Report: Continued spread of VOC 202012/01 in England
31 December 2020

An update to:

**Estimated transmissibility and severity
of novel SARS-CoV-2 Variant of Concern 202012/01 in England**

23 December 2020

Nicholas G. Davies[1], Rosanna C. Barnard*, Christopher I. Jarvis*, Adam J. Kucharski*, James Munday*, Carl A. B. Pearson*, Timothy W. Russell*, Damien C. Tully*, Sam Abbott, Amy Gimma, William Waites, Kerry LM Wong, Kevin van Zandvoort, CMMID COVID-19 Working Group, Rosalind M. Eggo, Sebastian Funk, Mark Jit, Katherine E. Atkins, W. John Edmunds

Centre for Mathematical Modelling of Infectious Diseases
London School of Hygiene and Tropical Medicine
Keppel St, London, WC1E 7HT
United Kingdom

[1] Corresponding author
* Equal contribution

We present a brief update to our analysis of 23 December 2020 below.

1. Spread of VOC 202012/01 in England

As of our previous report from 23rd December 2020[1], the latest data from COG-UK[2] showed VOC 202012/01 at moderate frequencies (20–60%) in the South East, London, and East of England NHS regions. Updated data from COG-UK, as well as Pillar 2 testing data from Public Health England, now show that the frequency of the variant has grown substantially in all regions of England. Because of Δ69/Δ70 deletions in spike for VOC 202012/01, the Thermo Fisher TaqPath testing kit does not detect the spike gene in samples of this variant (S gene target failure, SGTF). For labs processing NHS Pillar 2 testing data with this testing kit, SGTF can be used as a proxy for detecting VOC 202012/01[3]. A comparison of the growth of VOC 202012/01 in all 7 NHS England regions, using both COG-UK data and Pillar 2 testing SGTF, is shown in **Fig. U1A**.
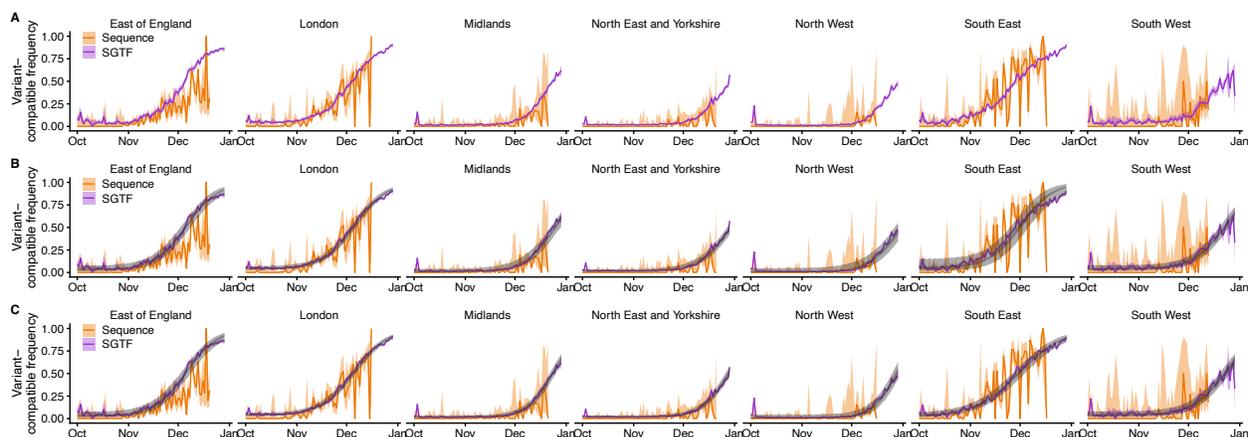

Fig. U1. Spread of VOC 202012/01 in all regions of England. (A) Relative frequency of VOC 202012/01 from COG-UK sequence data, and of S gene target failure from Pillar 2 testing data, in NHS regions of England. (B) Overlaid with logistic beta-binomial model (grey) assuming the same growth rate across all regions. (C) Overlaid with logistic beta-binomial model (grey) assuming different growth rates across regions. Mean and 95% credible intervals shown.

---

[1] Davies et al., 2020. Estimated transmissibility and severity of novel SARS-CoV-2 Variant of Concern 202012/01 in England. *MedRxiv* https://www.medrxiv.org/content/10.1101/2020.12.24.20248822v1, also https://cmmid.github.io/topics/covid19/uk-novel-variant.html.

