

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

Technical briefing 33

23 December 2021

This briefing provides an update on previous briefings up to 17 December 2021

Contents

Summary	3
Published information on variants	6
Part 1. Surveillance overview	7
1.1 Variants under surveillance	7
1.2 VOC and VUI overview	9
1.3 Variant prevalence	10
Part 2. Enhanced analysis on Omicron VOC-21NOV-01 (B.1.1.529)	15
2.1 Genomic diversity	15
2.2 Comparative demographics	18
2.3 Severity	21
2.4 Vaccine effectiveness	24
2.5 Reinfections	28
2.6 Growth rate and advantage	30
2.6 Wastewater analysis	36
Sources and acknowledgments	
Data sources	
Repository of human and machine-readable genomic case definitions	39
Variant Technical Group	
Acknowledgements	41

Summary

This report has been published to share the detailed variant surveillance analyses which contribute to the variant risk assessments and designation of new variants of concern (VOC) and variants under investigation (VUI). This specialist technical briefing contains early data and analysis on emerging variants and findings have a high level of uncertainty.

A <u>separate report is published</u> covering surveillance data on all other VOCs and VUIs. In summary:

Current VOCs and VUIs

There are 5 current VOCs and 6 VUIs (Table 1).

Data cutoff

Unless stated otherwise, the technical briefing uses a data cut-off of 20 December to allow time for analyses. At the data cut off, there were 56,066 confirmed cases of Omicron VOC-21NOV-01 (B.1.1.529) (hereafter referred to as Omicron), identified through sequencing or genotyping in England.

Growth

Omicron has continued to increase sharply as a proportion of cases in England as measured by S gene target failure, genotyping and sequencing. It is predominant in all regions of England (<u>Daily overview data</u>). The increase is also visible in wastewater, particularly in London and the South East. The proportion of S gene target failure cases in a particular area correlates strongly with the overall increase in coronavirus (COVID-19) cases in that area.

Genomic diversity

There is as yet little diversity within the Omicron BA.1 clade. Two acquired mutations in spike have been noted in the UK data set, A701V and R346K. Each of these is primarily associated with a single large subclade. These clades do not have an increased growth rate compared to the rest of the Omicron clade.

Comparative demographics

Relative to Delta, Omicron is currently more concentrated in young adult age groups (20 to 29) and is less prevalent in children. Whilst there were initially higher rates of Omicron cases in persons of Black ethnicity, the rates of all ethnic groups have now converged reflecting widespread community transmission. These demographic factors should be borne in mind when interpreting comparative analyses.

Hospitalisation and death

Using data up until 20 December, 132 individuals with laboratory confirmed Omicron have been admitted or transferred from emergency departments. Over 40% of

admissions were in London. Of those patients admitted to hospital, 17 (12.9%) had received a booster dose, 74 (56.1%) a second dose and 27 (20.5%) were not vaccinated (less than 10 were unlinked or had one dose). At the data cut off, 14 people were reported to have died within 28 days of an Omicron diagnosis, age range 52 to 96 years.

Severity

The risk of hospital admission for a person detected as a case of Omicron appears reduced compared to a case of Delta. This analysis excludes known reinfections. The current hazard ratio is 0.62 (95%CI 0.55-0.69) for emergency department attendance or admission, and 0.38 (95% CI 0.3-0.5) for admission alone. This analysis is preliminary because of the small numbers of Omicron cases currently in hospital and the limited spread of Omicron into older age groups as yet. It has not been adjusted for undiagnosed reinfections. It will be iterated regularly. In addition, Imperial reported analysis using the same data set but imputing a potential previous infection variable and estimated the intrinsic risk difference between Delta and Omicron as between 0 to 30% and the reduced risk of hospitalisation in those previously infected estimated as 55 to 70%. In the Scottish study, the range of estimates for their analysis was similar, though based on only 18 total admissions detected for Omicron in the study and only 7 individuals admitted with 7 or more days of follow-up.

Vaccine effectiveness

Repeated VE analysis continues to show lower VE for symptomatic Omicron disease compared to Delta. There is evidence of waning of protection against symptomatic disease with increasing time after dose 2, and by 10 weeks after the booster dose, with a 15 to 25% reduction in vaccine effectiveness after 10 weeks. This waning is faster for Omicron than for Delta infections. There are insufficient severe cases of Omicron as yet to analyse vaccine effectiveness against hospitalisation, but this is expected to be better sustained, for both primary and booster doses. This analysis will be iterated next week, although numbers may still restrict a robust analysis of protection against more severe outcomes. The VE data will also appear in the weekly COVID-19 vaccine surveillance report published routinely on a Thursday.

Reinfections

The population reinfection rate has increased sharply and disproportionately to the number of first infections. 9.5% of Omicron infections have been identified to have previous confirmed infections, which is likely to be a substantial underestimate of the proportion of reinfections. The first infections of the individuals with Omicron reinfections occurred in both the Alpha and Delta waves and are likely to have been undetected if in the first wave. There were 69 identified cases with Omicron as a third episode of infection and 290 cases where the Omicron infection was between a 60 to 89 day interval after a confirmed first infection.

Secondary attack rates

Iterated secondary attack rates calculated using routine contact tracing continue to show higher secondary attack rates for Omicron than for Delta. The difference between Omicron and Delta is currently greater for non-household contacts than for household contacts.

Updated risk assessment

An updated <u>risk assessment</u> for Omicron VOC-21NOV-01 (B.1.1.529) has been published.

All <u>risk assessments</u> are published separately online, except for Gamma, which was published within <u>technical briefing 7</u> and Alpha within <u>technical briefing 9</u>. As Delta is the dominant variant in the UK, epidemiological data in the <u>weekly surveillance report</u> is also relevant.

Sequencing coverage data has moved to the variant data update.

Published information on variants

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

The UK Health Security Agency (UKHSA), formerly Public Health England (PHE), has curated a repository from 5 March 2021 containing the up-to-date genomic definitions for all VOCs and VUIs. The repository is accessible on <u>GitHub</u>.

World Health Organization (WHO) nomenclature from 31 May 2021 is incorporated. A table incorporating WHO and UK designations with Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin lineages) is provided below (<u>Table 1</u>). Following the table, variants are referred to using their WHO designation where this exists and the UK designation where it does not.

<u>Technical briefings</u> 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 (RBDA) to identify variant and mutation (VAM) profiles from genotype assay mutation profiles. Genotyping is used to identify variants Alpha, Beta, Delta, Gamma and Mu. 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 detected and not detected in the UK as of 21 December 2021.

Variants of concern	Variants under Investigation	Variants in monitoring
Alpha (B.1.1.7) VOC-20DEC-01	VUI-210CT-01 (AY.4.2)†	B.1.640
Beta (B.1.351) VOC-20DEC-02	VUI-21JUL-01 (B.1.621)	B.1.617.2 + E484K
Gamma (P.1) VOC-21JAN-02	VUI-21APR-03 (B.1.617.3)	
Delta (B.1.617.2 and sub-lineages) VOC-21APR-02		
Omicron (B.1.1.529, BA.1, BA.2, BA.3) VOC-21NOV-01		

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

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

Variants of concern	Variants under investigation	Variants in monitoring
	VUI-21JAN-01 (P.2)	C.37*
	VUI-21FEB-04 (B.1.1.318)	B.1.526
	VUI-21FEB-03 (B.1.525)	B.1 with 214insQAS
		B.1.630, B.1.631/B.1.628
		P.1.8
		C.1.2
		<u>B.1.1.7 + B.1.617.2</u> possible recombinant
		C.37 descendant (S:L5F, G75V, D614G, L452Q, E484K, P499R, N501T, H655Y, P681R)
		B.1.427/B.1.429

*Previously VUI-21JUN-01, de-escalated on 20 October 2021.

