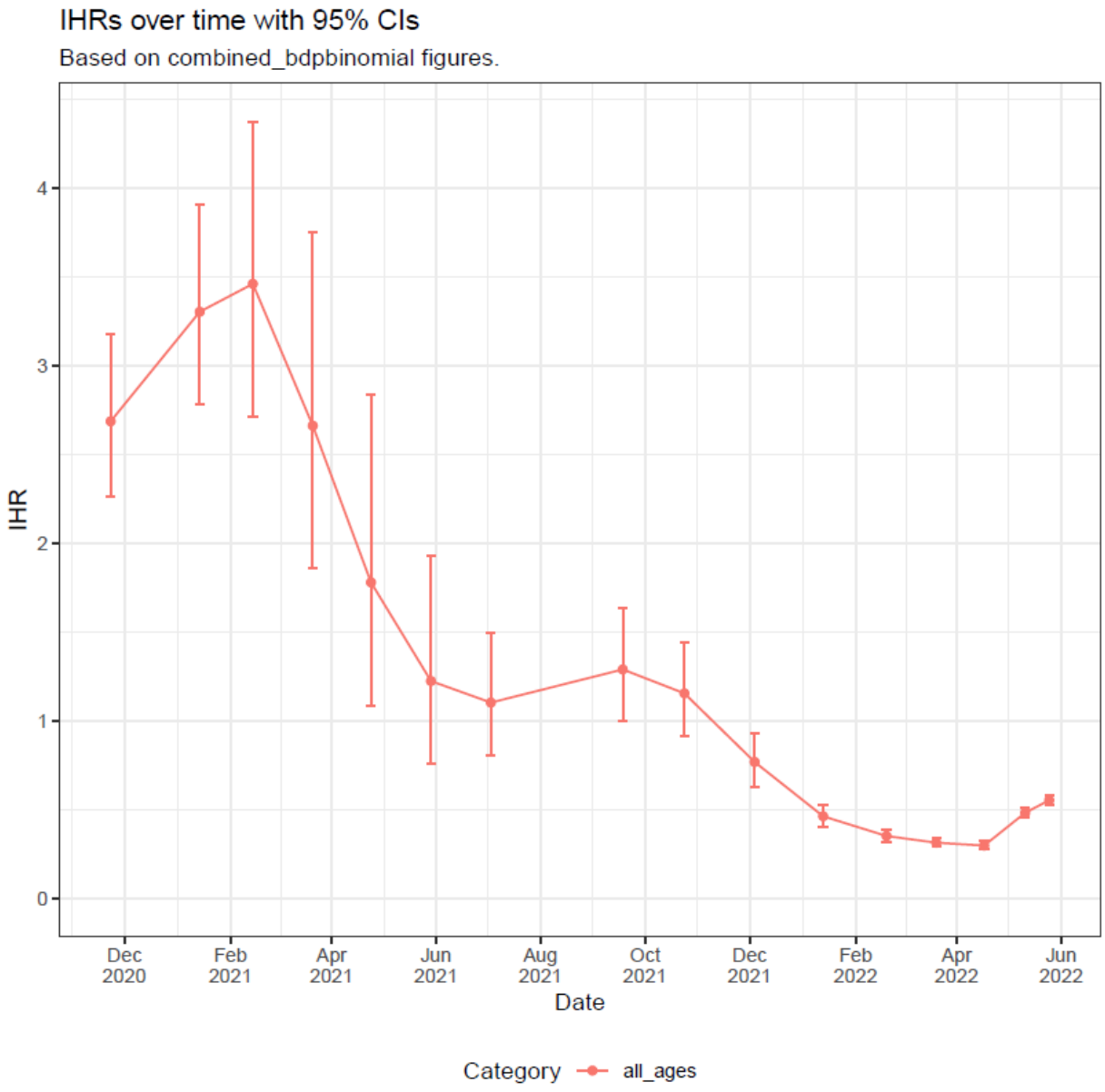
Real time infection hospitalisation risk (IHR)

To calculate the real time infection hospitalisation risk, we produced a combined Office of National Statistics (ONS) and REACT estimate for incidence until April 2022. From April onwards ONS is the only included incidence estimate. The method converts these prevalence estimates to incidence, accounting for time to test and the duration of test positivity. For model combination we estimate posterior samples from a binomial outcome where an informative prior is used. The prior weight is determined using a Weibull discount function. Parameters for the temporal infection adjustment and infection length of each round are modelled as moving parameters. Time delay distribution for hospitalisation given infection are modelled using a doubly interval censored model adjusting for right truncation. PCR positivity length for each variant is modelled using an accelerated failure time model.

Leading up to January 2021, (Figure 9) the Real Time Infection-Hospitalisation Risk (IHR) was increasing, driven by a combination of the more severe Alpha variant and increased age profile of cases. Since January 2021, the IHR steadily decreased until August 2021 when we observed a rise due to waning immunity in the oldest age groups. Since April 2022, a rise in the estimate of the IHR has been observed.

It is unclear why the IHR may be rising and at present this is a small effect. Close monitoring is required.

Figure 9. Estimated IHR for the combined ONS and REACT prevalence studies



Supplementary data is not available for this figure.

1.5 Vaccine effectiveness

There are insufficient data for a robust assessment of the effectiveness of COVID-19 vaccines against mild or severe disease with BA.4 and BA.5. However, preliminary analyses indicate that the vaccination status of cases infected with BA.4 and BA.5 is not significantly different to that of cases infected with BA.2, suggesting that protection conferred by the vaccines likely remains comparable to that observed previously.

Cases were identified from hospital (pillar 1) and community (pillar 2) testing data from the period from 18 April to 29 May 2022 and classified as BA.2, BA.4 and BA.5 based on sequencing information. Logistic regression was used to estimate the vaccination status of BA.4 or BA.5 cases as compared to BA.2 control cases. Previous positivity, testing pillar, health and social care worker status, clinical risk status, age, gender, and week of test were adjusted for. The vaccination status of those recently vaccinated (within the last 25 weeks) with either a second, third or fourth dose was compared to a baseline group of those with a 'waned' (>25 weeks since vaccination) second or third dose. Vaccine types were combined.

