Epidemiology and Infection

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Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021

M. R. Smallman-Raynor[1], A. D. Cliff[2] and The COVID-19 Genomics UK (COG-UK) Consortium[3,†]

[1]School of Geography, University of Nottingham, Nottingham, UK; [2]Department of Geography, University of Cambridge, Cambridge, UK and [3]https://www.cogconsortium.uk

Original Paper

†Full list of consortium names and affiliations are in the appendix

Cite this article: Smallman-Raynor MR, Cliff AD, The COVID-19 Genomics UK (COG-UK) Consortium (2022). Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021. *Epidemiology and Infection* **150**, e145, 1–13. https://doi.org/10.1017/S0950268822001285

Received: 30 January 2022
Revised: 4 May 2022
Accepted: 14 July 2022

Key words:
COVD-19; England; geography; SARS-CoV-2; spatial analysis

Author for correspondence:
M. R. Smallman-Raynor,
E-mail: matthew.smallman-raynor@nottingham.ac.uk

Abstract

This paper uses a robust method of spatial epidemiological analysis to assess the spatial growth rate of multiple lineages of SARS-CoV-2 in the local authority areas of England, September 2020–December 2021. Using the genomic surveillance records of the COVID-19 Genomics UK (COG-UK) Consortium, the analysis identifies a substantial (7.6-fold) difference in the average rate of spatial growth of 37 sample lineages, from the slowest (Delta AY.4.3) to the fastest (Omicron BA.1). Spatial growth of the Omicron (B.1.1.529 and BA) variant was found to be 2.81× faster than the Delta (B.1.617.2 and AY) variant and 3.76× faster than the Alpha (B.1.1.7 and Q) variant. In addition to AY.4.2 (a designated variant under investigation, VUI-21OCT-01), three Delta sublineages (AY.43, AY.98 and AY.120) were found to display a statistically faster rate of spatial growth than the parent lineage and would seem to merit further investigation. We suggest that the monitoring of spatial growth rates is a potentially valuable adjunct to outbreak response procedures for emerging SARS-CoV-2 variants in a defined population.

Introduction

Emerging lineages of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have the potential to place significant pressure on public health systems due to increased infectivity, transmissibility, virulence, immune escape or other fitness advantage [1, 2]. Global genomic surveillance has identified >1700 SARS-CoV-2 lineages since the beginning of the COVID-19 pandemic [3, 4], of which Alpha (B.1.1.7 and Q), Beta (B.1.351), Gamma (P.1), Delta (B.1.617.2 and AY) and Omicron (B.1.1.529 and BA) have been designated as variants of concern by the World Health Organization (WHO) on account of their global public health significance [5]. Additional lineages are currently classified on the basis of properties that are suggestive of an emerging (variants of interest) or possible future (variants under monitoring) risk to global public health [5]. The risk is well illustrated by the recent and rapid emergence of Omicron as the dominant variant in the UK, South Africa and the USA, among other countries, in late November and December 2021 [6–8].

One important epidemiological facet of an emerging SARS-CoV-2 lineage is its propensity to grow in a defined population [9]. There are well-established methods for assessing the rate of temporal growth by, for example, examining the trajectory of case doubling times or estimating the basic reproduction number, R_0, of the agent in question [10, 11]. Viewed from a geographical perspective, these measures are essentially aspatial in that they provide very little information on the geographical growth, or spatial expansion, of the associated infection wave. To extend the examination of SARS-CoV-2 growth rates into the spatial domain, the present paper applies a robust method of spatial epidemiological analysis that is known as the *swash-backwash model of the single epidemic wave* [12] to the genomic surveillance records of the COVID-19 Genomics UK (COG-UK) Consortium [13]. Using the spatial sequence of detection of sample variants as a proxy for the spatial wave front of infection, our examination yields estimates of the spatial growth rate of multiple SARS-CoV-2 lineages in the local authority areas of England, September 2020–December 2021.

For a total of 37 sample lineages under investigation, we present evidence of a substantial (7.6-fold) difference in the average rate of spatial growth, from the slowest (Delta AY.4.3) to the fastest (Omicron BA.1). Whilst the overall results for the Alpha, Delta and Omicron variants are consistent with the documented growth advantages for these lineages, several emergent Delta sublineages (AY.4.2, AY.43, AY.98 and AY.120) are found to have had a statistically significant growth advantage over the parent lineage. To our knowledge, this is the first comparative study of the spatial growth rate of multiple emerging SARS-CoV-2 lineages at the national level. It is also the first report of a spatial growth advantage for the Delta AY.43, AY.98

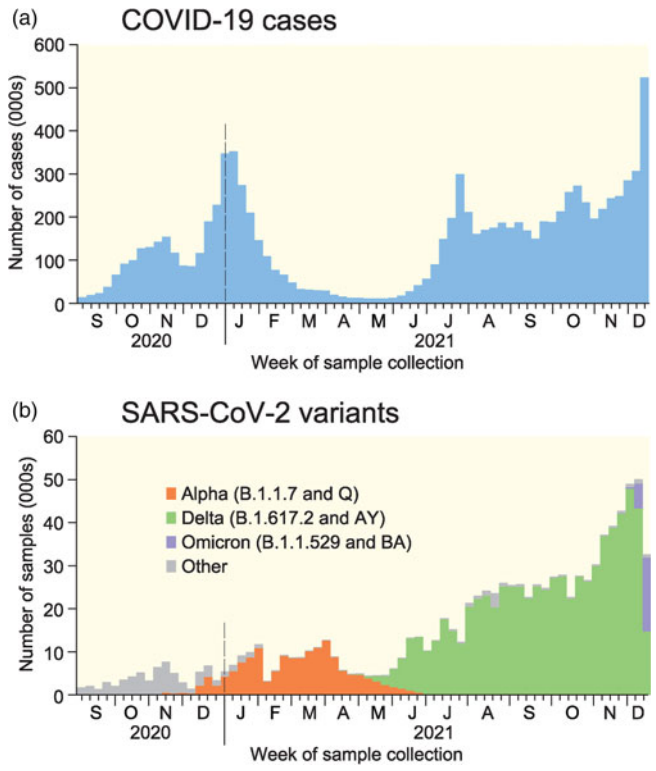

Fig. 1. COVID-19 cases in England, September 2020–December 2021. (a) Positive COVID-19 test specimens as recorded by the UK Government. (b) Number of sample genomes of SARS-CoV-2 in the COG-UK database by variant to 18 December 2021. All data are plotted by week of sample collection. Sources: data from GOV.UK Coronavirus (COVID-19) in the UK [17] and COVID-19 Genomics UK (COG-UK) Consortium [18].

and AY.120 lineages, and the first to document an apparently reduced spatial growth rate for a substantial number of other AY lineages that emerged in the spring and summer of 2021. The modelling of spatial growth rates is equally applicable to the analysis of RT-PCR gene target data, and we suggest it to be a potentially valuable adjunct to outbreak response procedures for SARS-CoV-2 variants in a defined population.

Data and methods

Since September 2020, successive waves of SARS-CoV-2 infection with emerging lineages of the Alpha (September 2020 onset), Delta (March 2021 onset) and Omicron (November 2021 onset) variants have been recorded in England [14–16]. The weekly record of COVID-19 cases to mid-December 2021 is plotted in Figure 1a, whilst the underpinning sequence of variants is depicted in Figure 1b. As Figure 1b shows, Alpha, Delta and Omicron achieved the status of dominant variants in December 2020, May 2021 and December 2021, respectively.

Data

We draw on the integrated national-level SARS-CoV-2 genomic surveillance records of the COG-UK Consortium [13]. These records are based on unselected (random sample) sequencing of positive SARS-CoV-2 test samples that have been identified through standard ('pillar 2') diagnostic pathways in the UK. Lineages are assigned using the Phylogenetic Assignment of Named Global Outbreak Lineages (pangolin) tool, with lineage counts made available by local authority area and week of sample collection. For further information on the data under examination, see COG-UK Consortium, COVID-19 Genomic Surveillance [18].