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

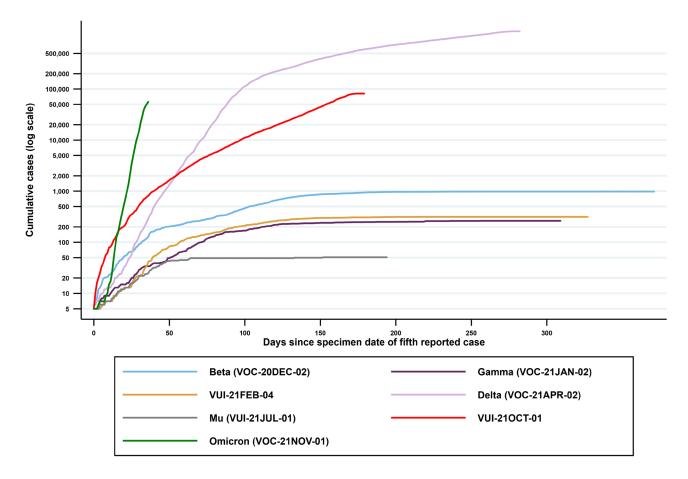
Zeta and Theta were de-escalated by WHO and are no longer WHO variants under monitoring. Kappa, lota, Eta and Epsilon were de-escalated by WHO and are now WHO variants under monitoring.

1.2 VOC and VUI overview

Summary epidemiology for each variant and case numbers are updated online.

Figure 1 shows the cumulative number of cases per variant indexed by days since the first report.

Figure 1. Cumulative cases in England of variants indexed by days since the fifth reported case as of 20 December 2021



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

1.3 Variant prevalence

The prevalence of different variants amongst genotyped cases is presented in <u>Figure 2</u>. The prevalence of different variants amongst sequenced cases is split by travel status in <u>Figure 3</u>.

Genotyping provides probable variant results with a shorter turnaround time of 12 to 24 hours after initial confirmation of coronavirus (COVID-19) by PCR. 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 Figure 2 and Figure 3 includes genomes where the quality is insufficient to determine variant status and genomes that do not meet the current definition for a VUI or VOC. The supplementary data for figures is available.

The Omicron genome (lineage BA.1) contains the spike deletion at position 69-70 which is associated with SGTF in some widely used PCR tests. Such PCR tests evaluate the presence of 3 SARS-CoV-2 genes: Spike (S), N and ORF1ab. SGTF is defined as a PCR test where the N and ORF1ab genes are detected (with Ct values <=30) but the S gene is not. SGTF patterns can be used to assess the spread of Omicron. The number of COVID-19 cases with S gene positive/SGTF by day, among those tested in TaqPath labs is shown in Figure 4. COVID-19 cases with detectable S gene/SGTF and percentage with SGTF among those tested in TaqPath Labs by region is now published in the Omicron daily overview.

Figure 2. Variant prevalence for all England available genotyped cases from 1 February 2021 as of 20 December 2021 (Find accessible data used in this graph in <u>underlying data</u>.)

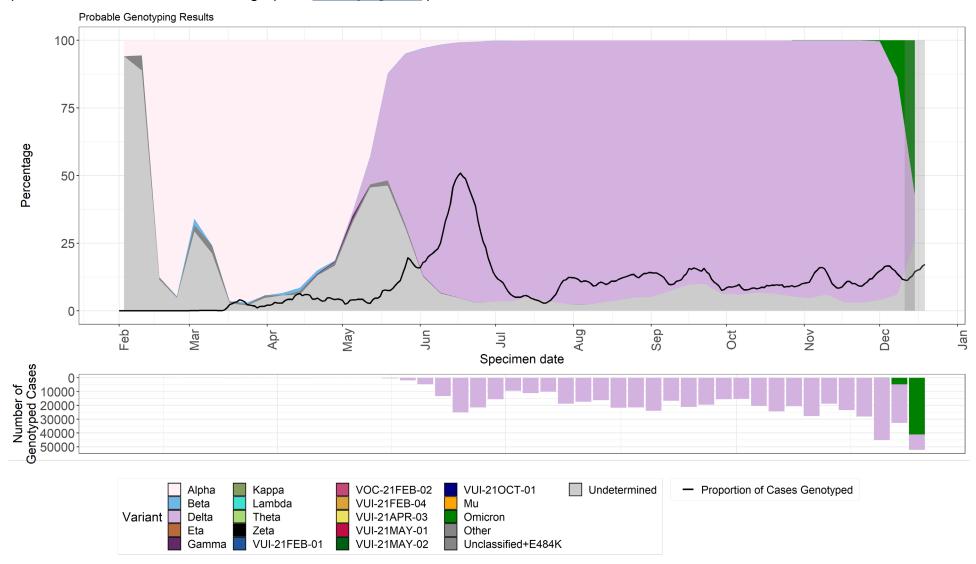


Figure 3. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 20 December 2021. (excluding 907 cases where the travel status or specimen date were unknown).

(Find accessible data used in this graph in <u>underlying data</u>.)

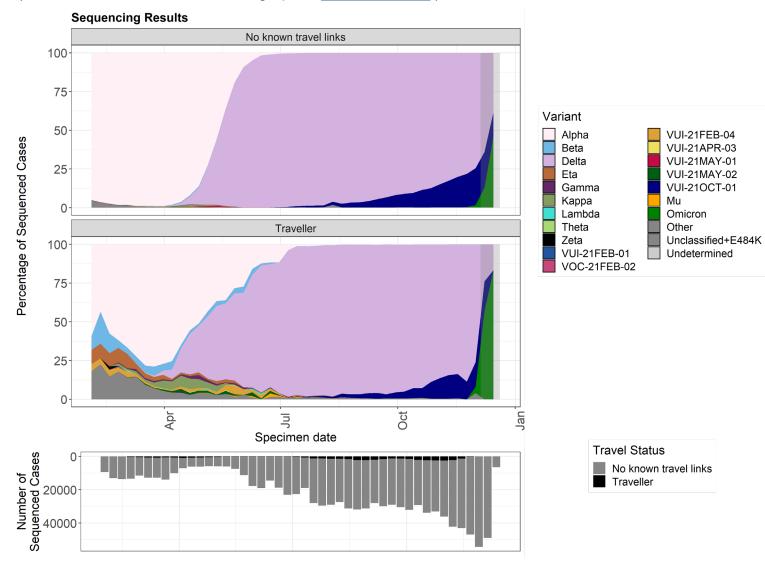
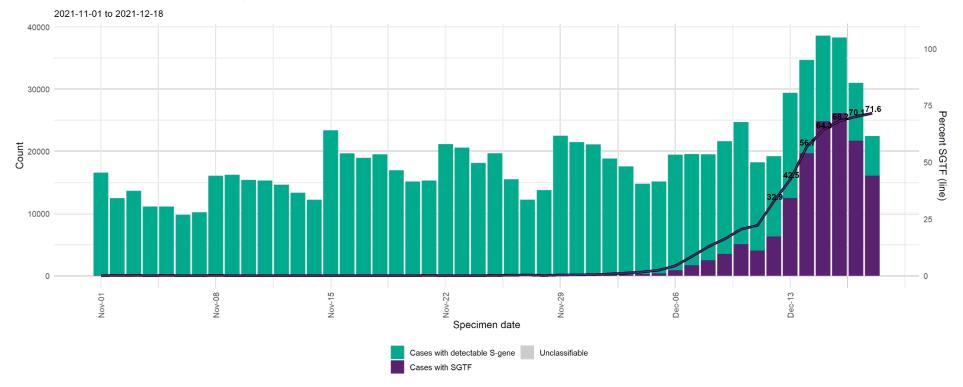


Figure 4. Number of COVID-19 cases with S gene positive/SGTF by day, among those tested in TagPath labs as of 20 December 2021. (95% confidence intervals indicated by grey shading).