The vaccination status of BA.4 and BA.5 cases did not differ significantly from that of BA.2 cases; (adjusted odd ratio- aOR 1.13; 95% CI 0.88-1.44 and aOR 0.83; 95% CI 0.88-1.44, respectively) (Table 4). These early data do not indicate a difference in vaccine effectiveness against BA.4 or BA.5 as compared to BA.2; however, a formal analysis using a test-negative case control design will be conducted as the data become available.

Table 4. Adjusted odds ratios of BA.4 and BA.5 cases as compared to BA.2 controls by vaccination status

Doses	Interval	Controls	Cases	Adjusted odds ratio	95% Confidence interval
		BA.2	**BA.4**		
Dose 2/3/4	< 25 weeks	8,663	123	1.13	(0.88-1.44)
Dose 2/3	>= 25 weeks	10,896	214	Baseline	
		BA.2	**BA.5**		
Dose 2/3/4	< 25 weeks	8,663	103	0.83	(0.64-1.08)
Dose 2/3	>= 25 weeks	10,896	232	Baseline	

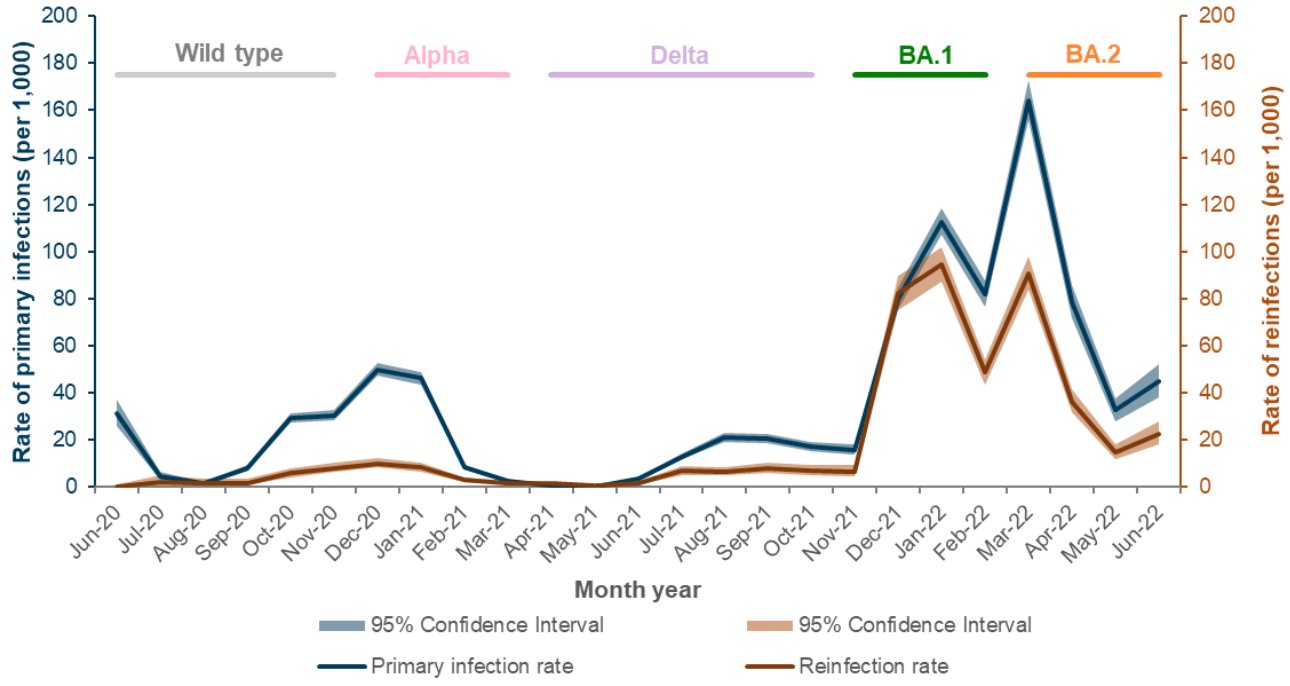
1.6 Update on the SARS-CoV-2 Immunity and Reinfection EvaluatioN (SIREN) a cohort study in healthcare workers

The SARS-CoV-2 Immunity and Reinfection EvaluatioN (SIREN) is a cohort over 44,000 National Health Service healthcare workers, recruited from 135 hospital sites UK-wide. Participants under active follow-up undergo asymptomatic SARS-CoV-2 PCR testing every 2 weeks. This cohort had high seropositivity on recruitment (30% before the second wave) and is now highly vaccinated (more than 95%). The incidence of new infections and potential reinfections in SIREN is monitored.

Reinfections were defined as a new PCR positive infections 90 days after a previous PCR positive date or 28 days after antibody positivity consistent with prior infection. Monthly primary infection rate calculated as primary infection detection in the month divided by the number of participants undergoing PCR testing with the month. Monthly reinfection rate calculated as reinfections detected in the month divided by the number of participants in the positive cohort undergoing PCR testing within the month. Positive cohort status was calculated at the beginning of each month.

Figure 10 shows the rate of primary infections and reinfections in the SIREN cohort has slightly increased in the first few weeks of June 2022.

Figure 10. Rate of primary infection (per 1,000 tests in those without prior infection) and reinfections (per 1,000 test in those with prior infection) in SIREN participants per month in the UK, June 2020 to June 2022



Supplementary data is not available for this figure.