Lineage counts for England were accessed from the COG-UK website [18] for a 68-week period, September 2020 (epidemiological week 36, ending 5 September) to December 2021 (epidemiological week 50, ending 18 December) (Fig. 1b). The data set included geo-coded information on 979 075 SARS-CoV-2 samples assigned to the 309 Lower Tier Local Authority (LTLA) divisions of England. Here, we define the 309 LTLAs according to their most recent (May 2021) status. Information on the lineage of 20 655 samples (2.1%) was either suppressed (1105) or not recorded (19 550). Of the remaining 958 420 samples, the majority (93.8%) were classified as belonging to the B.1.1.7 and Q (Alpha, 153 405 samples), B.1.617.2 and AY (Delta, 722 133 samples) and B.1.1.529 and BA (Omicron, 23 137 samples) lineages (Table 1). Samples belonging to these lineages form the basis of all our analysis.

Methods

To assess the spatial growth rate of a given SARS-CoV-2 lineage, we draw on the *swash-backwash model of the single epidemic wave* [12]. In essence, the model represents a spatial derivative of the generic *SIR* mass action models of infectious disease transmission [19]. Using the binary (presence/absence) of a disease, the model (i) allows the disaggregation of an infection wave into phases of spatial expansion and retreat and (ii) provides a means of measuring the phase transitions of geographical units from susceptible *S*, through infective *I* to recovered *R* status. See, for example, Smallman-Raynor and Cliff [20] and Smallman-Raynor *et al.* [21].

Measuring the spatial growth rate

Full details of the modelling procedure are outlined by Cliff and Haggett [12]. For the purposes of the present analysis, we focus on the spatial expansion phase (i.e. the change of state from *S* to *I* across a set geographical units) for a given SARS-CoV-2 lineage. Specifically, let the first week in which the lineage was detected in England be coded as $t = 1$. Subsequent weeks were then coded serially as $t = 2, 3, \ldots, T$, where T is the number of weekly periods from the beginning to the end of the detected occurrence of the lineage. For any given geographical unit, we refer to the first week in which the lineage was detected as the *leading edge* (*LE*) of the infection wave. The average time (in weeks) to the detection of the lineage across the set of units can then be defined by a time-weighted mean, $\bar{t}_{LE}$, of the form

$$\bar{t}_{LE} = \frac{1}{N}\sum_{t=1}^{T} tn_t. \quad (1)$$

Here, n_t is the number of units whose leading edge, *LE*, occurred in week t and $N = \sum n_t$. Formed in this manner, SARS-CoV-2 lineages with relatively *high* rates of spatial expansion (or rapidly developing *LE*) take on relatively *low* values of $\bar{t}_{LE}$ (i.e. short average times to detection). Conversely, lineages with relatively *low* rates of spatial expansion (or slowly developing *LE*) take on relatively *high* values of $\bar{t}_{LE}$ (i.e. long average times to detection).

https://doi.org/10.1017/S0950268822001285 Published online by Cambridge University Press

Table 1. Estimated rate of spatial growth ($\bar{t}_{LE}$) of sample SARS-CoV-2 lineages in England, September 2020–December 2021

Variant/lineage	LTLAs (*n*)	Number of detections[a]	Earliest detection[b] (*t* = 1)	$\bar{t}_{LE}$ (95% CI) (weeks)
Alpha (B.1.1.7 and Q)	307	153 405	39/2020 (26 Sept.)	9.90 (9.56–10.23)
Delta (B.1.617.2 and AY)	307	722 133	12/2021 (27 March)	7.40 (7.12–7.68)
B.1.617.2	307	17 504	13/2021 (3 April)	9.11 (8.48–9.74)
AY.3	168	620	27/2021 (10 July)	14.12 (13.26–14.98)
AY.4	307	547 403	12/2021 (27 March)	9.45 (9.24–9.66)
AY.4.1	133	416	25/2021 (26 June)	9.50 (8.61–10.40)
AY.4.2	307	77 391	25/2021 (26 June)	6.21 (5.86–6.57)
AY.4.2.1	307	11 541	29/2021 (24 July)	9.43 (8.91–9.94)
AY.4.3	188	781	19/2021 (15 May)	19.93 (18.92–20.93)
AY.4.5	158	742	24/2021 (19 June)	15.06 (13.76–16.37)
AY.5	307	26 111	15/2021 (17 April)	9.83 (9.38–10.28)
AY.6	306	17 405	17/2021 (1 May)	8.88 (8.48–9.27)
AY.7	276	3627	18/2021 (8 May)	9.02 (8.39–9.65)
AY.8	141	1241	16/2021 (24 April)	8.60 (7.90–9.29)
AY.9	304	10 136	14/2021 (10 April)	10.88 (10.33–11.42)
AY.9.2	251	1990	28/2021 (17 July)	10.44 (9.70–11.17)
AY.10	118	683	15/2021 (17 April)	8.50 (7.96–9.04)
AY.25	130	486	31/2021 (7 Aug.)	13.02 (12.26–13.78)
AY.33	105	319	25/2021 (26 June)	17.84 (16.63–19.05)
AY.34	268	3088	30/2021 (31 July)	10.88 (10.19–11.57)
AY.36	256	1999	28/2021 (17 July)	12.69 (12.05–13.32)
AY.42	115	338	27/2021 (10 July)	10.08 (8.81–11.34)
AY.43	307	23 068	27/2021 (10 July)	5.56 (5.27–5.86)
AY.46	305	9461	21/2021 (29 May)	11.23 (10.72–11.74)
AY.46.5	304	8649	23/2021 (12 June)	10.13 (9.66–10.61)
AY.87	172	688	20/2021 (22 May)	10.28 (9.28–11.29)
AY.89	173	544	21/2021 (29 May)	13.97 (13.17–14.77)
AY.90	218	1202	21/2021 (29 May)	13.52 (12.54–14.50)
AY.98	307	22 465	22/2021 (5 June)	6.34 (5.99–6.70)
AY.98.1	172	621	25/2021 (26 June)	15.77 (14.80–16.75)
AY.109	116	441	25/2021 (26 June)	17.59 (16.67–18.52)
AY.111	296	4649	21/2021 (29 May)	15.25 (14.46–16.04)
AY.120	306	18 400	20/2021 (22 May)	6.56 (6.16–6.97)
AY.122	302	5018	21/2021 (29 May)	13.80 (13.07–14.53)
AY.124	119	424	25/2021 (26 June)	12.99 (11.93–14.05)
AY.125	162	534	26/2021 (3 July)	16.65 (15.79–17.51)
Omicron (B.1.1.529 and BA)	304	23 137	47/2021 (27 Nov.)[c]	2.63 (2.56–2.71)[d]
Average	233	46 450		11.27 (10.03–12.50)

aExcludes 1105 detections for which lineage data are suppressed and 19 550 detections for which lineage data are not available.
[b]Epidemiological week/year, with the last day of the week given in parentheses.
[c]Excludes a lone detection in week 43 (30 October).
[d]Indexed to week 47; $\bar{t}_{LE}$ = 6.62 (6.53, 6.70) when indexed to week 43.