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

Number COVID19 cases with S gene +ve/SGTF and percentage SGTF by day, among those tested in TagPath Labs 95% confidence intervals indicated by gray shading. Percentages for most recent 7 days shown. Data updated on 2021-12-20



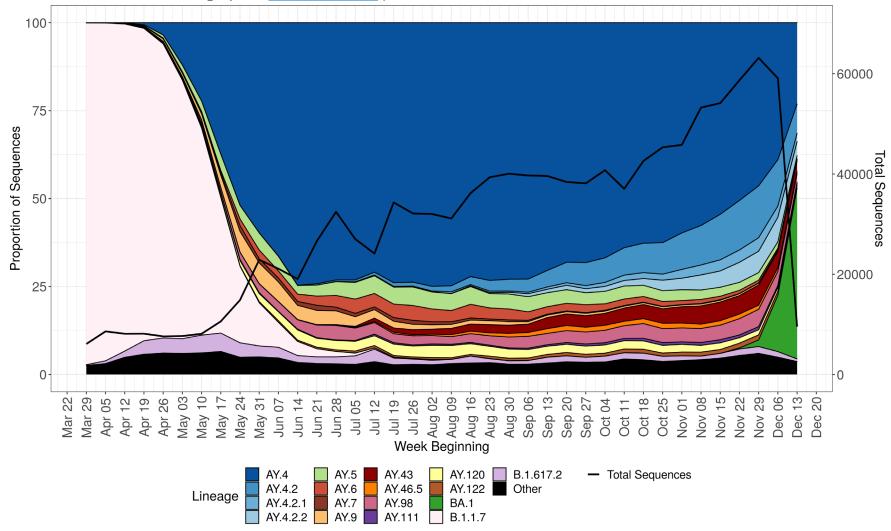
A detectable S gene is a proxy for Delta since April 2021. SGTF was a surveillance proxy for VOC-20DEC-01 however has largely consisted of Delta since August 2021.

Local trends in these data may be affected by decisions to direct the processing of samples via a TaqPath laboratory. Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene results included, from Newcastle, Alderley Park, Milton Keynes and Glasgow Lighthouse Labs. SGTF refers to non-detectable S gene and <=30 CT values for N and ORF1ab genes. Detectable S-gene refers to <=30 CT values for S, N, and ORF1ab genes.

Produced by Outbreak Surveillance Team, UKHSA.

Figure 5. Prevalence of Pangolin lineages within sequence data from 1 April 2021 to 19 December 2021

The total number of valid sequence results per week is shown by the black line. Only lineages with more than 5000 sequences. Smaller lineages are either merged with parent lineages (for example, AY.3.1 is included in AY.3) or are included in 'Other'. (Find accessible data used in this graph in <u>underlying data</u>.)



Part 2. Enhanced analysis on Omicron VOC-21NOV-01 (B.1.1.529)

A new variant with a novel combination of mutations was detected on GISAID on 23 November 2021 and designated B.1.1.529 on 24 November 2021. This variant was designated VUI-21NOV-01 by the UKHSA Variant Technical Group and on review re-designated as VOC-21NOV-01 on 27 November 2021.

2.1 Genomic diversity

Spike mutations are monitored within BA.1 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. Two acquired mutations in Spike have been identified in BA.1: R346K and A701V (Figure 6). Both mutations occur within distinct clades (Figure 7).

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%

Table 2. Criteria used to assess e	emerging mutations
------------------------------------	--------------------

Figure 6. Proportion of sequences containing a given mutation within UK BA.1 sequences that meet more than one criterion and are present in at least 10 sequences

Data shown is sequence data from 20 September 2021 to 20 December 2021. The proportion of sequences is indicated by the colour and the number of genomes is shown within the tile. Proportion is calculated based on the total number of sequences where the amino acid can be called. Mutations expected to be in all Omicron genomes are shown separately to those considered to have been acquired since initial emergence of the lineage. The total number of sequences per week is shown by the black line in the lower plot.

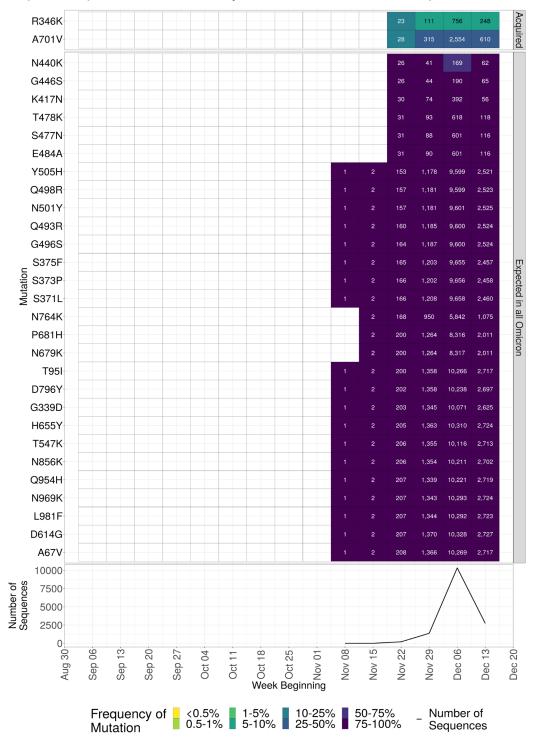
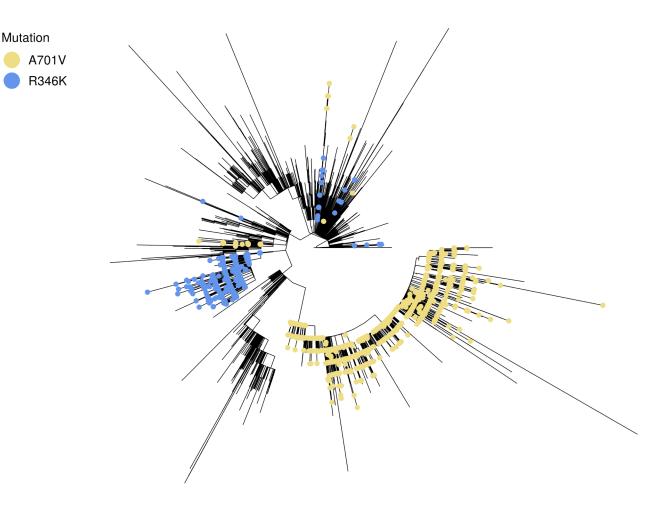


Figure 7. Maximum likelihood phylogeny of UK BA.1 genomes (n=14,416) as of 20 December 2021

BA.1 sequences with lower data quality were removed (n=87). Tip colour indicates whether R346K (blue) or A701V (yellow) are present in each sequence. Both mutations are decreasing in frequency over time among omicron cases (R346K -0.839 per week, A701V -1.039 per week, both p<0.001). There are no sequences that contain both mutations. Data quality issues mean that some sequences with these mutations are misplaced in the tree and do not group with the larger tree.

Supplementary data is not available for this figure.



2.2 Comparative demographics

Omicron cases described below are those identified by sequencing or genotyping.

A summary of case data for Omicron is published in the COVID-19: Omicron daily overview.