Part 2. VOC-22APR-03 (BA.4)

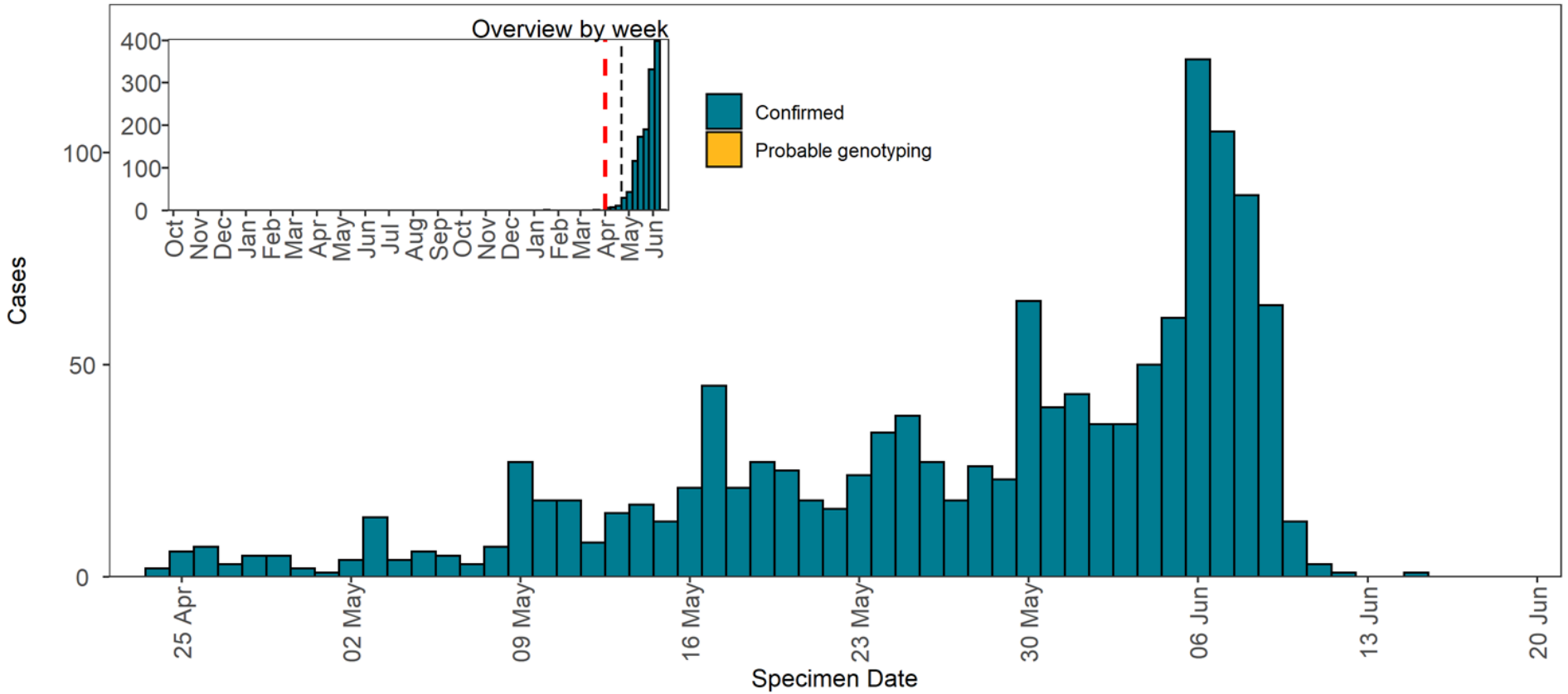
Omicron sub-lineage BA.4 was identified as part of horizon scanning on 4 April 2022. On 6 April 2022, the Variant Technical Group classified Omicron sub-lineage BA.4 as V-22APR-03. On 18 May 2022, UKHSA re-classified V-22APR-03 as VOC-22APR-03.

The revised genomic case definition for V-22APR-03 is available in Technical Briefing 41.

2.1 Epidemiology of VOC-22APR-03 (BA.4) in England

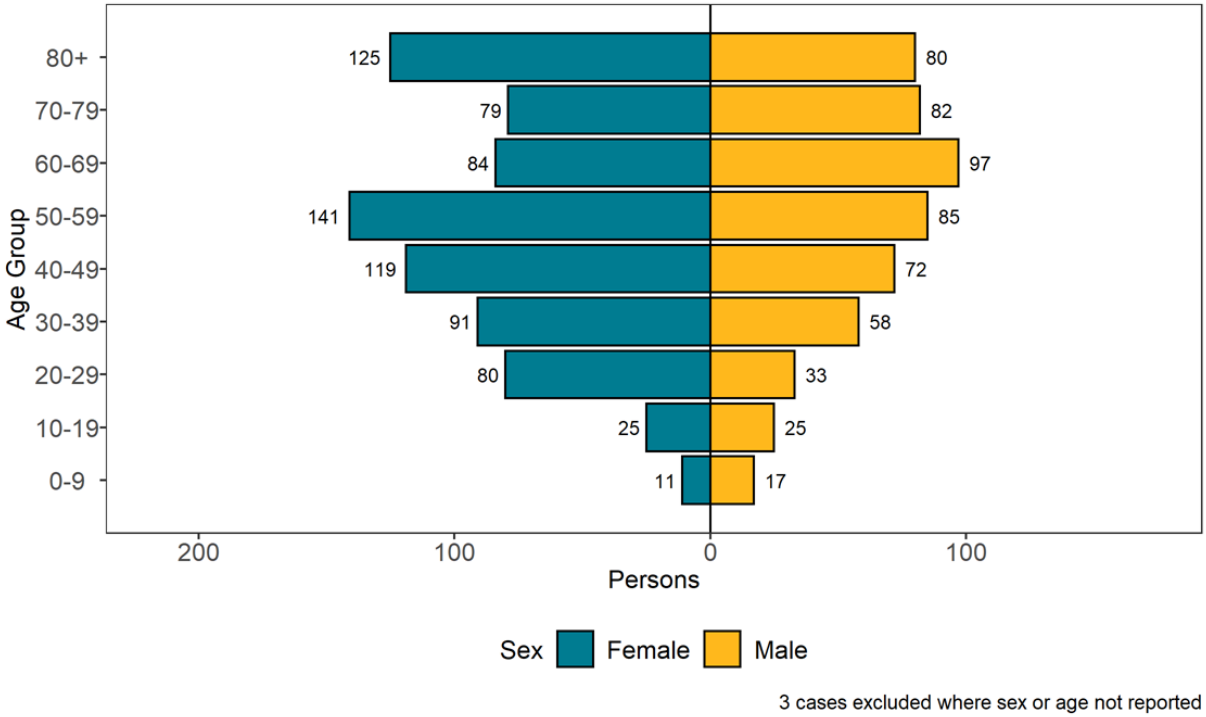
One thousand three hundred and seven sequences assigned to the BA.4 in the UK genomics dataset up to 20 June 2022, of these 1,307 were associated with England, 1,289 of which were linked to patient information. Cases are increasing and geographically distributed across England with most cases in London and the South East.