[2] Covid-19 Genomics UK Consortium. https://www.cogconsortium.uk/data/

[3] Public Health England, 2020. *Investigation of novel SARS-COV-2 variant Variant of Concern 202012/01.* https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/947048/Technical_Briefing_VOC_SH_NJL2_SH2.pdf

We fitted models of logistic growth accounting for false positives (modelled as regionally-varying background rates of SGTF associated with non-VOC 202012/01 variants) to the SGTF data in Fig. U1A. Two versions of the model were used, one with the same growth rate of VOC 202012/01 across all NHS regions (**Fig. U1B, Table U1**) and one with different growth rates for each NHS region (**Fig. U1C, Table U2**).

2. Spatial patterns of VOC 202012/01

To visualize patterns of the spread of VOC 202012/01, we show the frequency of S gene target failure (SGTF) by upper-tier local authority in **Fig. U2.** Two fairly distinct growth phases are seen, one in the south-east of England and one in rest of England (**Fig. U3**).
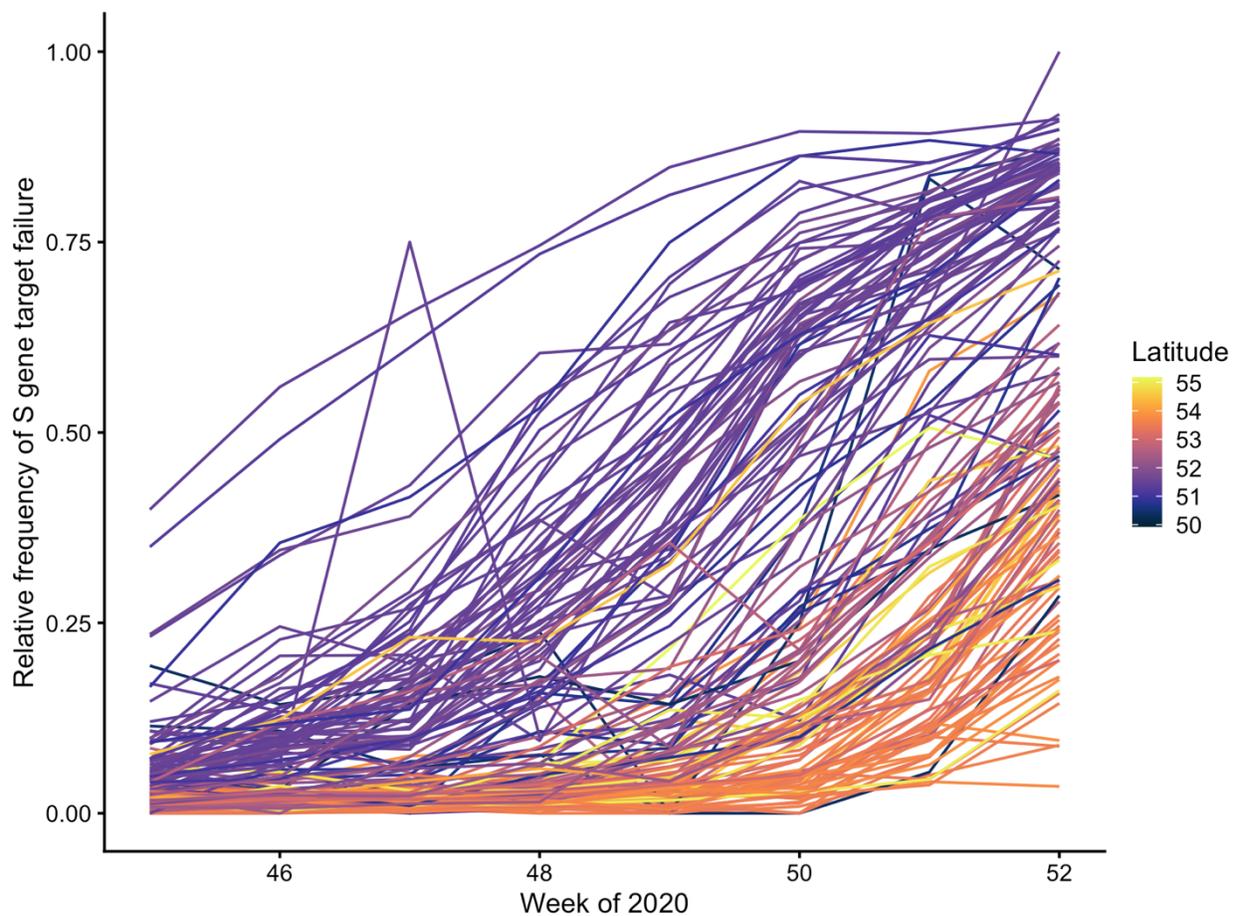