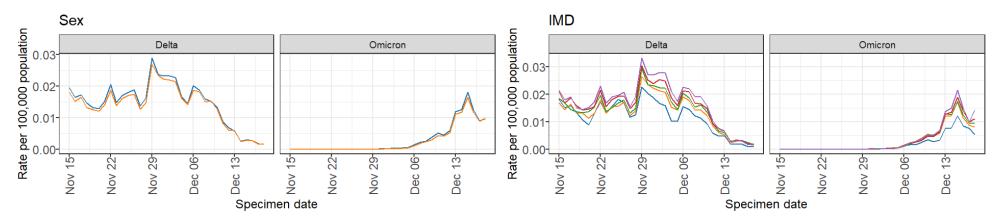
<u>Table 3</u> shows the demographic distribution of Omicron cases with specimen dates in December, as compared to Delta. Figure 8 demonstrates this further as rates over time. Omicron was initially at increased frequency in Black ethnic group, however since mid-December the rates within specific ethnic groups have converged, reflecting more community transmission. Omicron is particularly concentrated in 20 to 29 and 30 to 39 year old groups. Differences in trends by deprivation may at least partially reflect the fact that London and the South East, regions with lower deprivation Lower layer Super Output Areas, also those with the highest Omicron rates.

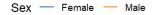
Table 3. Comparison of Delta (VOC-21APR-02) and Omicron (VOC-21NOV-01) cases by
sex, age group, ethnic group and Index of Multiple Deprivation (IMD) quintile from 1
December to 18 December 2021

Characteristic	Delta, N = 116,939	Omicron, N = 53,842		
Sex				
Female	60,571 (52%)	28,265 (52%)		
Male	56,368 (48%)	25,577 (48%)		
Age group				
0-9	19,514 (17%)	1,418 (2.6%)		
10-19	23,516 (20%)	6,334 (12%)		
20-29	11,457 (9.8%)	17,552 (33%)		
30-39	19,295 (17%)	12,411 (23%)		
40-49	21,795 (19%)	8,097 (15%)		
50-59	13,327 (11%)	5,292 (9.8%)		
60-69	5,220 (4.5%)	1,845 (3.4%)		
70-79	1,682 (1.4%)	640 (1.2%)		
80+	1,133 (1.0%)	253 (0.5%)		
Ethnic group				
White	101,631 (87%)	42,230 (78%)		
Asian	7,802 (6.7%)	4,366 (8.1%)		
Black	2,806 (2.4%)	4,584 (8.5%)		
Mixed	3,427 (2.9%)	1,960 (3.6%)		
Other	1,273 (1.1%)	702 (1.3%)		
IMD quintile				
1 (most deprived)	16,788 (14%)	7,117 (13%)		
2	22,217 (19%)	10,767 (20%)		
3	24,761 (21%)	11,171 (21%)		
4	25,024 (21%)	11,453 (21%)		
5 (least deprived)	28,149 (24%)	13,334 (25%)		

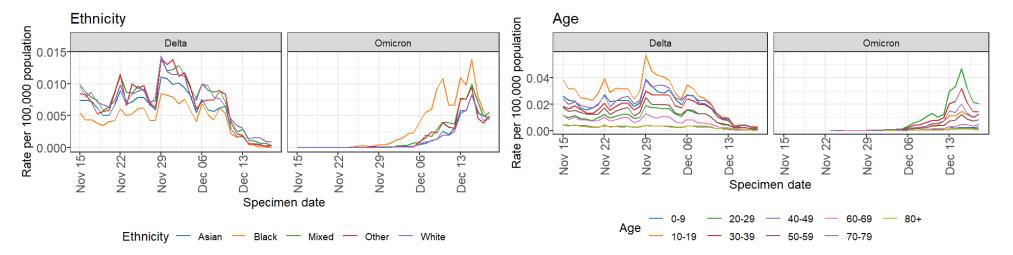
Figure 8. Comparison of sequenced and genotyped Delta (VOC-21APR-02) and Omicron (VOC-21NOV-01) case rate over time by sex, age group, ethnic group and IMD quintile from 15 November to 18 December 2021

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









2.3 Severity

Descriptive epidemiology of severe outcomes of Omicron in England

To monitor the severe outcomes of Omicron infections, Omicron cases are linked to NHS data on presentation to emergency care and to UKHSA data on deaths following confirmed COVID-19 test results. Hospitalisation was defined as attendance to emergency care which resulted in admission or transfer, and the Omicron specimen date was between 14 days prior to attendance and 1 day after attendance.

Using data up until 20 December 2021, a total of 132 individuals with laboratory-confirmed (sequencing, genotyping or SGTF) Omicron have been admitted or transferred from emergency departments. Of these, 54 (40.9%) admissions were in London.

The age range of admitted individuals was 0 to 98, years (median: 45.5); 74 (56.1%) were aged 40 years or more; 25.8% were aged 70 years or more. 55% of Omicron hospitalisations occurred in people whose self-reported ethnicity was White (British) and 8% among Black (African) people.

A total of 14 people have been reported to have died within 28 days of an Omicron COVID-19 diagnosis. The median time from Omicron specimen date to death was 4 days (range 1 to 10). The age of those dying ranged from 52 to 96 years.

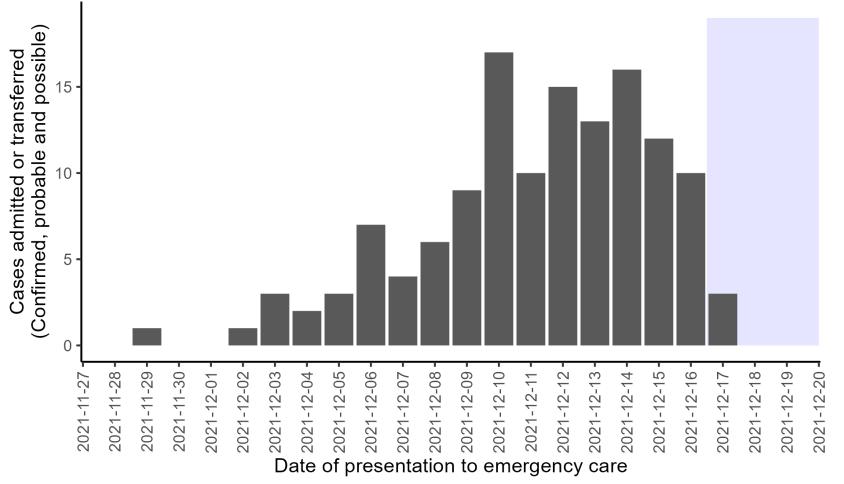


Figure 9. Omicron cases in England being admitted or transferred to hospital at the end of presentation to emergency care

Shaded area indicates dates most likely to be affected by data lags.

Table 4. Number of Omicron cases admitted or transferred to hospital at the end ofpresentation to emergency care by vaccination status, England. Data to 20 December2021

Vaccination status	Count (n)	Percentage (%)
Unlinked*	6	4.5
Not vaccinated	27	20.5
Received one dose (1 to 20 days before specimen date)	1	0.8
Received one dose, ≥21 days before specimen date	7	5.3
Second dose ≥14 days before specimen date	74	56.1
Third dose or Booster ≥14 days before specimen date	17	12.9

* Individuals whose NHS numbers were unavailable to link to the National Immunisation Management System.

When interpreting Table 4 it should be understood that in a population with high vaccine coverage, the majority of cases will occur in vaccinated individuals. In comparison to the vaccination uptake in England there are higher proportions of cases in unvaccinated individuals and lower proportions who have received their third dose or booster. Vaccine effectiveness cannot be inferred from this table and vaccine effectiveness is described in section 2.4 below.

Risk of hospitalisation in England

Based on a record linkage of sequenced or genotyped, probable and possible Omicron cases and Delta cases (COVID-19 cases with sequenced or genotyped variant or based on S-gene negativity/positivity), a preliminary analysis of 114,144 Omicron cases and 461,772 Delta cases occurring between 22 November and 19 December, was undertaken to assess the risk of hospital admission and emergency care attendance among cases. This analysis excludes known cases of reinfection (individuals with a positive PCR result more than 90 days before the current test).