Application of the model

Equation (1) was used to estimate the spatial growth rate of sample SARS-CoV-2 lineages for which the earliest detection in England occurred in the time period covered by the dataset (September 2020–December 2021) and for which substantial geographical spread had been documented. To ensure the inclusion

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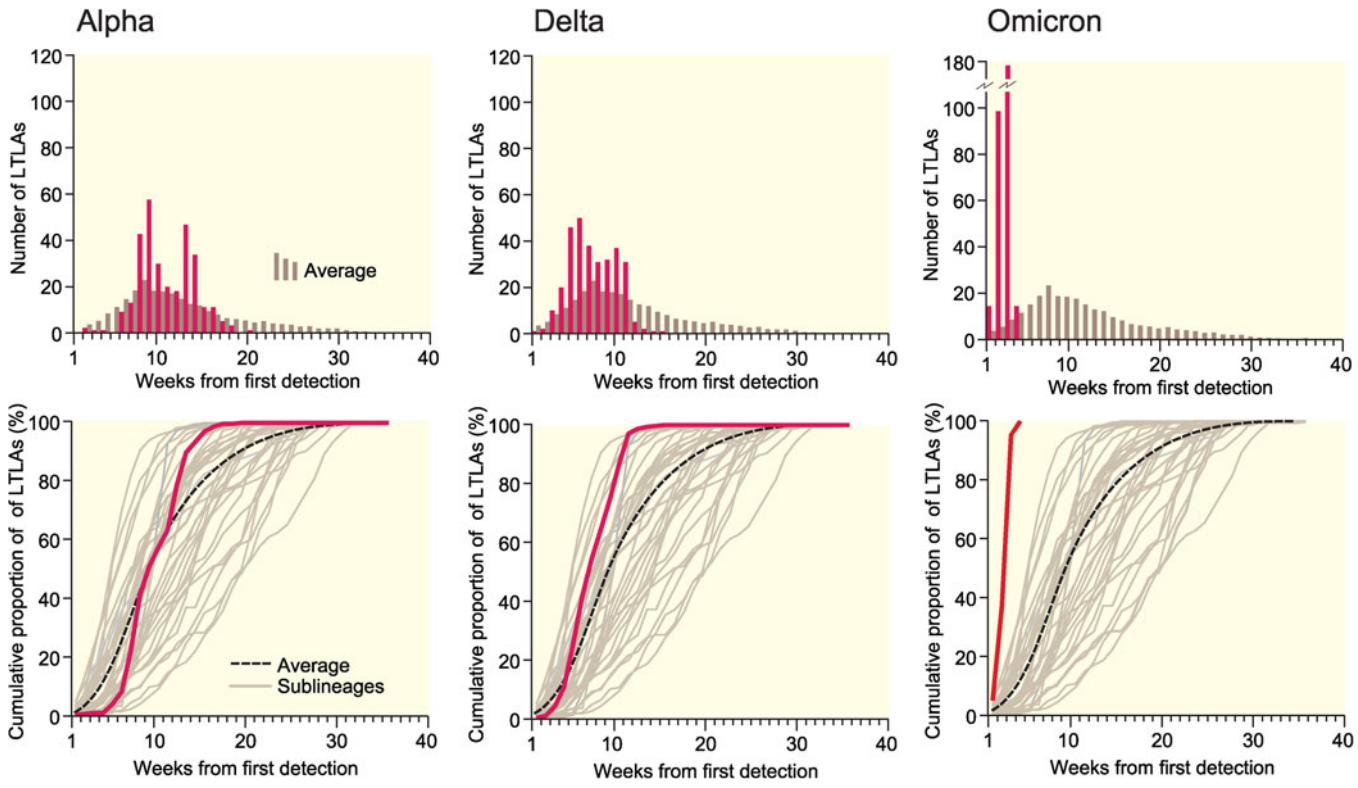

Fig. 2. Spatial leading edges (*LE*) of the Alpha (B.1.1.7 and Q), Delta (B.1.617.2 and AY) and Omicron (B.1.1.529 and BA) variants in England, September 2020–December 2021. The graphs plot, on a weekly basis, the non-cumulative count (upper) and cumulative proportion (lower) of LTLAs in which each of the three variants was first detected. The horizontal (time) axes are indexed to the epidemiological week of first detection ($t = 1$) of the corresponding variant. Average curves, formed across the set of sample lineages in Table 1, are plotted for reference.

of sufficient observations for geographical analysis, the sample was limited to lineages that had been detected in at least one-third of the 309 LTLAs by December 2021. Based on these criteria, the sample consisted of 37 lineages. Summary details of the sample, including the number of LTLAs in which each lineage was detected, the total count of detections over the study period and the earliest date of detection, are provided in Table 1.

For each lineage, equation (1) was fitted with $t = 1$ set to the week of earliest detection in Table 1. In the instance of Omicron, retrospective analysis has identified a lone detection of the BA.1 lineage in epidemiological week 43 of 2021 (week ending 30 October), 4 weeks prior to the subsequent detection and apparent onset of widespread transmission of the variant in epidemiological week 47 (week ending 27 November). For the purposes of the present analysis, we set week 47 as $t = 1$ for Omicron, but we also report the computed value of $\bar{t}_{LE}$ based on the earlier detection in week 43. Finally, we exclude two LTLAs (City of London and Isles of Scilly) from all analysis on account of the suppression of lineage data due to their small populations. Data analysis was performed in Minitab®17 (Minitab Inc., Pennsylvania, USA) and data mapping in QGIS 3.10.14-A Coruña (QGIS.org) using Local Authority Districts (May 2021) UK and Regions (December 2020) EN shapefiles from the Office for National Statistics (ONS) [22].

Results

Table 1 confirms that the 37 sample lineages were geographically extensive in their transmission, with 29 having been detected in >150 LTLAs, 21 in >250 LTLAs, 16 in >300 LTLAs and nine in the complete set of 307 LTLAs under examination. The majority (23) were associated with >1000 detections, 13 with > 10 000 detections and three with > 100 000 detections. Delta (B.1.617.2 and AY) was the most common lineage (722 133 detections) and AY.4 the most common sublineage (547 403 detections), with AY lineages accounting for 33 of the spread events under examination. In turn, the majority of lineages emerged (as judged by the date of earliest detections) in the spring and summer of 2021, as the Delta infection wave was evolving both domestically and internationally.

Spatial growth curves and leading edge (LE) maps

The upper graphs in Figure 2 plot the count of LTLAs by week of earliest detection of the Alpha (B.1.1.7 and Q), Delta (B.1.617.2 and AY) and Omicron (B.1.1.529 and BA) variants, where weeks are indexed to the earliest detection of the respective variants (Table 1). The lower graphs are spatial growth curves, formed by replotting the information in the upper graphs as a cumulative proportion of LTLAs. Average curves for the set of sample lineages in Table 1 are shown for reference.

Together, the graphs in Figure 2 portray the temporal development of the spatial leading edges (*LE*) for each variant. The geographical expression of these *LE* is captured by the choropleth maps in Figure 3 which plot the week of earliest detection of each variant in the set of LTLAs. The sequentially more rapid spatial growth of the variants (Alpha → Delta → Omicron) is evidenced by the sequentially steeper spatial growth curves (Fig. 2) and the sequentially shorter periods to earliest detection (Fig. 3). The latter feature is emphasised when earliest detections are formed as regional averages in Figure 4.