Fig. U2. Growth of VOC 202012/01, as indicated by the proxy of S gene target failure in Pillar 2 SARS-CoV-2 tests across upper-tier local authorities in England. Lines are shaded according to the latitude of each local authority. Two phases of growth are seen, with the frequency of VOC 202012/01 rising in southern regions of England first (darker lines) followed by northern regions (lighter lines).
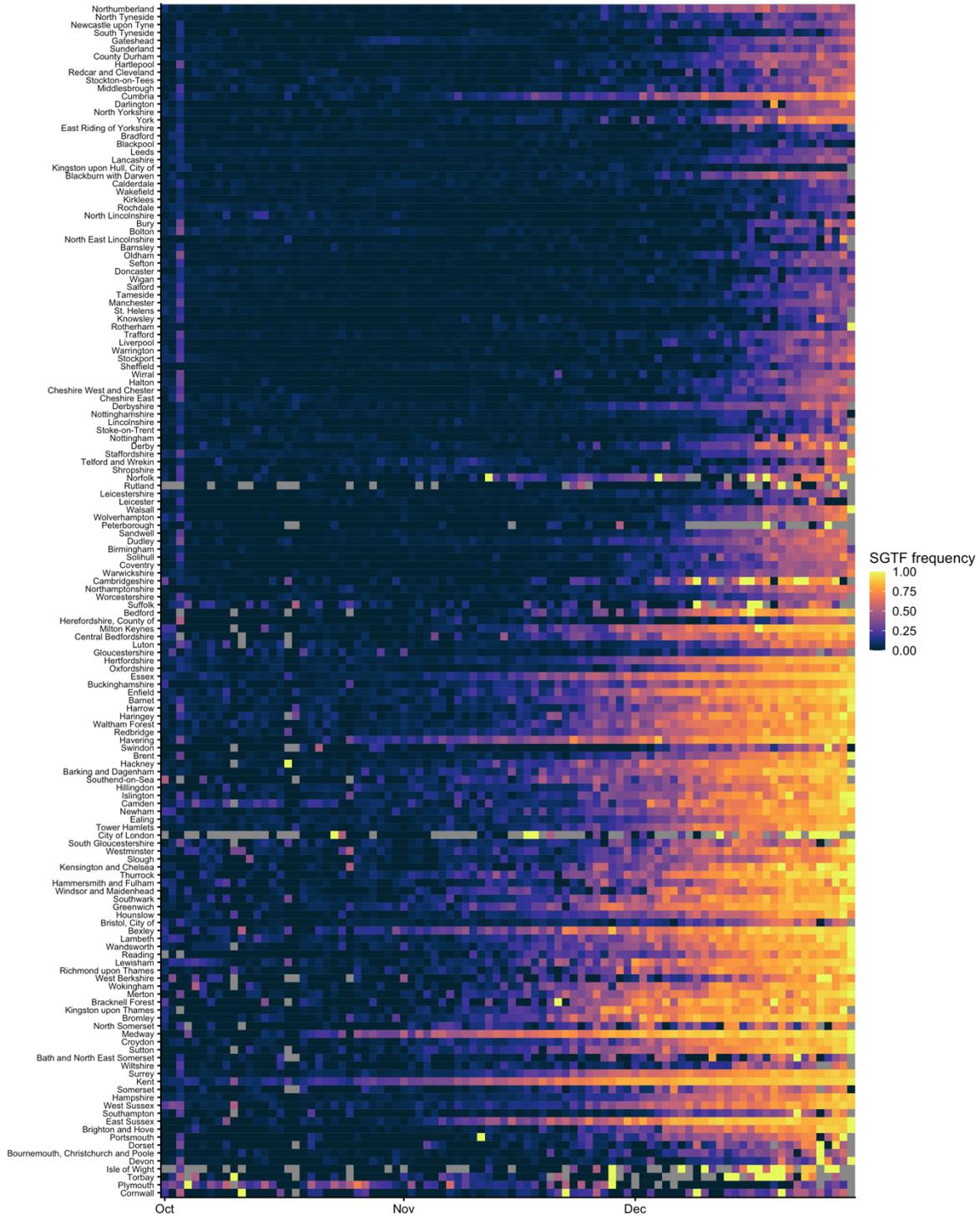
Fig. U3. Growth of VOC 202012/01, as indicated by the proxy of S gene target failure in Pillar 2 SARS-CoV-2 tests across upper-tier local authorities in England. Local authorities are arranged from north to south (top to bottom in the plot). The early emergence of VOC 202012/01 in Kent is seen, followed by rapid dissemination throughout south-east England, reaching local authorities in the north of England later.