Stratified Cox proportional hazard regression assessed that the risk of presentation to emergency care or hospital admission with Omicron was approximately three-fifths of that for Delta (Hazard Ratio 0.62, 95% CI: 0.55 to 0.69). The risk of hospital admission alone with Omicron was approximately two-fifths of that for Delta (Hazard Ratio 0.38, 95% CI: 0.30 to 0.50). These analyses stratified on week of specimen and area of residence and further adjusted for age, exact calendar date, sex, ethnicity, local area deprivation, international travel and vaccination status.

This effect is still present when stratified by vaccination status. However, this is preliminary analysis including only 431 attendances to the emergency department and 70 hospital admissions with Omicron. These analyses also are not adjusted for undiagnosed previous COVID-19 infection, or co-morbidities of these individuals. It is not an assessment of in hospital severity, which will take further time to access. Despite adjusting for calendar week, there may

still be reporting delays for hospital events. It is important to highlight that these lower risks do not necessarily imply reduced hospital burden over the epidemic wave given the higher growth rate and immune evasion observed with Omicron.

Using a very similar data set, Imperial College, provided estimates that Omicron cases had a 15 to 25% (Hazard ratio 0.8; 95% CI 0.75-85) reduced risk of emergency department attendance (hospitalisations in their data set) and 40 to 49% (HR 0.55, 95% CI 0.51-59) reduced risk of a hospitalisation with a stay of one or more nights. Importantly, this group attempt to impute the effect of prior infection, highlighting that while 17% of the population have tested positive for COVID-19, this is likely to capture only one-third of total infections that have occurred in England. Including the likelihood of previous infection, in addition to vaccination in their model, they have estimated the intrinsic risk difference between Delta and Omicron as between 0 to 30% and the reduced risk of hospitalisation in those previously infected estimated as 55 to 70%. Scotland, using their national data, performed a <u>cohort study</u>, to determine the risk of COVID-19 hospitalisation. The calculated rate of S gene negative reinfection was approximately 10 times that of previously detected S gene positive. Only 6.6% of S gene negative cases were detected in the 60-plus age group and 49.2% were detected in 20 to 39%. Using their model there were less individuals admitted to hospital than expected with 3 estimates highlighted:

- all cases: 36% of expected (95% CI 22-56%), based on 18 admissions for S negative
- all cases, followed for 7 days: 33% of expected (95% CI 15-65%), based on 7 admissions for S negative followed for 7 days
- all cases, aged 20 to 59 years: 34.4% of expected (95% CI 25-70%), based on 15 admissions for S negative

However, there are a number of important caveats to this data:

- limited circulation of S negative among the over 60s and therefore this estimate will lean to an over optimistic conclusion for this group
- it does not include those tested in the NHS hospital laboratories which may give an underestimate for admissions and biases towards individuals who test in the community compared to those that test in hospitals
- an incomplete assessment of undiagnosed previous infection of COVID-19 and any impact of waning of vaccine effectiveness in the over 60s who received their vaccination more than 8 to 10 weeks ago

2.4 Vaccine effectiveness

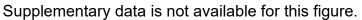
A test-negative case control design was used to estimate vaccine effectiveness against symptomatic COVID-19 with the Omicron variant compared to the Delta variant. Here, vaccination rates in PCR-positive cases are compared to vaccination rates in those who test negative. Individuals who reported symptoms and were tested in pillar 2 (community testing)

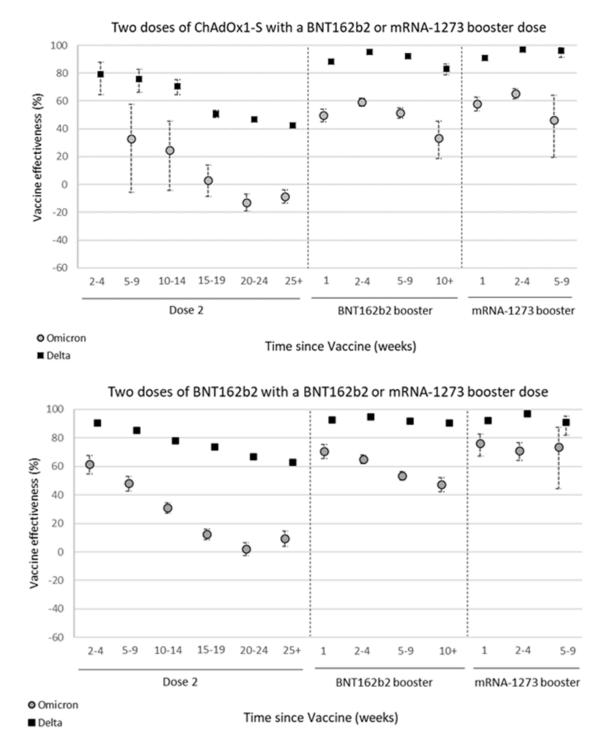
between 27 November and 17 December 2021 were included in the analysis. Those who reported recent foreign travel were excluded from the analysis due to differences in exposure risk and possible misclassification of vaccination status in this group.

Cases were defined as the Omicron variant or Delta variant based on whole genome sequencing, genotyping or S-gene target status on PCR testing. The Omicron variant has been associated with a negative S-gene target result on PCR testing with the Taqpath assay whereas with the Delta variant the S-gene target is almost always positive. A priori, we considered that S-gene target failure would be used to define the Omicron variant when Omicron accounts for at least 80% of S-gene target failure cases. This meant that S-gene target status could be used from 27 November onwards.

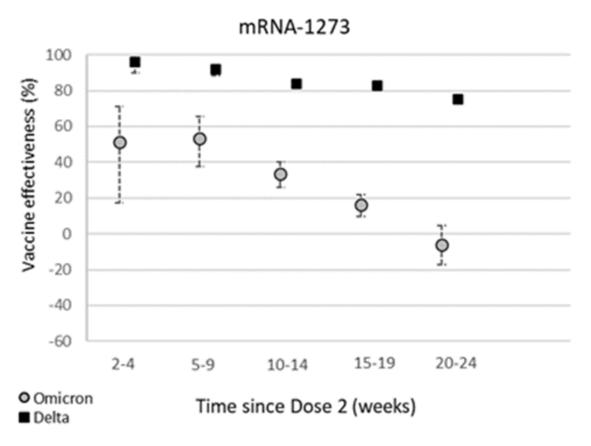
Vaccine effectiveness was estimated by period after dose 2 and dose 3. The final analysis included 147,597 Delta and 68,489 Omicron cases. Vaccine effectiveness against symptomatic disease by period after dose 2 and dose 3 is shown in <u>Figure 7</u> for those who received a primary course of the AstraZeneca vaccine (Figure 10A), Pfizer (Figure 10B) or Moderna (Figure 10C). Booster estimates are separated for Pfizer and Moderna boosters. In all periods, effectiveness was lower for Omicron compared to Delta. Among those who received an AstraZeneca primary course, vaccine effectiveness was around 60% 2 to 4 weeks after either a Pfizer or Moderna booster, then dropped to 35% with a Pfizer booster and 45% with a Moderna booster by 10 weeks after the booster. Among those who received a Pfizer primary course, vaccine effectiveness was around 70% after a Pfizer booster, dropping to 45% after 10-plus weeks and stayed around 70 to 75% after a Moderna booster up to 9 weeks after booster.

Figure 10. Vaccine effectiveness against symptomatic diseases by period after dose 1 and dose 2 for Delta (black squares) and Omicron (grey circles) for (A) recipients of 2 doses of AstraZeneca (ChAdOx1) vaccine as the primary course and (B) recipients of 2 doses of Pfizer (BNT162b2) vaccine as the primary course (C) recipients of 2 doses of Moderna (mRNA-1273) vaccine* as the primary course





26



* Numbers were too low to estimate booster vaccine effectiveness amongst recipients of a primary course of the Moderna vaccine.