Figure 11. Confirmed (sequencing) and probable (genotyping) VOC-22APR-03 (BA.4) cases in England by specimen date and detection method as of 20 June 2022



Find accessible data used in this graph in underlying data.

Figure 12. Age-sex pyramid of VOC-22APR-03 (BA.4) cases as of 20 June 2022



Find accessible data used in this graph in underlying data.

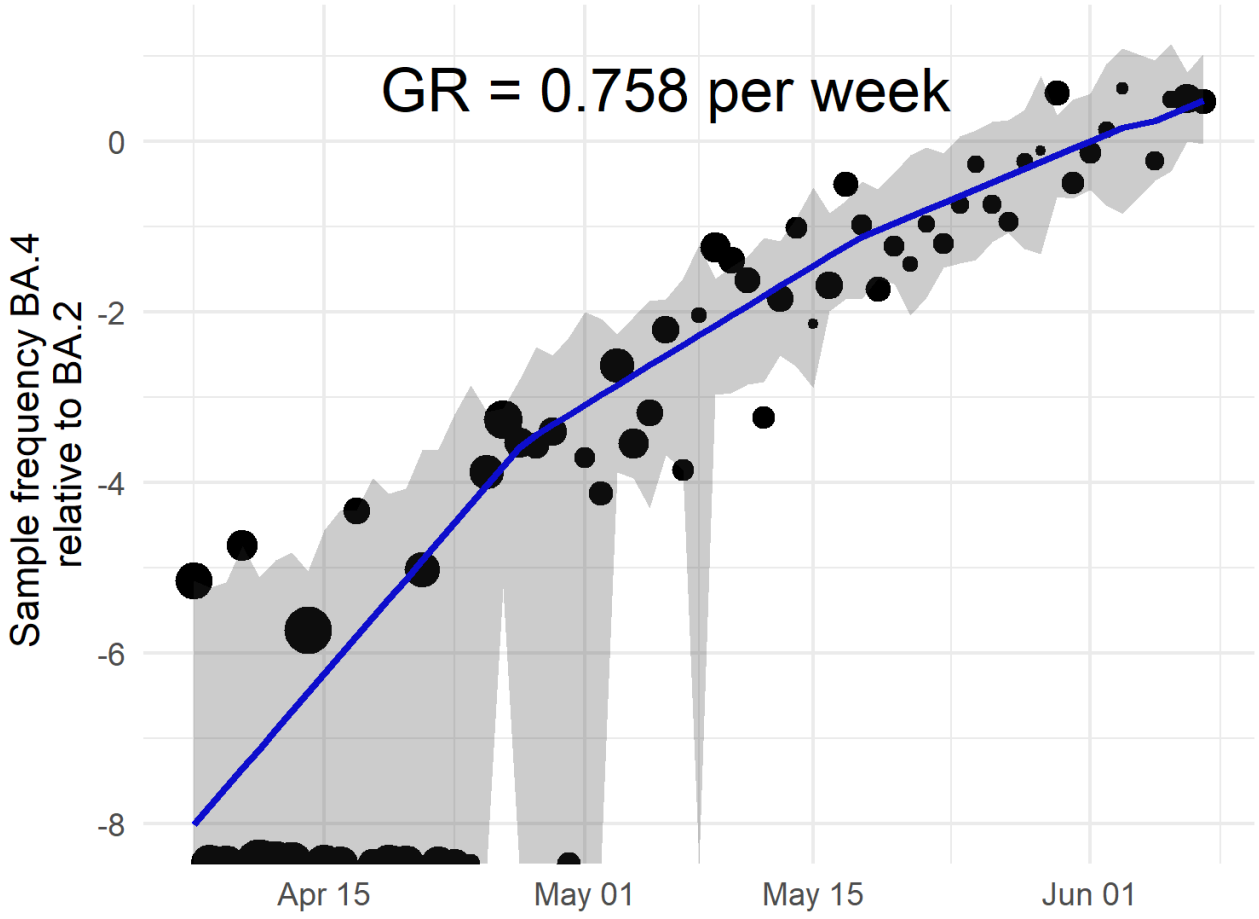
2.2 Growth rate

The growth rate of a novel variant is calculated relative to a matched control. Matched controls are samples of other circulating variants selected from the same time and location. For BA.4, genomes identified as BA.4 are compared to co-circulating BA.2 only. A statistical model was run to calculate the probability of a sampled genome being from the novel variant versus from the control over time. Growth rates are calculated per week or per day and are expressed on a log scale. A logistic growth rate of 0.5 per week indicates that the variant is increasing by a multiplicative factor of exp (0.5) =1.65 per week in comparison to the control. A logistic growth rate of zero would indicate no difference in growth rates between the 2 variants.

Using a control adjusts for geographic and temporal variation in case numbers, but despite these adjustments, differences in growth rates can be due to epidemiological factors such as founder effects and sampling, especially early on. Over time, the growth rate of a variant will converge towards an estimate of the variant's inherent transmissibility in comparison to other circulating variants. The growth rate is estimated by logistic regression of the number of genomes sampled with the BA.4 and BA.2 lineages on time of sample collection.