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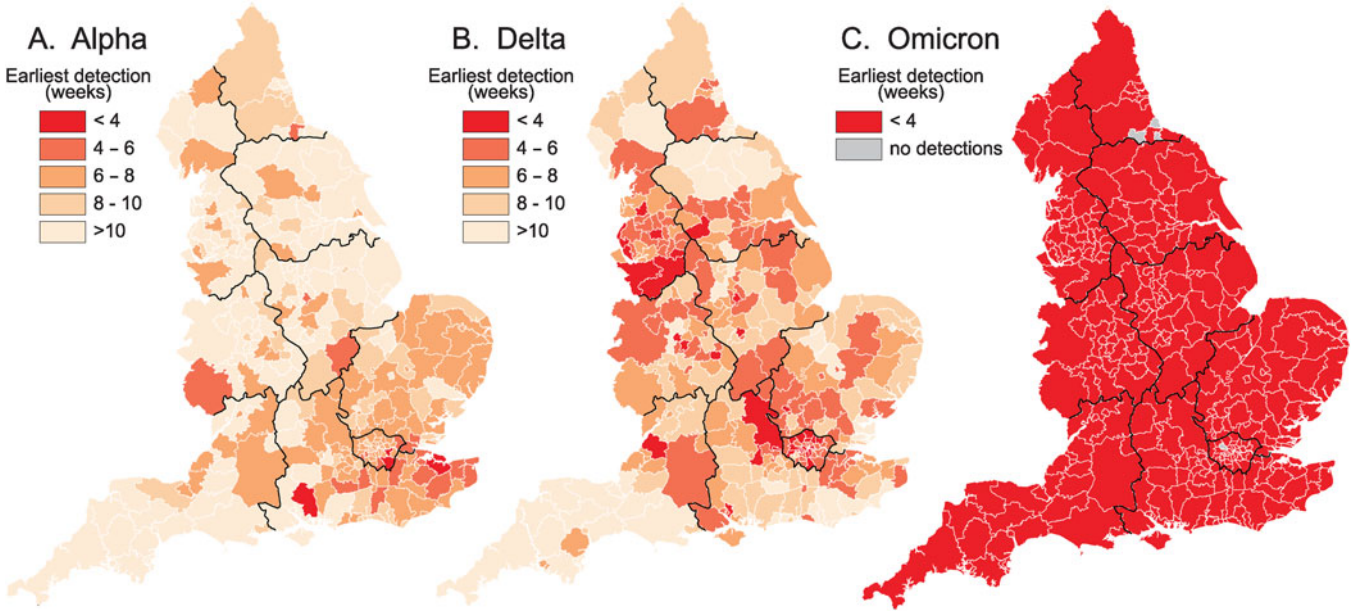

Fig. 3. Spatial leading edges (*LE*) of the Alpha (B.1.1.7 and Q), Delta (B.1.617.2 and AY) and Omicron (B.1.1.529 and BA) variants in the LTLAs of England, September 2020–December 2021. Maps are indexed to the epidemiological week of first detection (= week 1) of the corresponding variant and plot the number of weeks to first detection in each LTLA.

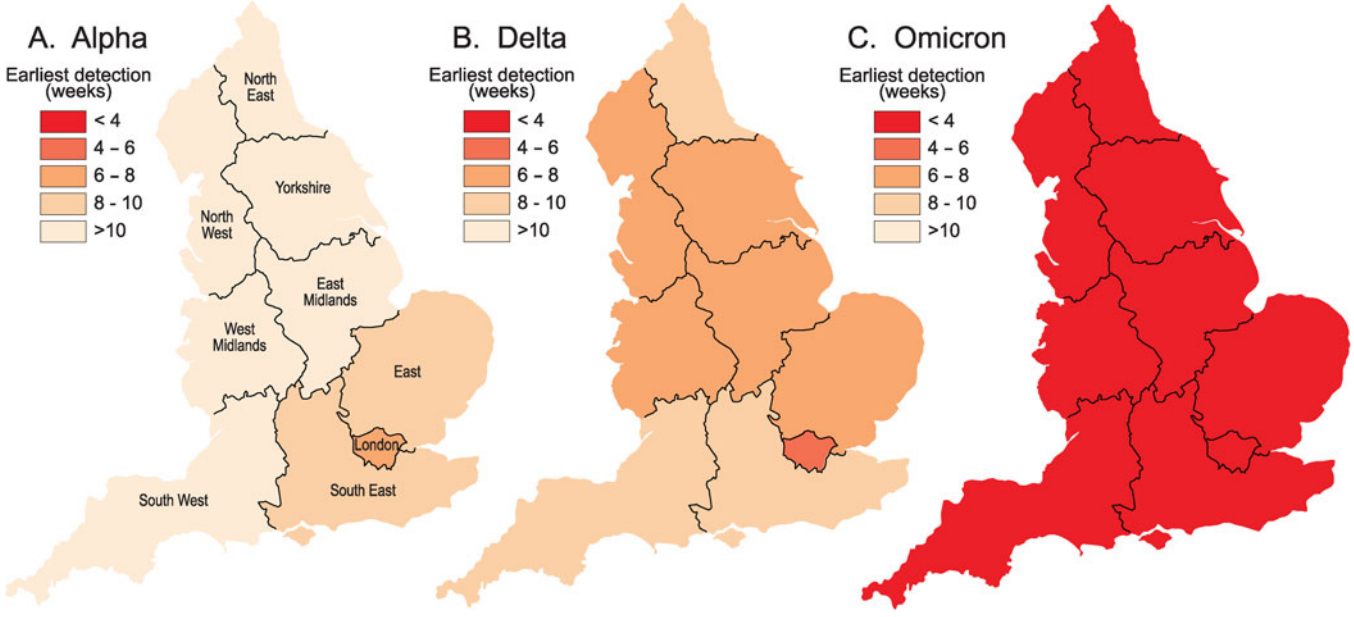

Fig. 4. Spatial leadings edges (*LE*) of the Alpha (B.1.1.7 and Q), Delta (B.1.617.2 and AY) and Omicron (B.1.1.529 and BA) variants in the nine standard regions of England, September 2020–December 2021. Maps plot the average time (in weeks) to first detection of a given variant in each regional subset of LTLAs.

Rates of spatial growth ($\bar{t}_{LE}$)

The right-hand column in Table 1 summarises the results of the application of equation (1) to each of the sample lineages. Computed values of $\bar{t}_{LE}$ and associated 95% confidence intervals (95% CI) are given, along with an overall average value of $\bar{t}_{LE}$ for the entire sample. As noted above, lineages with relatively *high* rates of spatial expansion (or rapidly developing *LE*) are represented by relatively *low* values of $\bar{t}_{LE}$ (i.e. short average times to detection), while lineages with relatively *low* rates of spatial expansion (or slowly developing *LE*) take on relatively *high* values of $\bar{t}_{LE}$ (i.e. long average times to detection). In this manner, the table confirms the sequential increase in the spatial growth rate for Alpha, Delta and Omicron. On average, the earliest detection of the Alpha variant in a given LTLA occurred at $\bar{t}_{LE} = 9.90$ (95% CI 9.56–10.23) weeks after the earliest sampled detection in England. This reduced to 7.40 (95% CI 7.12–7.68) weeks for Delta and 2.63 (95% CI 2.56–2.71) weeks for Omicron.

Delta AY lineages

Figure 5 is based on the information in Table 1 and plots the values of $\bar{t}_{LE}$ for B.1.617.2 and AY lineages in order, from the lowest (left, high values of $\bar{t}_{LE}$) to the highest (right, low values of

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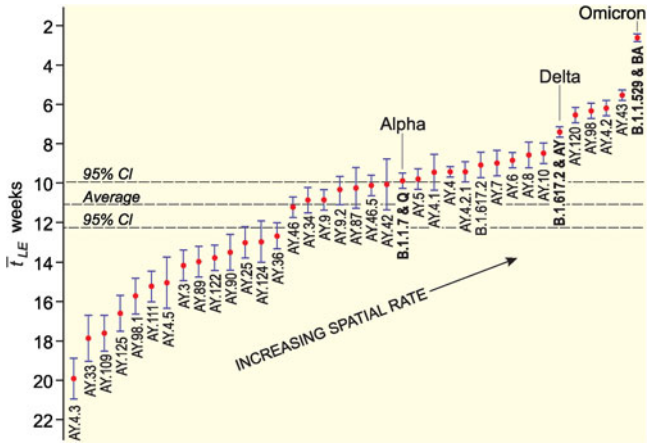

Fig. 5. Estimated rate of spatial growth of sample SARS-CoV-2 lineages in England, September 2020–December 2021. The graph plots values of $\bar{t}_{LE}$ and associated 95% CI from Table 1. Values are ordered from the lowest (left, high values of $\bar{t}_{LE}$) to the highest (right, low values of $\bar{t}_{LE}$) rates of spatial growth. Values are plotted on an inverted vertical scale to facilitate interpretation. The average value of $\bar{t}_{LE}$ for the sample is shown for reference.