These results should be interpreted with caution due to the low counts and the possible biases related to the populations with highest exposure to Omicron (including travellers and their close contacts) which cannot fully be accounted for.

With previous variants, vaccine effectiveness against severe disease, including hospitalisation and death, has been significantly higher than effectiveness against mild disease (that is, those detected through community testing and included here). Initially to estimate effectiveness against hospitalisation the risk of symptomatic cases going on to be hospitalised in vaccinated compared to unvaccinated as assessed in a survival model can be combined with symptomatic disease effectiveness in a 2-step approach. Although this analysis has been trialled, the number of cases admitted to hospital following testing positive in the community is too small. It will be a few weeks before effectiveness against severe disease with Omicron can be estimated, however based on experience with previous variants, this is likely to be substantially higher than the estimates against symptomatic disease. After the emergence of Delta in the UK, early estimates of vaccine effectiveness against mild infection after 2 doses of vaccine were substantially attenuated in comparison to alpha. Analysis of protection against hospitalisation however, showed no diminution of protection when comparing the 2 variants.

2.5 Reinfections

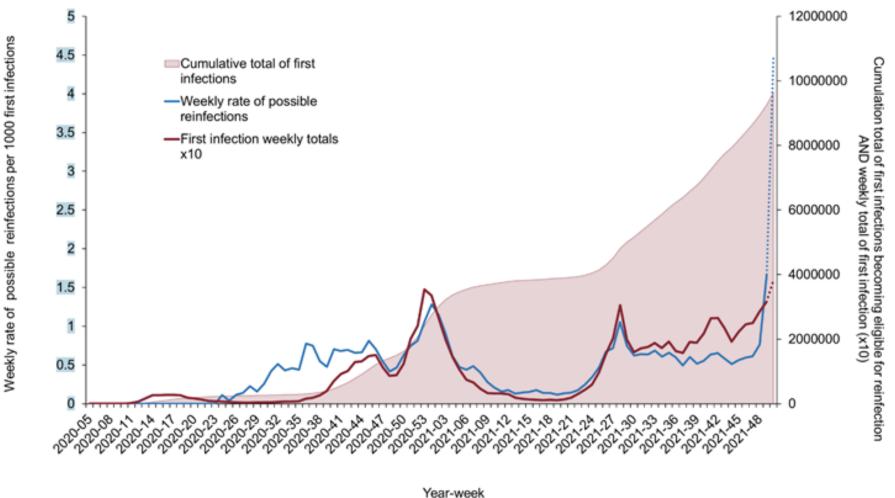
Cases of reinfection (at any interval) extracted on 19 December 2021 were identified amongst confirmed and probable Omicron variant SARS-CoV-2 positive cases with a specimen date between 1 November and 18 December 2021. Of 116,683 individuals identified with an Omicron infection in this period, 11,103 individuals (9.5%) were linked to previous confirmed infection (by PCR or LFD testing) and had an interval from the previous test positive of >=90 days. These cases would therefore have been identified as a reinfection based on the diagnosis used in ongoing surveillance (an interval between 2 sequential positive SARS-CoV-2 test results of >=90 days).

The case ages ranged from infants to people in their 90s (median 27 years) and the interval to reinfection from previous SARS-CoV-2 infection ranged from 90 to 650 days (median 343 days) with first episodes occurring both within periods of Alpha and Delta variant dominance and earlier. There were 69 individuals for whom the Omicron infection was their third episode of infection (>=90 days between each episode). There were 290 individuals with a possible reinfection between a 60 to 89 day interval after an earlier confirmed infection but in those with an interval of <90 days between episodes it can be difficult to distinguish reinfection from persistent detection of virus.

Reinfection rates are usually generated using the population of previous infections eligible to become a reinfection (that is with a previous positive test result >=90 earlier). Using this as a measure of current reinfection rates in the population there is now a marked increase in overall reinfection rates, this is disproportionate to the increase in first infections (Figure 11). Further information on overall reinfections is published in the <u>UKHSA National flu and COVID-19</u> surveillance reports (week 51).

Figure 11. The weekly rate of possible COVID-19 reinfections with cumulation of first infections becoming eligible for reinfection and weekly total of first infection* (England only to week 50 of 2021, provisional)

Supplementary data is not available for this figure.



* This data has been derived independently based on Pillar 1 and Pillar 2 data sets and may therefore differ to previously published data.

2.6 Growth rate and advantage

The growth in frequency of adjusted SGTF which are likely to originate from Omicron cases in England is shown in Figure 12 and for each region in England in Figure 13.

Growth rates are computed relative to the number of S gene positive cases. Sample inclusion criteria are:

- 1. a non-traveller as determined by matching each case against passenger locator forms and managed quarantine service test codes
- 2. collected from Pillar 2 testing
- 3. less than 30 cycle threshold (Ct) on targets other than the S-gene in order to reduce false positives in patients with low viral loads

SGTF has variable specificity for detection of the Omicron variant because Delta cases will occasionally produce SGTF. Before Omicron was detected, the majority of SGTF originated from non-Omicron cases in the first half of November. The probability that an SGTF originates from an Omicron case over time was estimated using a generalised additive model applied to SGTF cases paired with sequence data between 20 November and 18 December 2021. The true positive rate for using SGTF as a marker for Omicron increased from 20% on 20 November to >99% by 10 December 2021. Before estimating growth rates, SGTF counts were adjusted by redistributing cases from negative to positive in proportion to the true positive rate of SGTF for Omicron.

The growth rate is estimated by logistic regression of the number of SGTF on the time of sample collection. A growth rate of 0 would indicate parity with S-gene positive cases. Confidence intervals were computed by parametric bootstrap.

Lines show a logistic regression fit to the data and shaded region a 95% confidence interval.

Figure 12. Sample frequency of log odds adjusted SGTF cases as compared to S gene positive cases

Supplementary data is not available for this figure. A linear increase, using log odds, is consistent with exponential growth.

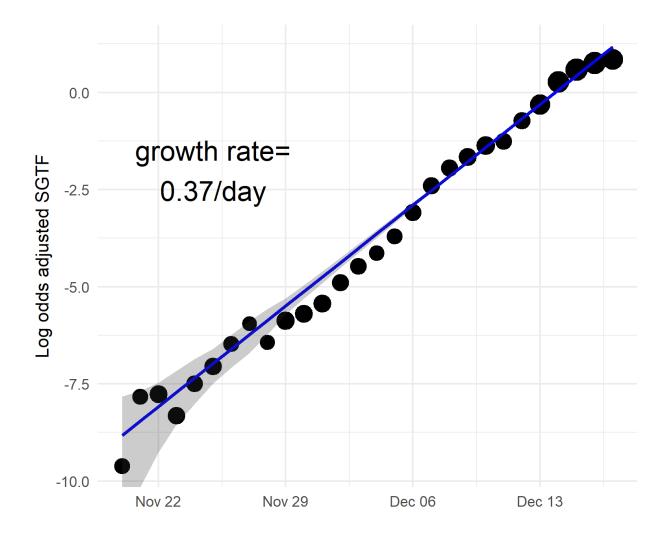
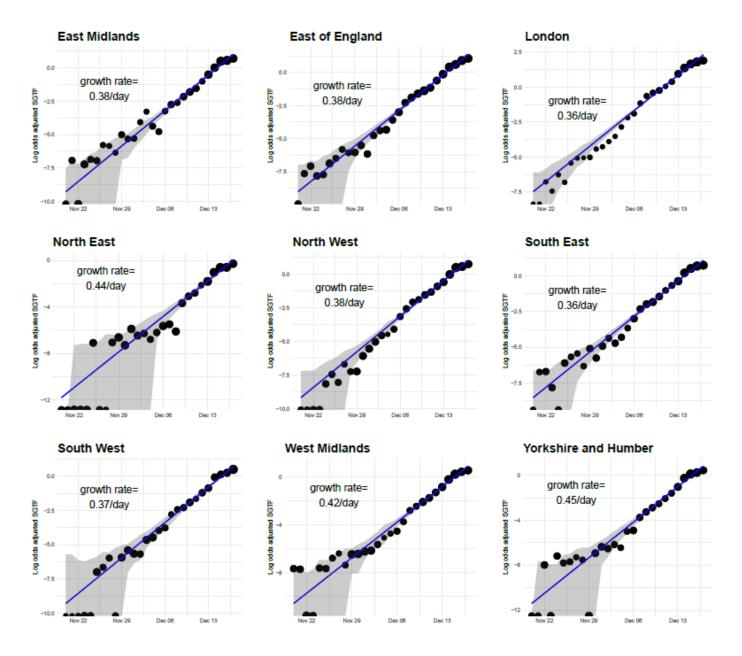