To adjust for geographic variation in case growth rates, BA.4 growth rates were estimated relative to a geographically matched sample of BA.2 genomes. Data sampled between 8 April 2022 and 8 June 2022 were included. The median growth rate is 75.8% per week (Figure 13). Patterns across regions are inconsistent and not reported.

Figure 13. Sample frequency of BA.4 (VOC-22APR-03) relative to Omicron (BA.2) over time



Supplementary data is not available for this figure.

Part 3. Enhanced analyses of VOC-22APR-04 (BA.5)

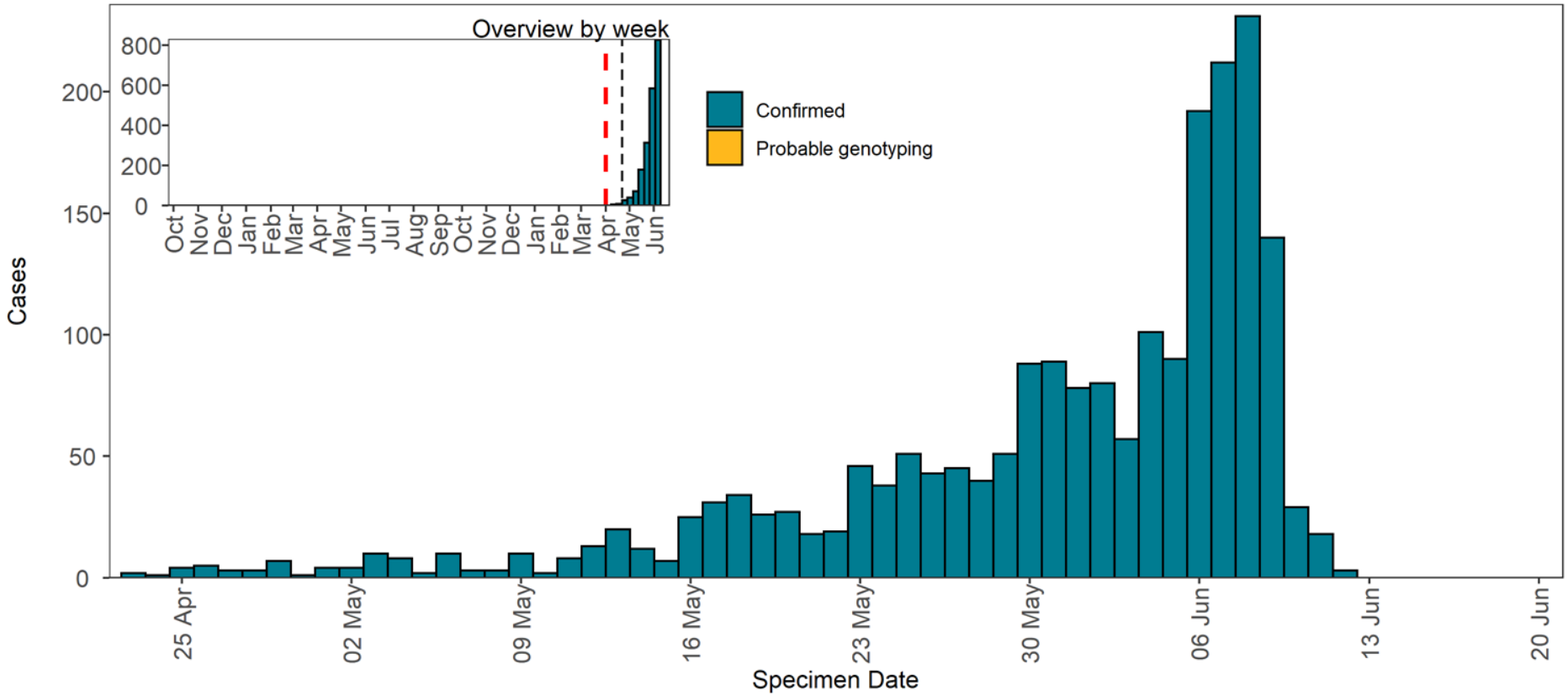
Omicron sub-lineage BA.5 was identified as part of horizon scanning on 4 April 2022. On 6 April 2022, the Variant Technical Group classified Omicron sub-lineage BA.5 as V-22APR-04. On 18 May 2022, UKHSA re-classified V-22APR-04 as VOC-22APR-04.

The revised genomic case definition for V-22APR-04 is available in Technical Briefing 41.