$\bar{t}_{LE}$) rates of spatial growth. Values are plotted on an inverted vertical scale to facilitate interpretation. The average value of $\bar{t}_{LE}$, formed across the sample set of lineages in Table 1, is indicated for reference as are the $\bar{t}_{LE}$ for the Alpha (B.1.1.7 and Q), Delta (B.1.617.2 and AY) and Omicron (B.1.1.529 and BA) variants. Spatial growth curves, formed in the manner of Figure 2, are plotted for a sample of 20 AY lineages with relatively high and low rates of spatial growth in Figure 6.

There is a 7.6-fold difference in the range of values of $\bar{t}_{LE}$ in Figure 5, from Delta AY.4.3 with the lowest spatial growth rate (19.93 weeks) to Omicron with the highest (2.63 weeks). A group of four AY lineages (AY.4.2, AY.43, AY.98 and AY.120), first detected in the period from mid-May to mid-July 2021, are positioned between Delta and Omicron in Figure 5 and display rates of spatial growth that are significantly higher (as judged by 95% CI) than the aggregate rate for the Delta variant. In contrast, the overwhelming majority of AY lineages display statistically lower – in many instances substantially lower – spatial growth rates (as judged by 95% CI) than the aggregate rate for the Delta variant.

Discussion

Recent experience has underscored the importance of the ongoing tracking, monitoring and analysis of emerging SARS-CoV-2 lineages with a view to mitigating the impacts of the COVID-19 pandemic [23]. We have used a robust model of spatial epidemiological analysis to estimate the rate of spatial growth of multiple lineages of the virus in England over a 68-week period, September 2020–December 2021. We have shown that the Alpha, Delta and Omicron variants took an average of 9.90, 7.40 and 2.63 weeks, respectively, to reach the set of LTLAs under examination (Table 1 and Fig. 5). Expressed in relative terms, the leading spatial edges were 1.34× faster (Delta *vs.* Alpha), 2.81× faster (Omicron *vs.* Delta) and 3.76× faster (Omicron *vs.* Alpha). Our estimates scale to the approximate length of time that Alpha (12 weeks), Delta (8 weeks) and Omicron (3 weeks) took to establish themselves as the dominant variants in England [18], and are consistent with evidence for the fitness advantage of Delta over Alpha and Omicron over Delta [11, 24, 25].

Of the 121 Delta AY lineages detected in England to December 2021 and included in the genomic surveillance records of the COG-UK Consortium, 33 lineages met the geographical criterion for inclusion in the current analysis. In interpreting the results for these lineages, we note that AY designations are phylogenetically defined and do not necessarily denote any fundamental biological differences between the lineages [26]. Moreover, results of the type documented in this paper are context dependent and cannot be interpreted as evidence of a change in biological transmissibility, immune escape or other fitness advantage. Subject to these caveats, we have identified four AY lineages (AY.4.2, AY.43, AY.98 and AY.120) for which the rate of spatial growth exceeded the aggregate rate for the Delta variant. These lineages had been detected in all (AY.4.2, AY.43 and AY.98) or most (AY.120) of the local authority areas under investigation, and each had been associated with considerably more than 10 000 detections (Table 1). Table 2 summarises the global status of these four lineages as of 9 January 2022. With the exception of the AY.43 lineage, which was prevalent in a number of European countries and associated with >267 000 detections worldwide, the majority of detections of these lineages originated from the UK.

Our findings for the AY.4.2 and AY.43 lineages are consistent with their respective designations by the UK Health Security Agency as a distinct variant under investigation (VUI-21OCT-01) and a variant of concern [32, 33]. Preliminary investigations indicated the AY.4.2 lineage to be associated with a higher growth rate and a higher household secondary attack rate, but with no significant reduction in vaccine effectiveness, as compared to the parent lineage [32, 34]. Although the factors underpinning the higher growth rate of AY.4.2 remain to be established [32, 35, 36], we observe that this lineage accounted for a maximum of 24.4% of all detections (week ending 4 December 2021) before being outcompeted by Omicron [18]. Similarly, the status of the AY.43 lineage in terms of transmission advantage and/or immune escape remains to be determined, although further investigation is merited as new AY.43 sublineages have recently been reported from Brazil [37]. Finally, our identification of a rapid rate of spatial growth for the AY.98 and AY.120 lineages, approximating the estimated rates for AY.4.2 and AY.43, is noteworthy. Whilst very little has been documented on the epidemiological facets of these lineages, both have been identified in a number of countries in Europe and elsewhere (Table 2) and would seem to merit further investigation on the basis of the findings presented here.

With the foregoing exceptions, our analysis has shown that many emerging AY lineages in England in the spring and summer of 2021 were associated with spatial growth rates that were lower (in some instances, substantially lower) than the aggregate rate for the Delta variant (Table 1 and Fig. 5). Multiple biological (e.g. reduced infectivity or transmissibility) and contextual (e.g. progressive expansion of the national COVID-19 vaccination programme) factors may account for this observation. Importantly, there is no evidence of a temporal trend in the observed rates of spatial growth that would be suggestive of either (i) a biological selection pressure in favour of a growth advantage of emerging lineages or (ii) a progressive contextual effect in the form of, for example, increasing levels of vaccination coverage or natural immunity that would serve to retard growth rates.

It is important to emphasise the broader societal and epidemiological context to the spread of SARS-CoV-2 lineages that will have influenced our estimates of $\bar{t}_{LE}$ in Table 1 and