Figure 13. Sample frequency of log odds adjusted SGTF cases as compared to S gene positive cases for each region in England

Supplementary data is not available for this figure. A linear increase, using log odds, is consistent with exponential growth. Observed growth is consistent across regions.



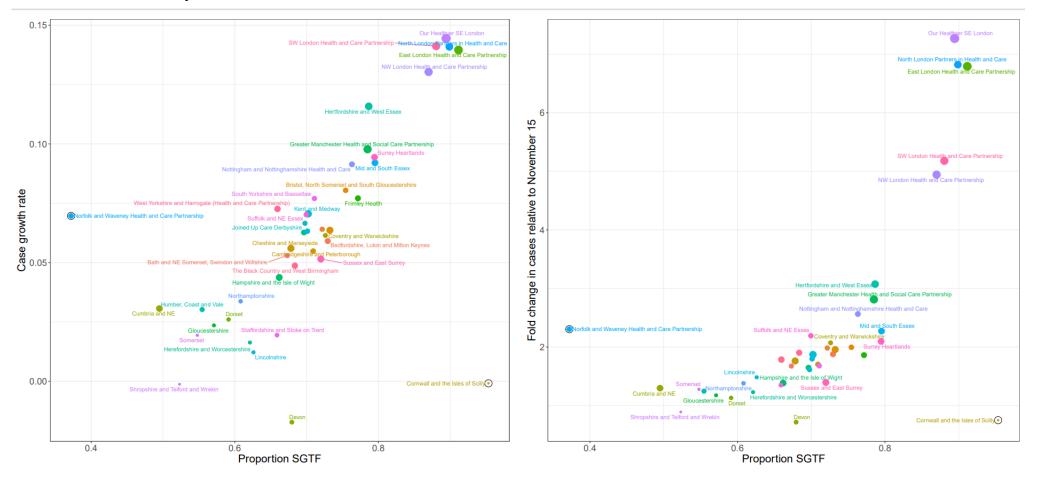
Growth rate and incidence

Incidence has increased rapidly in Sustainability and Transformation Partnerships (STPs) where the proportion of SGTF cases is highest, as shown in <u>Figure 14</u>.

Case growth rate was calculated as the daily change in number of diagnoses. The case growth rate across STPs is positively correlated with the proportion of SGTF.

Figure 14. Change in COVID-19 case growth rate versus proportion of SGTF across Sustainability and Transformation Partnerships as of 18 December 2021.

Supplementary data is not available for this figure. The size of the points is proportional to the number of cases on 18 December 2021. Norfolk and Waveney Health and Care Partnership, and Cornwall and the Isles of Scilly are circled because they performed fewer than 10 PCR tests that identify SGTF on 18 December 2021.



Secondary attack rates

This section is based on cases with test dates in the period 15 November to 14 December 2021. Secondary attack rates and odds ratios are based on positive tests amongst contacts named to NHS Test and Trace by an original case identified with confirmed or genotyped Omicron or Delta, with date of symptom onset or positive test of the secondary case occurring 2 to 7 days after original exposure. This shortened follow up period was used to expedite analysis on Omicron in the context of limited data so far.

Only close contacts named by the original case to NHS Test and Trace 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. Contacts not named by the case but identified as part of contact tracing of international travellers on flights are excluded.

There are a number of limitations to this work. Enhanced identification and testing for contacts of cases with Omicron may still be contributing to higher case ascertainment amongst those contacts and hence higher observed secondary attack rates; this effect is likely to have lessened since the previous briefing. Differences in demographics and activities of Omicron and Delta cases may also be contributing to different patterns of risk of onwards transmission to their contacts. A higher proportion (37.3%) of named close contacts of Omicron cases were outside of the household compared to Delta (20.8%), which is suggestive of differing contact patterns between these groups in the study period.

<u>Table 5</u> shows the secondary attack rates split by type of contact. Secondary attack rates amongst contacts of Omicron cases in households (13.6%; 95% CI:13.1%-14.1%) and non-household settings (7.6%; 95% CI: 7.2%-8.0%) are higher than those for Delta (household: 10.1%; 95% CI:10.0%-10.2%, non-household: 2.8%; 95% CI: 2.7%-2.9%), but are lower than previous estimates, suggesting that the effect of enhanced identification and testing amongst Omicron contacts may have reduced in most recent data.

<u>Table 6</u> shows crude and adjusted odds ratios of a close contact becoming a case for Omicron compared to Delta index cases, stratified by household or non-household contacts. In both settings this odds ratio indicated significantly more transmission to contacts of Omicron cases than those of Delta cases. Adjusted odds ratio of a non-household contact of an Omicron case (versus a Delta case) becoming a contact was 2.63 (95% CI: 2.43-2.84), the adjusted odds ratio for household contacts was 1.42 (95% CI: 1.36-1.49).

Table 5. Secondary attack rates for contacts of cases with Omicron VOC-21NOV-01 (B.1.1.529) and Delta

(Case test dates 15 November to 14 December 2021, exposure dates 15 November to 11 December 2021, variant data as of 20 December 2021 and contact tracing data as of 21 December 2021)

Variant	Count of cases	Household contacts becoming cases / all household contacts	-	Non-household contacts becoming cases / all non- household contacts	Secondary attack rate amongst non-household contacts (95% CI)
Delta	256,854	40,644 / 403,162	10.1% (10.0%-10.2%)	2,922 / 102,997	2.8% (2.7%-2.9%)
Omicron	27,803	2,539 / 18,682	13.6% (13.1%-14.1%)	1,109 / 14,606	7.6% (7.2%-8.0%)

Secondary attack rates from NHS Test and Trace should generally be considered lower bounds due to the nature of contact tracing and testing, and specifically so here because of the restricted (7 days) time period for follow up. Data provided is for exposures in the period until 11 December 2021 in order to allow some time for contacts to become cases, hence case counts are lower than other sources. Contacts are included in secondary attack rates if their date of exposure if the contact is a non-household contact, or onset or test of exposing case if the contact is a household contact, is during the period of study.

Table 6. Odds ratio of a close contact becoming a case for contacts of Omicron VOC-21NOV-01 (B.1.1.529) compared to Delta index cases, crude and adjusted

(Case test dates 15 November to 14 December 2021, exposure dates 15 November to 11 December 2021, variant data as of 20 December 2021 and contact tracing data as of 21 December 2021)

Setting	OR (crude)	OR (adjusted*)
Household	1.40 (1.34-1.46, p<0.001)	1.42 (1.36-1.49, p<0.001)
Non-household	2.81 (2.62-3.02, p<0.001)	2.63 (2.43-2.84, p<0.001)

* Adjusted for the age and sex of exposing case and close contact and home region of exposing case.