3.1 Epidemiology of VOC-22APR-04 (BA.5) in England

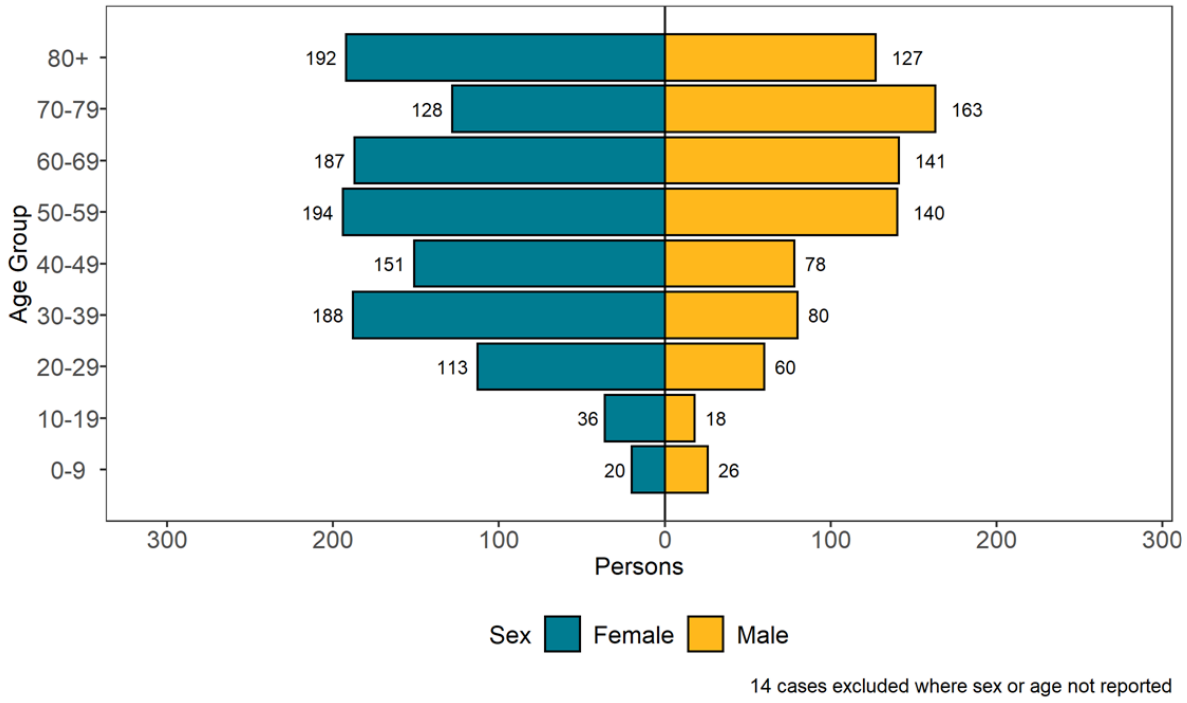
Two thousand and fifty-six sequences assigned to the BA.5 in the UK genomics dataset up to 20 June 2022, of these 2,056 were associated with England, 2,038 of which were linked to patient information. Cases are geographically distributed across England with most cases in the South East and London.

Figure 14. Confirmed (sequencing) and probable (genotyping) VOC-22APR-04 (BA.5) cases in England by specimen date and detection method as of 20 June 2022



Find accessible data used in this graph in underlying data.

Figure 15. Age-sex pyramid of VOC-22APR-04 (BA.5) cases as of 20 June 2022



Find accessible data used in this graph in underlying data.

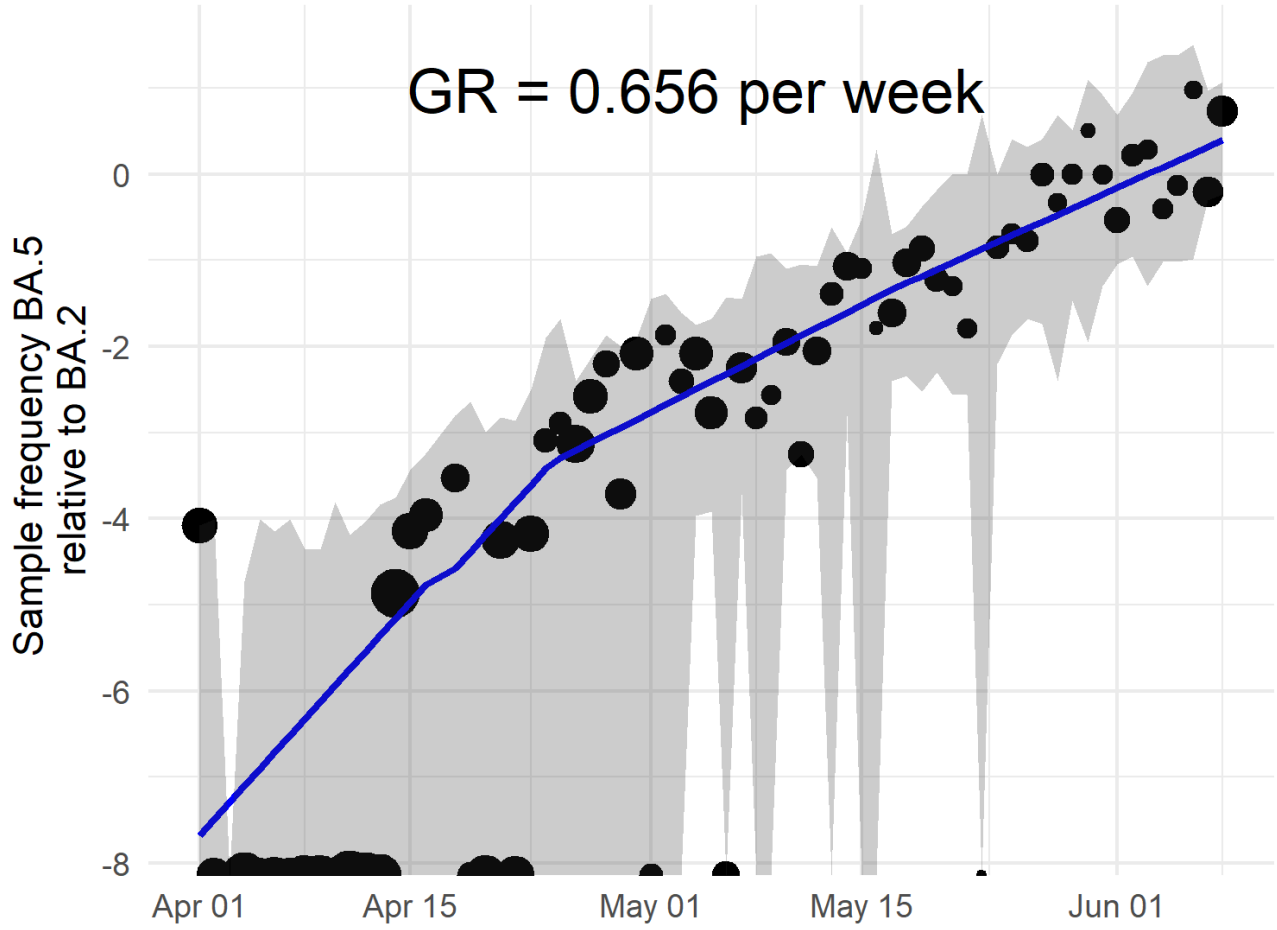
3.2 Growth rate

The growth rate of a novel variant is calculated relative to a matched control. Matched controls are samples of other circulating variants selected from the same time and location. For BA.5, genomes identified as BA.4 are compared to co-circulating BA.2 only. A statistical model was run to calculate the probability of a sampled genome being from the novel variant versus from the control over time. Growth rates are calculated per week or per day and are expressed on a log scale. A logistic growth rate of 0.5 per week indicates that the variant is increasing by a multiplicative factor of exp (0.5) =1.65 per week in comparison to the control. A logistic growth rate of zero would indicate no difference in growth rates between the 2 variants.