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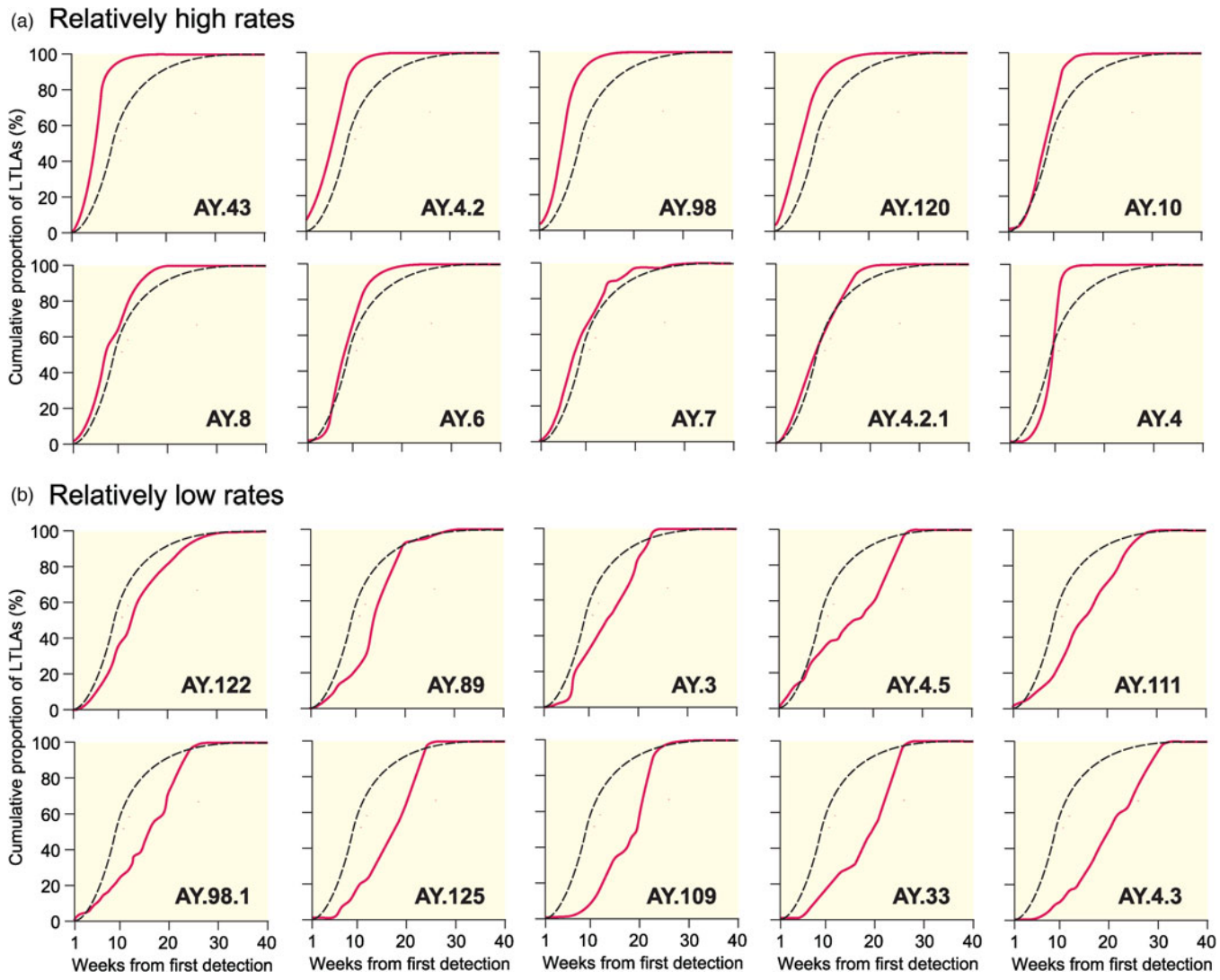

Fig. 6. Spatial growth curves for sample Delta sublineages in England, March–December 2021. Curves have been formed in the manner of the lower graphs in Figure 2, with the average curve plotted for reference. Lineages are ordered according to the values of $\bar{t}_{LE}$ in Table 1 and are defined as having relatively high (i.e. low values of $\bar{t}_{LE}$; upper graphs, a) and relatively low (i.e. high values of $\bar{t}_{LE}$; lower graphs, b) rates of spatial growth.

Table 2. Worldwide detection of sample Delta AY lineages with relatively high estimated rates of spatial growth (status: 9 January 2022)

Variant	Countries	Global prevalence (%)	Number of detections	Predominant countries (proportion of global detections)
AY.4.2	52	1	82 038	UK (90%), Denmark (4%), Germany (1%), Poland (1%), France (1%)
AY.43	128	4	267 426	Germany (15%), UK (13%), Denmark (13%), France (12%), Belgium (5%)
AY.98	66	1	41 507	UK (91%), USA (2%), Germany (1%), Denmark (1%), Ireland (1%)
AY.120	74	1	30 320	UK (85%), India (3%), USA (3%), Germany (2%), France (1%)

Sources: data from cov-lineages.org [27] and Latif *et al.* [28–31].

Figure 5. For the time period covered by the present study, non-pharmaceutical interventions (NPIs) included: a tier system of local lockdown in October 2020; two periods of national lockdown (November–December 2020 and January–March 2021); a phased lifting of national restrictions in the period to July 2021; and the implementation of 'Plan B' control guidelines against the Omicron variant in December 2021 [38]. Whilst the phases of national lockdown had significant impacts on population mobility, mixing and associated opportunities for SARS-CoV-2 transmission [39], it is noteworthy that the majority (27) of lineages included in the present analysis were first detected in the period from May to July 2021 (Table 1). This corresponded with the final steps in the Government's four-stage roadmap for the lifting of lockdown measures and was marked by a substantial

https://doi.org/10.1017/S0950268822001285 Published online by Cambridge University Press

easing and eventual removal of restrictions on social mixing [38]. To set against this easing of restrictions, lineage growth rates will have been retarded to an unknown extent by the immunity afforded by prior infection with antigenically similar SARS-CoV-2 variants (B.1.617.2 and AY sublineages, in particular) and by the phased rollout of the national COVID-19 vaccination programme [40].

The results we have presented are subject to the limitations of the available lineage data. Although the COG-UK Consortium genomic surveillance data are recognised for their extent and reliability [41], the data are formed as a sample of positive SARS-CoV-2 test results and are subject to the limitations and biases of sample data. In this context, we note that the cumulative coverage of the COG-UK records for England was estimated at 13.7% of people with positive SARS-CoV-2 test results to October 2021 [42]. We also note that the sample test data are derived from a laboratory system with testing capabilities that vary by region and time period [9]. Such space-time variations have potentially important implications for analyses, of the type outlined in the present paper, that are dependent on the dates of first detection of SARS-CoV-2 lineages in a multi-region setting.

Our results are also subject to the underpinning assumptions of the analytical procedure. In particular, the computation of $\bar{t}_{LE}$ is dependent on the specification of the index week (i.e. the week that a given lineage was first detected in England) and the degree to which this reflects the date of actual emergence of the lineage in England. The extent to which the sample data accurately track the spatial expansion of the *LE* for a given lineage, the variable contributions of international travel- and community-related transmission to the development of the *LE*, and the geographical starting point(s) of a given lineage in the national transmission network, will also have influenced our results in unknown ways. For example, the early involvement and high degree of geographical connectivity of London and the South East may have served to accelerate the spatial transmission of the Alpha variant in the latter months of 2020 [14]. The observed rapid spread of the Delta variant may reflect international importations and onwards transmission from multiple different geographical locations in the spring of 2021 [15, 43], whilst early cases of the Omicron variant were observed in highly connected regions at a time of reduced NPIs in November and December 2021 [44].

For the purposes of the present analysis, our application of the swash-backwash model has utilised genomic surveillance data. We note, however, that the modelling approach is equally applicable to the analysis of RT-PCR gene target data. As such, the approach may be used to facilitate timely assessments of the spatial growth of emerging SARS-CoV-2 variants and thereby contribute to rapid outbreak responses [9, 45].

Further insights into the spatial growth and decay of SARS-CoV-2 lineages may be gained by application of the full swash-backwash model, but this is dependent on the substantial spatial retreat of any given lineage from the population. Here we note that, with the exception of AY.10 (last detected in July 2021) and AY.8 and Alpha (B.1.1.7 and Q) (both last detected in August/September 2021), there is evidence of the circulation of all the lineages included in Table 1 in the weeks to December 2021.

We have demonstrated, for the first time, a robust method for assessing and comparing the rate of spatial growth of multiple SARS-CoV-2 lineages in a set of geographical areas. We suggest that this approach represents a potentially valuable adjunct to outbreak response procedures for emerging SARS-CoV-2 variants in a defined population.

Acknowledgements. COG-UK is supported by funding from the Medical Research Council (MRC) part of UK Research & Innovation (UKRI), the National Institute of Health Research (NIHR) [grant code: MC_PC_19027], and Genome Research Limited, operating as the Wellcome Sanger Institute. The authors acknowledge use of data generated through the COVID-19 Genomics Programme funded by the Department of Health and Social Care. The views expressed are those of the author and not necessarily those of the Department of Health and Social Care or PHE or UKHSA.

Conflict of interest. None.

Data availability statement. The data that support the findings of this study are available at Wellcome Sanger Institute COVID–19 Genomic Surveillance (https://covid19.sanger.ac.uk/lineages/raw).