Discussion

The continued rapid spread of VOC 202012/01 in England to high frequencies (50% or greater in all NHS regions as of 29 December 2020) makes it less likely that the spread of this variant is due to a founder effect or an otherwise selectively neutral effect. The spread of this variant is now apparent from both sequencing data from COG-UK and S gene target failure data from Pillar 2 testing (**Fig U1**). There is a pattern of spread in two distinct phases, involving south-east England followed by the north of England (**Fig U2, U3**). We will continue to update our analyses, and will make a new estimation of the relative severity and transmissibility of VOC 202012/01 in the coming week.

Methods and tables

Our logistic beta-binomial model of VOC 202012/01 growth is as follows:

$$slope \sim normal(mean = 0, sd = 1)$$
$$intercept \sim normal(mean = 0, sd = 1000)$$
$$falsepos \sim beta(\alpha = 1.5, \beta = 15)$$
$$conc \sim normal(mean = 0, sd = 500) \geq 2$$

$$f(t) = \frac{\exp[slope \times (t - intercept)]}{1 + \exp[slope \times (t - intercept)]}$$
$$s(t) = f(t) + \big(1 - f(t)\big) \times falsepos$$

$$k_t \sim beta\text{–}binomial(n = n_t, \alpha = s(t) \times (conc - 2) + 1, \beta = (1 - s(t)) \times (conc - 2) + 1)$$

Here, *f*(*t*) is the model-predicted frequency of VOC 202012/01 at time *t* based on the terms *slope* and *intercept*, *s*(*t*) is the model-predicted frequency of S gene target failure at time *t* owing to a background false positive rate *falsepos*, *conc* is the "concentration" parameter ($= \alpha + \beta$) of a beta distribution with mode *s*(*t*), k_t is the number of S gene target failures detected at time *t* and n_t is the total number of tests at time *t*. We either fit the models simultaneously with the same *slope* parameter across all NHS regions but different *intercept*, *falsepos* and *conc* parameters for each NHS region (**Fig. U1B, Table U1**), or with all parameters completely independent for each NHS region (**Fig. U1C, Table U2**).

Table U1. Model posteriors (median and 95% CrI), shared slope.

NHS region	Relative growth rate	Intercept (f_VOC = 50%)	SGTF false positive rate	Data precision
East of England	0.104 (0.102 - 0.107)	06 Dec (05 Dec - 06 Dec)	0.0329 (0.0275 - 0.0384)	174 (126 - 236)
London	0.104 (0.102 - 0.107)	05 Dec (05 Dec - 06 Dec)	0.0434 (0.0396 - 0.0472)	456 (311 - 652)
Midlands	0.104 (0.102 - 0.107)	25 Dec (25 Dec - 26 Dec)	0.0104 (0.00764 - 0.0129)	174 (129 - 227)
North East & Yorkshire	0.104 (0.102 - 0.107)	30 Dec (29 Dec - 30 Dec)	0.0152 (0.0132 - 0.0171)	296 (225 - 384)
North West	0.104 (0.102 - 0.107)	31 Dec (30 Dec - 01 Jan)	0.00454 (0.00185 - 0.00731)	95.7 (72.6 - 123)
South East	0.104 (0.102 - 0.107)	01 Dec (30 Nov - 02 Dec)	0.0523 (0.0412 - 0.0631)	57.8 (44.4 - 77.3)
South West	0.104 (0.102 - 0.107)	23 Dec (22 Dec - 24 Dec)	0.0404 (0.0356 - 0.0453)	196 (129 - 303)

Table U2. Model posteriors (median and 95% CrI), independent slopes.

NHS region	Relative growth rate	Intercept (f_VOC = 50%)	SGTF false positive rate	Data precision
East of England	0.104 (0.0988 - 0.109)	05 Dec (05 Dec - 06 Dec)	0.0318 (0.0254 - 0.039)	171 (122 - 244)
London	0.0983 (0.0957 - 0.101)	05 Dec (05 Dec - 05 Dec)	0.0393 (0.0356 - 0.0431)	580 (405 - 807)
Midlands	0.13 (0.124 - 0.137)	24 Dec (23 Dec - 24 Dec)	0.0153 (0.0134 - 0.0172)	324 (234 - 433)
North East & Yorkshire	0.123 (0.118 - 0.129)	28 Dec (27 Dec - 29 Dec)	0.018 (0.0162 - 0.0198)	400 (297 - 537)
North West	0.138 (0.129 - 0.15)	28 Dec (27 Dec - 29 Dec)	0.0093 (0.00656 - 0.0115)	134 (101 - 173)
South East	0.0752 (0.0724 - 0.0782)	30 Nov (30 Nov - 01 Dec)	0.0239 (0.0157 - 0.0328)	223 (157 - 302)
South West	0.1 (0.0926 - 0.109)	23 Dec (22 Dec - 24 Dec)	0.0391 (0.0333 - 0.0443)	193 (126 - 280)