Using a control adjusts for geographic and temporal variation in case numbers, but despite these adjustments, differences in growth rates can be due to epidemiological factors such as founder effects and sampling, especially early on. Over time, the growth rate of a variant will converge towards an estimate of the variant's inherent transmissibility in comparison to other circulating variants. The growth rate is estimated by logistic regression of the number of genomes sampled with the BA.5 and BA.2 lineages on time of sample collection.

To adjust for geographic variation in case growth rates, BA.4 growth rates were estimated relative to a geographically matched sample of BA.2 genomes. Data sampled between 8 April 2022 and 8 June 2022 were included. The median growth rate is 65.6% per week (Figure 16). Patterns across regions are inconsistent and not reported.

Figure 16. Sample frequency of BA.5 (VOC-22APR-04) relative to Omicron (BA.2) over time



Supplementary data is not available for this figure.

Part 4. Omicron VOC-22JAN-01 (BA.2)

The mutation profile of the Omicron sub-lineages was previously reported in Technical Briefing 31.

BA.2 has been reclassified as a VOC under the new classification on 1 April 2022.

4.1 Genomic diversity

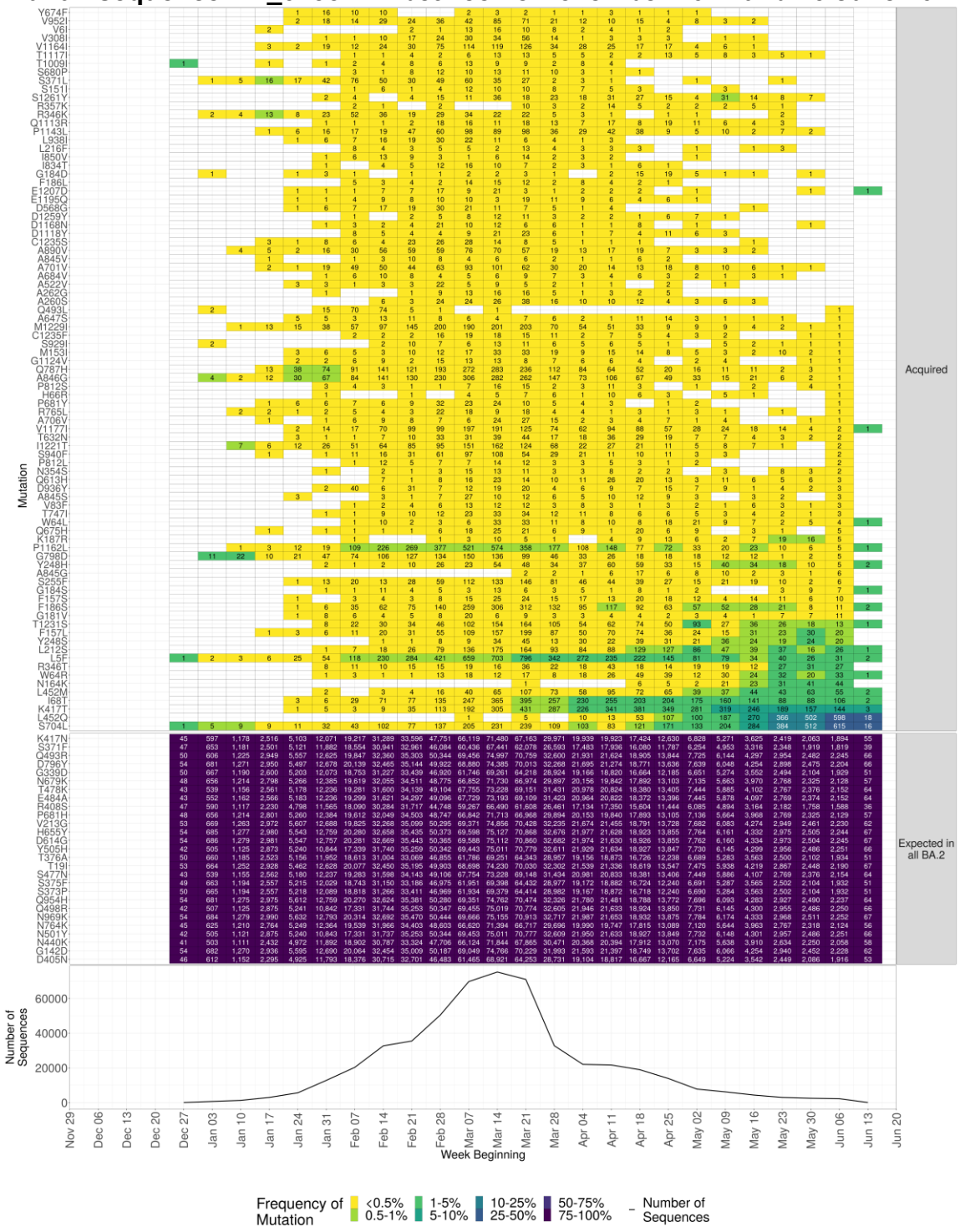
Diversity in Spike

Spike mutations are monitored within BA.2 using 4 criteria (Table 2). A mutation is investigated further if it meets more than one of these criteria and is present in at least 10 sequences. Eighty-five additional mutations have been observed in BA.2 sequences according to the criteria in Table 2 (Figure 17). The criteria for mutation monitoring are currently being reviewed and amended.