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Appendix: The COVID-19 Genomics UK (COG-UK) Consortium

Funding acquisition, Leadership and supervision, Metadata curation, Project administration, Samples and logistics, Sequencing and analysis, Software and analysis tools, and Visualisation:
Samuel C Robson [13, 84]

Funding acquisition, Leadership and supervision, Metadata curation, Project administration, Samples and logistics, Sequencing and analysis, and Software and analysis tools:
Thomas R Connor [11, 74] and Nicholas J Loman [43]

Leadership and supervision, Metadata curation, Project administration, Samples and logistics, Sequencing and analysis, Software and analysis tools, and Visualisation:
Tanya Golubchik [5]

Funding acquisition, Leadership and supervision, Metadata curation, Samples and logistics, Sequencing and analysis, and Visualisation:
Rocio T Martinez Nunez [46]

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Andrew Rambaut [104]

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https://doi.org/10.1017/S0950268822001285 Published online by Cambridge University Press

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https://doi.org/10.1017/S0950268822001285 Published online by Cambridge University Press

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Tanya Curran [3], Sian Morgan [10], Patrick Maxwell [20], Ken Smith [20], Sahar Eldirdiri [21], Anita Kenyon [21], Alison H Holmes [38, 57], James R Price [38, 57], Tim Wyatt [69], Alison E Mather [75], Timofey Skvortsov [77] and John A Hartley [96]

Metadata curation:
Martyn Guest [11], Christine Kitchen [11], Ian Merrick [11], Robert Munn [11], Beatrice Bertolusso [33], Jessica Lynch [33], Gabrielle Vernet [33], Stuart Kirk [34], Elizabeth Wastnedge [56], Rachael Stanley [58], Giles Idle [64], Declan T Bradley [69, 77], Jennifer Poyner [79] and Matilde Mori [110]

Project administration:
Owen Jones [11], Victoria Wright [18], Ellena Brooks [20], Carol M Churcher [20], Mireille Fragakis [20], Katerina Galai [20, 70], Andrew Jermy [20], Sarah Judges [20], Georgina M McManus [20], Kim S Smith [20], Elaine Westwick [20], Stephen W Attwood [23], Frances Bolt [38, 57], Alisha Davies [74], Elen De Lacy [74], Fatima Downing [74], Sue Edwards [74], Lizzie Meadows [75], Sarah Jeremiah [97], Nikki Smith [109] and Luke Foulser [116]

Samples and logistics:
Themoula Charalampous [12, 46], Amita Patel [12], Louise Berry [15], Tim Boswell [15], Vicki M Fleming [15], Hannah C Howson-Wells [15], Amelia Joseph [15], Manjinder Khakh [15], Michelle M Lister [15], Paul W Bird [16], Karlie Fallon [16], Thomas Helmer [16], Claire L McMurray [16], Mina Odedra [16], Jessica Shaw [16], Julian W Tang [16], Nicholas J Willford [16], Victoria Blakey [17], Veena Raviprakash [17], Nicola Sheriff [17], Lesley-Anne Williams [17], Theresa Feltwell [20], Luke Bedford [26], James S Cargill [27], Warwick Hughes [27], Jonathan Moore [28], Susanne Stonehouse [28], Laura Atkinson [29], Jack CD Lee [29], Dr Divya Shah [29], Adela Alcolea-Medina [32, 112], Natasha Ohemeng-Kumi [32, 112], John Ramble [32, 112], Jasveen Sehmi [32, 112], Rebecca Williams [33], Wendy Chatterton [34], Monika Pusok [34], William Everson [37], Anibolina Castigador [44], Emily Macnaughton [44], Kate El Bouzidi [45], Temi Lampejo [45], Malur Sudhanva [45], Cassie Breen [47], Graciela Sluga [48], Shazaad SY Ahmad [49, 70], Ryan P George [49], Nicholas W Machin [49, 70], Debbie Binns [50], Victoria James [50], Rachel Blacow [55], Lindsay Coupland [58], Louise Smith [59], Edward Barton [60], Debra Padgett [60], Garren Scott [60], Aidan Cross [61], Mariyam Mirfenderesky [61], Jane Greenaway [62], Kevin Cole [64], Phillip Clarke [67], Nichola Duckworth [67], Sarah Walsh [67], Kelly Bicknell [68], Robert Impey [68], Sarah Wyllie [68], Richard Hopes [70], Chloe Bishop [72], Vicki Chalker [72], Ian Harrison [72], Laura Gifford [74], Zoltan Molnar [77], Cressida Auckland [79], Cariad Evans [85, 109], Kate Johnson [85, 109], David G Partridge [85, 109], Mohammad Raza [85, 109], Paul Baker [86], Stephen Bonner [86], Sarah Essex [86], Leanne J Murray [86], Andrew I Lawton [87], Shirelle Burton-Fanning [89], Brendan AI Payne [89], Sheila Waugh [89], Andrea N Gomes [91], Maimuna Kimuli [91], Darren R Murray [91], Paula Ashfield [92], Donald Dobie [92], Fiona Ashford [93], Angus Best [93], Liam Crawford [93], Nicola Cumley [93], Megan Mayhew [93], Oliver Megram [93], Jeremy Mirza [93], Emma Moles-Garcia [93], Benita Percival [93], Megan Driscoll [96], Leah Ensell [96], Helen L Lowe [96], Laurentiu Maftei [96], Matteo Mondani [96], Nicola J Chaloner [99], Benjamin J Cogger [99], Lisa J Easton [99], Hannah Huckson [99], Jonathan Lewis [99], Sarah Lowdon [99], Cassandra S Malone [99], Florence Munemo [99], Manasa Mutingwende [99], Roberto Nicodemi [99], Olga Podplomyk [99], Thomas Somassa [99], Andrew Beggs [100], Alex Richter [100], Claire Cormie [102], Joana Dias [102], Sally Forrest [102], Ellen E Higginson [102], Mailis Maes [102], Jamie Young [102], Rose K Davidson [103], Kathryn A Jackson [107], Lance Turtle [107], Alexander J Keeley [109], Jonathan Ball [113], Timothy Byaruhanga [113], Joseph G Chappell [113], Jayasree Dey [113], Jack D Hill [113], Emily J Park [113], Arezou Fanaie [114], Rachel A Hilson [114], Geraldine Yaze [114] and Stephanie Lo [116]

Sequencing and analysis:
Safiah Afifi [10], Robert Beer [10], Joshua Maksimovic [10], Kathryn McCluggage [10], Karla Spellman [10], Catherine Bresner [11], William Fuller [11], Angela Marchbank [11], Trudy Workman [11], Ekaterina Shelest [13, 81], Johnny Debebe [18], Fei Sang [18], Marina Escalera Zamudio [23], Sarah Francois [23], Bernardo Gutierrez [23], Tetyana I Vasylyeva [23], Flavia Flaviani [31], Manon Ragonnet-Cronin [39], Katherine L Smollett [42], Alice Broos [53], Daniel Mair [53], Jenna Nichols [53], Kyriaki Nomikou [53], Lily Tong [53], Ioulia Tsatsani [53], Sarah O'Brien [54], Steven Rushton [54], Roy Sanderson [54], Jon Perkins [55], Seb Cotton [56], Abbie Gallagher [56], Elias Allara [70, 102], Clare Pearson [70, 102], David Bibby [72], Gavin Dabrera [72], Nicholas Ellaby [72], Eileen Gallagher [72], Jonathan Hubb [72], Angie Lackenby [72], David Lee [72], Nikos Manesis [72], Tamyo Mbisa [72], Steven Platt [72], Katherine A Twohig [72], Mari Morgan [74], Alp Aydin [75], David J Baker [75], Ebenezer Foster-Nyarko [75], Sophie J Prosolek [75], Steven Rudder [75], Chris Baxter [77], Sílvia F Carvalho [77], Deborah Lavin [77], Arun Mariappan [77], Clara Radulescu [77], Aditi Singh [77], Miao Tang [77], Helen Morcrette [79], Nadua Bayzid [96], Marius Cotic [96], Carlos E Balcazar [104], Michael D Gallagher [104], Daniel Maloney [104], Thomas D Stanton [104], Kathleen A Williamson [104], Robin Manley [105], Michelle L Michelsen [105], Christine M Sambles [105], David J Studholme [105], Joanna Warwick-Dugdale [105], Richard Eccles [107], Matthew Gemmell [107], Richard Gregory [107], Margaret Hughes [107], Charlotte Nelson [107], Lucille Rainbow [107], Edith E Vamos [107], Hermione J Webster [107], Mark Whitehead [107], Claudia Wierzbicki [107], Adrienn Angyal [109], Luke R Green [109], Max Whiteley [109], Emma Betteridge [116], Iraad F Bronner [116], Ben W Farr [116], Scott Goodwin [116], Stefanie V Lensing [116], Shane A McCarthy [116, 102], Michael A Quail [116], Diana Rajan [116], Nicholas M Redshaw [116], Carol Scott [116], Lesley Shirley [116] and Scott AJ Thurston [116]

