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


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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.

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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:

\[
\text{slope} \sim \text{normal}(\text{mean} = 0, \text{sd} = 1) \\
\text{intercept} \sim \text{normal}(\text{mean} = 0, \text{sd} = 1000) \\
\text{falsepos} \sim \text{beta}(\alpha = 1.5, \beta = 15) \\
\text{conc} \sim \text{normal}(\text{mean} = 0, \text{sd} = 500) \geq 2
\]

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

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

Here, \(f(t)\) is the model-predicted frequency of VOC 202012/01 at time \(t\) based on the terms \(\text{slope}\) and \(\text{intercept}\), \(s(t)\) is the model-predicted frequency of S gene target failure at time \(t\) owing to a background false positive rate \(\text{falsepos}\), \(\text{conc}\) 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 \(\text{slope}\) parameter across all NHS regions but different \(\text{intercept}\), \(\text{falsepos}\) and \(\text{conc}\) 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.

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

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

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