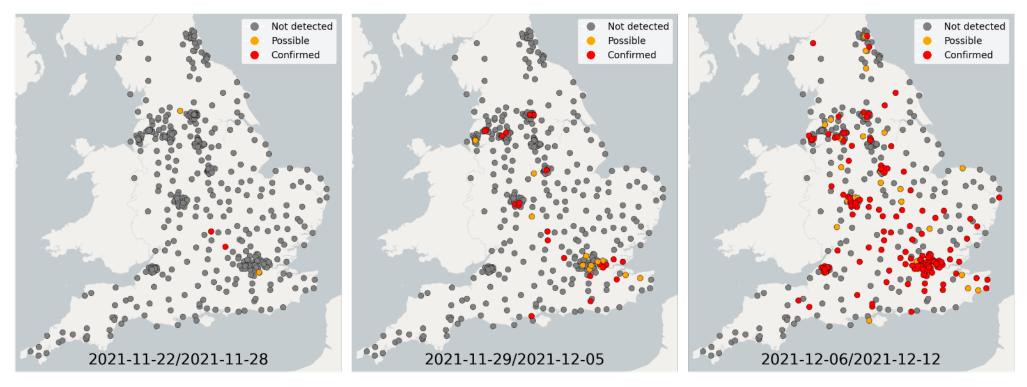
2.6 Wastewater analysis

Environmental monitoring of wastewater samples for the presence of SARS-CoV-2 variants is being undertaken across England and is in early stages of validation as an independent surveillance system. Wastewater is monitored for SARS-CoV-2 RNA at 477 sites including sewage treatment works (STW) and local sewer networks. Sampling is undertaken multiple times per week. This sampling framework is estimated to cover approximately 70% of the English population. It is possible to look for mutations associated with variants in the wastewater, but detection of variants can be transient and the correlation between population prevalence and wastewater variant detection has not been established for Omicron. Wastewater monitoring remains under development and is currently considered as supplementary data in variant monitoring.

Applying the definition provided in technical briefing 32, wastewater samples collected from sites across England up to 12 December 2021 have been analysed for the presence of Omicron. Between 22 November and 12 December there were confirmed or possible detections of Omicron in 311 wastewater samples amongst 3,673 sequenced (Table 7). Between 22 November and 5 December, 42 detections of Omicron in wastewater were reported, primarily in London, the South East and the North West (see technical briefing 32). In the week commencing 6 December, Omicron was identified in 264 wastewater samples across all regions, a 7-fold increase from the previous week, aligning with the rapid growth of confirmed and probable Omicron cases in England. Regionally, the highest percentage of samples in which Omicron was detected in the week commencing 6 December was in London and the South East.

Figure 15. Confirmed and Possible detections of Omicron VOC-21NOV-01 (B.1.1.529) in wastewater samples collected in England, data to 12 December 2021

Supplementary data is not available.



Region	22 to 28 November 2021			29 November to 5 December 2021*			6 to 12 December 2021		
	Sequenced samples	Confirmed Omicron	Possible Omicron	Sequenced samples	Confirmed Omicron	Possible Omicron	Sequenced samples	Confirmed Omicron	Possible Omicron
East Midlands	89	2	0	94	4	1	105	23	4
East of England	88	0	0	85	3	0	78	18	2
London	144	0	1	179	5	7	178	82	5
North East	67	0	0	103	0	0	52	2	3
North West	228	0	0	228	5	2	218	14	4
South East	86	1	0	77	6	2	78	26	4
South West	161	0	0	173	0	0	180	31	2
West Midlands	98	0	0	110	3	1	111	28	6
Yorkshire and the Humber	192	0	1	235	3	0	236	7	3
England	1,153	3	2	1,284	29	13	1,236	231	33

Table 7. Regional totals of wastewater samples sequenced and reported Omicron VOC-21NOV-01 (B.1.1.529) detections

* Please note, data was reanalysed after the publication of technical briefing 32 and a further 9 detections Omicron were found in wastewater samples (3 confirmed and 6 possible). Table reflects updated totals.

Wastewater samples will continue to be sequenced and results reported as they become available.

The data, including those presented here, is generated by non-accredited laboratories. They should be considered experimental and subject to change as methods are further developed. Monthly publication of this data on gov.uk as Experimental Statistics will commence in 2022.

Sources and acknowledgments

Data sources

Data used in this investigation is derived from the COG-UK and UKHSA genomic programme data set, the UKHSA Second Generation Surveillance System (SGSS), the Secondary Uses Service (SUS) data set, Emergency Care Data Set (ECDS), and the UKHSA Case and Incident Management System (CIMS).

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 UKHSA. 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 <u>briefings</u>.

Variant Technical Group

Authors of this report

UKHSA Genomics Cell UKHSA Outbreak Surveillance Team UKHSA Epidemiology Cell UKHSA Immunisations Team UKHSA Contact Tracing Data Team UKHSA Environmental Monitoring for Health Protection Team Contributions from the Variant Technical Group Members

Variant Technical Group members and contributors

Person	Institution	
Meera Chand (chair)	UKHSA	
Genomics and bioinformatics		
Andrew Rambaut	University of Edinburgh	

Person	Institution	
Nicholas Loman	UKHSA/University of Birmingham	
Richard Myers	UKHSA	
Jeffrey Barrett	Wellcome Sanger Institute	
Matt Holden	Public Health Scotland	
Natalie Groves	UKHSA	
Eileen Gallagher	UKHSA	
Nicholas Ellaby	UKHSA	
Virology and Immunology		
Wendy Barclay	Imperial College London	
Gavin Screaton	University of Oxford	
Maria Zambon	UKHSA	
Paul Kellam	Imperial College London	
Kevin Brown	UKHSA	
Susanna Dunachie	University of Oxford	
Lance Turtle	University of Liverpool	
Ravi Gupta	University of Cambridge	
Bassam Hallis	UKHSA	
Tim Wyatt	Northern Ireland Public Health Agency	
Thomas Peacock	Imperial College London	
Thushan da Silva	University of Sheffield	
Epidemiology and modelling		
Susan Hopkins	UKHSA	
Jamie Lopez-Bernal	UKHSA	
Nick Andrews	UKHSA	
Simon Thelwall	UKHSA	
Meaghan Kall	UKHSA	
Thomas Finnie	UKHSA	
Richard Elson	UKHSA	
Charlotte Anderson	UKHSA	
Charlie Turner	UKHSA	
Erik Volz	Imperial College London	
John Edmunds	London School of Hygiene and Tropical Medicine	
Neil Ferguson	Imperial College London	

SARS-CoV-2 variants of concern and variants under investigation in England: Technical briefing 33

Person	Institution
Daniela de Angelis	University of Cambridge
Maria Rossi	Public Health Scotland
Chris Williams	Public Health Wales
Anna Seale	UKHSA/University of Warwick
Julia Gog	SPI-M / University of Cambridge
International epidemiology	
Katherine Russell	UKHSA
Chris Lewis	Foreign, Commonwealth and Development Office
Leena Inamdar	UKHSA

The UK Health Security Agency Variant Technical Group includes members and contributors from the following organisations: UKHSA, 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, 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 University of Oxford, and the Genotype to Phenotype Consortium.

About the UK Health Security Agency

The <u>UK Health Security Agency</u> is an executive agency, sponsored by the <u>Department of</u> <u>Health and Social Care</u>.

© Crown copyright 2021 Version 1.0

Published: December 2021 Publishing reference: GOV-10738



You may re-use this information (excluding logos) free of charge in any format or medium, under the terms of the Open Government Licence v3.0. To view this licence, visit <u>OGL</u>. Where we have identified any third party copyright information you will need to obtain permission from the copyright holders concerned.



UKHSA supports the UN Sustainable Development Goals