Software and analysis tools:
Will Rowe [43], Amy Gaskin [74], Thanh Le-Viet [75], James Bonfield [116], Jennifier Liddle [116] and Andrew Whitwham [116]

1 Barking, Havering and Redbridge University Hospitals NHS Trust, **2** Barts Health NHS Trust, **3** Belfast Health & Social Care Trust, **4** Betsi Cadwaladr University Health Board, **5** Big Data Institute, Nuffield Department of Medicine, University of Oxford, **6** Blackpool Teaching Hospitals NHS Foundation Trust, **7** Bournemouth University, **8** Cambridge Stem Cell Institute, University of Cambridge, **9** Cambridge University Hospitals NHS Foundation Trust, **10** Cardiff and Vale University Health Board, **11** Cardiff University, **12** Centre for Clinical Infection and Diagnostics Research, Department of Infectious Diseases, Guy's and St Thomas' NHS Foundation Trust, **13** Centre for Enzyme Innovation, University of Portsmouth, **14** Centre for Genomic Pathogen Surveillance, University of Oxford, **15** Clinical Microbiology Department, Queens Medical Centre, Nottingham University Hospitals NHS Trust, **16** Clinical Microbiology, University Hospitals of Leicester NHS Trust, **17** County Durham and Darlington NHS Foundation Trust, **18** Deep Seq, School of Life Sciences, Queens Medical Centre, University of Nottingham, **19** Department of Infectious Diseases and Microbiology, Cambridge University Hospitals NHS Foundation Trust, **20** Department of Medicine, University of Cambridge, **21** Department of Microbiology, Kettering General Hospital, **22** Department of Microbiology, South West London Pathology, **23** Department of Zoology, University of Oxford, **24** Division of Virology, Department of Pathology, University of Cambridge, **25** East Kent Hospitals University NHS Foundation Trust, **26** East Suffolk and North Essex NHS Foundation Trust, **27** East Sussex Healthcare NHS Trust, **28** Gateshead Health NHS Foundation Trust, **29** Great Ormond Street Hospital for Children NHS Foundation Trust, **30** Great Ormond Street Institute of Child Health (GOS ICH), University College London (UCL), **31** Guy's and St. Thomas' Biomedical Research Centre, **32** Guy's and St. Thomas' NHS Foundation Trust, **33** Hampshire Hospitals NHS Foundation Trust, **34** Health Services Laboratories, **35** Heartlands Hospital, Birmingham, **36** Hub for Biotechnology in the Built Environment, Northumbria University, **37** Hull University Teaching Hospitals NHS Trust, **38** Imperial College Healthcare NHS Trust, **39** Imperial College London, **40** Infection Care Group, St George's University Hospitals NHS Foundation Trust, **41** Institute for Infection and Immunity, St George's University of London, **42** Institute of Biodiversity, Animal Health & Comparative Medicine, **43** Institute of Microbiology and Infection, University of Birmingham, **44** Isle of Wight NHS Trust, **45** King's College Hospital NHS Foundation Trust, **46** King's College London, **47** Liverpool Clinical Laboratories, **48** Maidstone and Tunbridge Wells NHS Trust, **49** Manchester University NHS Foundation Trust, **50** Microbiology Department, Buckinghamshire Healthcare NHS Trust, **51** Microbiology, Royal Oldham Hospital, **52** MRC Biostatistics Unit, University of Cambridge, **53** MRC-University of Glasgow Centre for Virus Research, **54** Newcastle University, **55** NHS Greater Glasgow and Clyde, **56** NHS Lothian, **57** NIHR Health Protection Research Unit in HCAI and AMR, Imperial

https://doi.org/10.1017/S0950268822001285 Published online by Cambridge University Press

College London, **58** Norfolk and Norwich University Hospitals NHS Foundation Trust, **59** Norfolk County Council, **60** North Cumbria Integrated Care NHS Foundation Trust, **61** North Middlesex University Hospital NHS Trust, **62** North Tees and Hartlepool NHS Foundation Trust, **63** North West London Pathology, **64** Northumbria Healthcare NHS Foundation Trust, **65** Northumbria University, **66** NU-OMICS, Northumbria University, **67** Path Links, Northern Lincolnshire and Goole NHS Foundation Trust, **68** Portsmouth Hospitals University NHS Trust, **69** Public Health Agency, Northern Ireland, **70** Public Health England, **71** Public Health England, Cambridge, **72** Public Health England, Colindale, **73** Public Health Scotland, **74** Public Health Wales, **75** Quadram Institute Bioscience, **76** Queen Elizabeth Hospital, Birmingham, **77** Queen's University Belfast, **78** Royal Brompton and Harefield Hospitals, **79** Royal Devon and Exeter NHS Foundation Trust, **80** Royal Free London NHS Foundation Trust, **81** School of Biological Sciences, University of Portsmouth, **82** School of Health Sciences, University of Southampton, **83** School of Medicine, University of Southampton, **84** School of Pharmacy & Biomedical Sciences, University of Portsmouth, **85** Sheffield Teaching Hospitals NHS Foundation Trust, **86** South Tees Hospitals NHS Foundation Trust, **87** Southwest Pathology Services, **88** Swansea University, **89** The Newcastle upon Tyne Hospitals NHS Foundation Trust, **90** The Queen Elizabeth Hospital King's Lynn NHS Foundation Trust, **91** The Royal Marsden NHS Foundation Trust, **92** The Royal Wolverhampton NHS Trust, **93** Turnkey Laboratory, University of Birmingham, **94** University College London Division of Infection and Immunity, **95** University College London Hospital Advanced Pathogen Diagnostics Unit, **96** University College London Hospitals NHS Foundation Trust, **97** University Hospital Southampton NHS Foundation Trust, **98** University Hospitals Dorset NHS Foundation Trust, **99** University Hospitals Sussex NHS Foundation Trust, **100** University of Birmingham, **101** University of Brighton, **102** University of Cambridge, **103** University of East Anglia, **104** University of Edinburgh, **105** University of Exeter, **106** University of Kent, **107** University of Liverpool, **108** University of Oxford, **109** University of Sheffield, **110** University of Southampton, **111** University of St Andrews, **112** Viapath, Guy's and St Thomas' NHS Foundation Trust, and King's College Hospital NHS Foundation Trust, **113** Virology, School of Life Sciences, Queens Medical Centre, University of Nottingham, **114** Watford General Hospital, **115** Wellcome Centre for Human Genetics, Nuffield Department of Medicine, University of Oxford, **116** Wellcome Sanger Institute, **117** West of Scotland Specialist Virology Centre, NHS Greater Glasgow and Clyde, **118** Whittington Health NHS Trust.

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