Table 2. Criteria used to assess emerging mutations

Criteria	Threshold
Cumulative count	Running total for the number of sequences containing mutation is at least 50
Proportion	1% of sequences classified as this variant contain this mutation within a single week
Difference in proportion	The difference in the proportion of sequences in 2 consecutive weeks is at least 0.25%
Percentage change in the number of sequences	The percentage change between the number of sequences containing the mutation in 2 consecutive weeks is at least 5%

Figure 17. Spike mutations found in BA.2 genomes in the UK dataset relative to the Wuhan sequence NC_045512.2 between 8 November 2021 and 19 June 2022

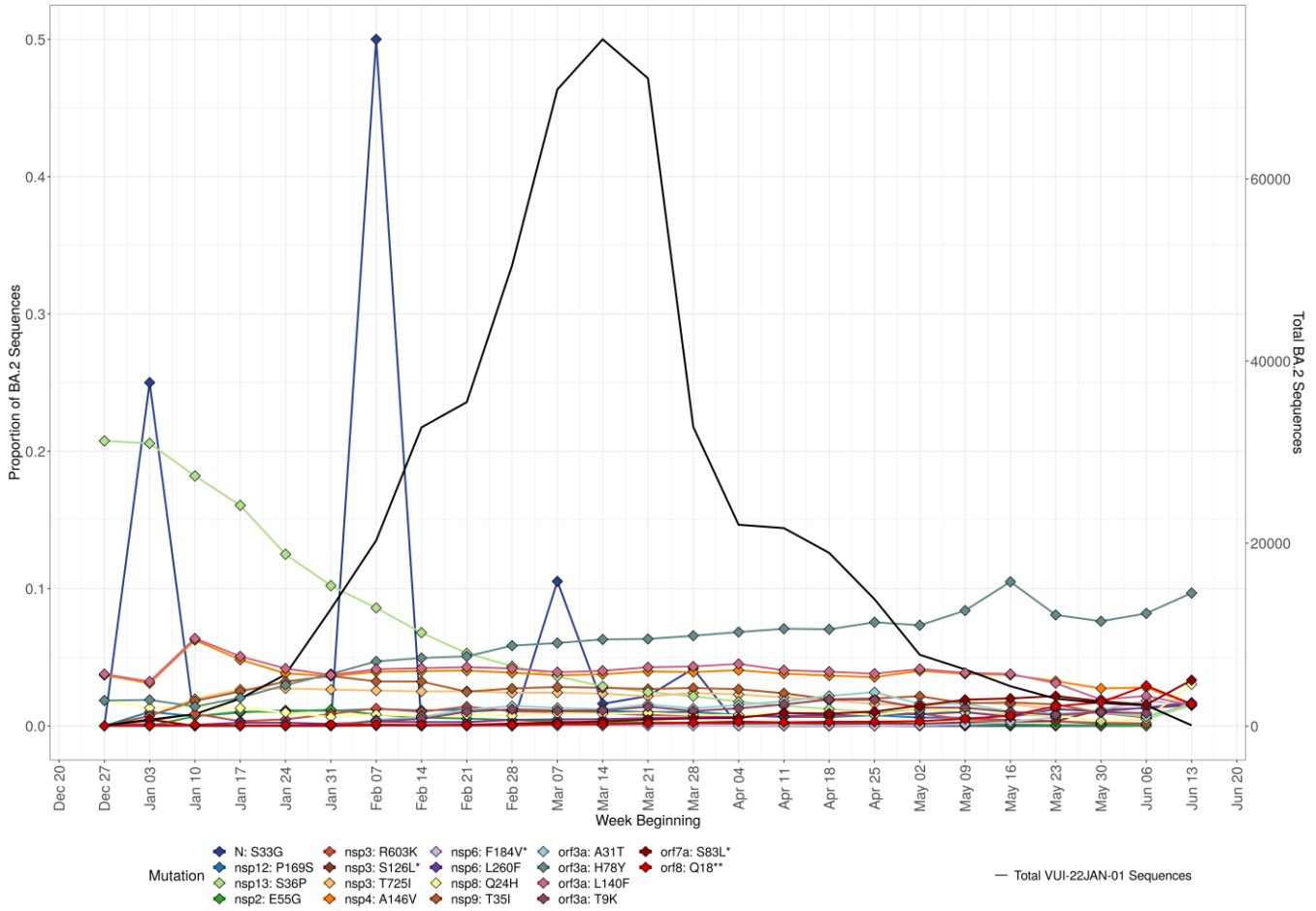


Find accessible data used in this graph in underlying data.

NB: all mutations in the sequence alignment are reported in these plots for review purposes.

Outside of Spike, there are 18 mutations that are present in at least 1% of BA.2 sequences for at least 3 consecutive weeks (Figure 18).

Figure 18. Mutations acquired by BA.2 outside Spike, shown as a proportion of total BA.2 sequences (6 December 2021 and 19 June 2022)



The total number of BA.2 sequences per week are indicated by the black line. Mutations for each genome are called relative to reference Wuhan NC_045512.2 and acquired mutations are those additional to the ancestral BA.2 mutation set. Those that are considered additional, and that are present in at least 1% of BA.2 sequences for at least 3 consecutive weeks in the UK dataset, are included in Figure 18 as a proportion of total BA.2 sequences. Mutations labelled with * are those that have been increasing as a proportion of VOC-22JAN-01 sequences for at least 3 consecutive weeks within the previous 6 weeks.

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 and UKHSA genomic programme data set, ONS COVID-19 Infection Survey, the UKHSA Second Generation Surveillance System, the Secondary Uses Service data set, Emergency Care Data Set and the UKHSA Case and Incident Management System.

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