

# Characteristics of SARS-CoV-2 variants of concern B.1.1.7, B.1.351 or P.1: data from seven EU/EEA countries, weeks 38/2020 to 10/2021

Tjede Funk<sup>1</sup>, Anastasia Pharris<sup>1</sup>, Gianfranco Spiteri<sup>1</sup>, Nick Bundle<sup>1</sup>, Angeliki Melidou<sup>1</sup>, Michael Carr<sup>2,3</sup>, Gabriel Gonzalez<sup>2,3</sup>, Alejandro Garcia-Leon<sup>4</sup>, Fiona Crispie<sup>5</sup>, Lois O'Connor<sup>6</sup>, Niamh Murphy<sup>6</sup>, Joël Mossong<sup>7</sup>, Anne Vergison<sup>7</sup>, Anke K. Wienecke-Baldacchino<sup>8</sup>, Tamir Abdelrahman<sup>8</sup>, Flavia Riccardo<sup>9</sup>, Paola Stefanelli<sup>9</sup>, Angela Di Martino<sup>9</sup>, Antonino Bella<sup>9</sup>, Alessandra Lo Presti<sup>9</sup>, Pedro Casaca<sup>10</sup>, Joana Moreno<sup>10</sup>, Vítor Borges<sup>11</sup>, Joana Isidro<sup>11</sup>, Rita Ferreira<sup>11</sup>, João Paulo Gomes<sup>11</sup>, Liidia Dotsenko<sup>12</sup>, Heleene Suija<sup>12</sup>, Jevgenia Epstein<sup>12</sup>, Olga Sadikova<sup>12</sup>, Hanna Sepp<sup>12</sup>, Niina Ikonen<sup>13</sup>, Carita Savolainen-Kopra<sup>13</sup>, Soile Blomqvist<sup>13</sup>, Teemu Möttönen<sup>13</sup>, Otto Helve<sup>13</sup>, Joana Gomes-Dias<sup>1</sup>, Cornelia Adlhoch<sup>1</sup>, on behalf of COVID study groups<sup>14</sup>

1. European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
2. National Virus Reference Laboratory (NVRL), University College Dublin, Dublin, Ireland
3. International Collaboration Unit, Research Center for Zoonosis Control, Hokkaido University, Sapporo, Japan
4. Centre for Experimental Pathogen Host Research, University College Dublin, Dublin, Ireland on behalf of the All Ireland Infectious Diseases (AIID) Cohort
5. Teagasc Food Research Centre, Moorepark, Fermoy, Ireland on behalf of the Irish Coronavirus Sequencing Consortium (ICSC)
6. Health Service Executive - Health Protection Surveillance Centre (HPSC), Dublin, Ireland
7. Health Directorate, Findel, Luxembourg
8. National Health Laboratory, Dudelange, Luxembourg
9. Istituto Superiore di Sanità, Rome, Italy
10. Directorate of Analysis and Information, Directorate-General of Health, Lisbon, Portugal
11. Bioinformatics Unit, Infectious Diseases Department, National Institute of Health Dr. Ricardo Jorge, Lisbon, Portugal
12. Health Board, Tallinn, Estonia
13. Finnish Institute for Health and Welfare (THL), Department of Health Security, Helsinki, Finland
14. The COVID study groups are listed at the end of this article under Acknowledgements

**Correspondence:** Cornelia Adlhoch (cornelia.adlhoch@ecdc.europa.eu)

## Citation style for this article:

Funk Tjede, Pharris Anastasia, Spiteri Gianfranco, Bundle Nick, Melidou Angeliki, Carr Michael, Gonzalez Gabriel, Garcia-Leon Alejandro, Crispie Fiona, O'Connor Lois, Murphy Niamh, Mossong Joël, Vergison Anne, Wienecke-Baldacchino Anke K., Abdelrahman Tamir, Riccardo Flavia, Stefanelli Paola, Di Martino Angela, Bella Antonino, Lo Presti Alessandra, Casaca Pedro, Moreno Joana, Borges Vítor, Isidro Joana, Ferreira Rita, Gomes João Paulo, Dotsenko Liidia, Suija Heleene, Epstein Jevgenia, Sadikova Olga, Sepp Hanna, Ikonen Niina, Savolainen-Kopra Carita, Blomqvist Soile, Möttönen Teemu, Helve Otto, Gomes-Dias Joana, Adlhoch Cornelia, on behalf of COVID study groups. Characteristics of SARS-CoV-2 variants of concern B.1.1.7, B.1.351 or P.1: data from seven EU/EEA countries, weeks 38/2020 to 10/2021. *Euro Surveill.* 2021;26(16):pii=2100348. <https://doi.org/10.2807/1560-7917.ES.2021.26.16.2100348>

Article submitted on 23 Mar 2021 / accepted on 21 Apr 2021 / published on 22 Apr 2021

**We compared 19,207 cases of SARS-CoV-2 variant B.1.1.7/S gene target failure (SGTF), 436 B.1.351 and 352 P.1 to non-variant cases reported by seven European countries. COVID-19 cases with these variants had significantly higher adjusted odds ratios for hospitalisation (B.1.1.7/SGTF: 1.7, 95% confidence interval (CI): 1.0–2.9; B.1.351: 3.6, 95% CI: 2.1–6.2; P.1: 2.6, 95% CI: 1.4–4.8) and B.1.1.7/SGTF and P.1 cases also for intensive care admission (B.1.1.7/SGTF: 2.3, 95% CI: 1.4–3.5; P.1: 2.2, 95% CI: 1.7–2.8).**

Here, we analyse coronavirus disease (COVID-19) cases infected with any of the three severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants of concern (VOC): B.1.1.7/S gene target failure (SGTF), B.1.351 or P.1. We compare them with cases reported as infected with non-VOC virus with a focus on disease severity.

## SARS-CoV-2 variant viruses

In December 2020, the United Kingdom (UK) reported an emerging SARS-CoV-2 VOC classified as Pangolin lineage B.1.1.7 [1]. In the UK, and shortly thereafter in

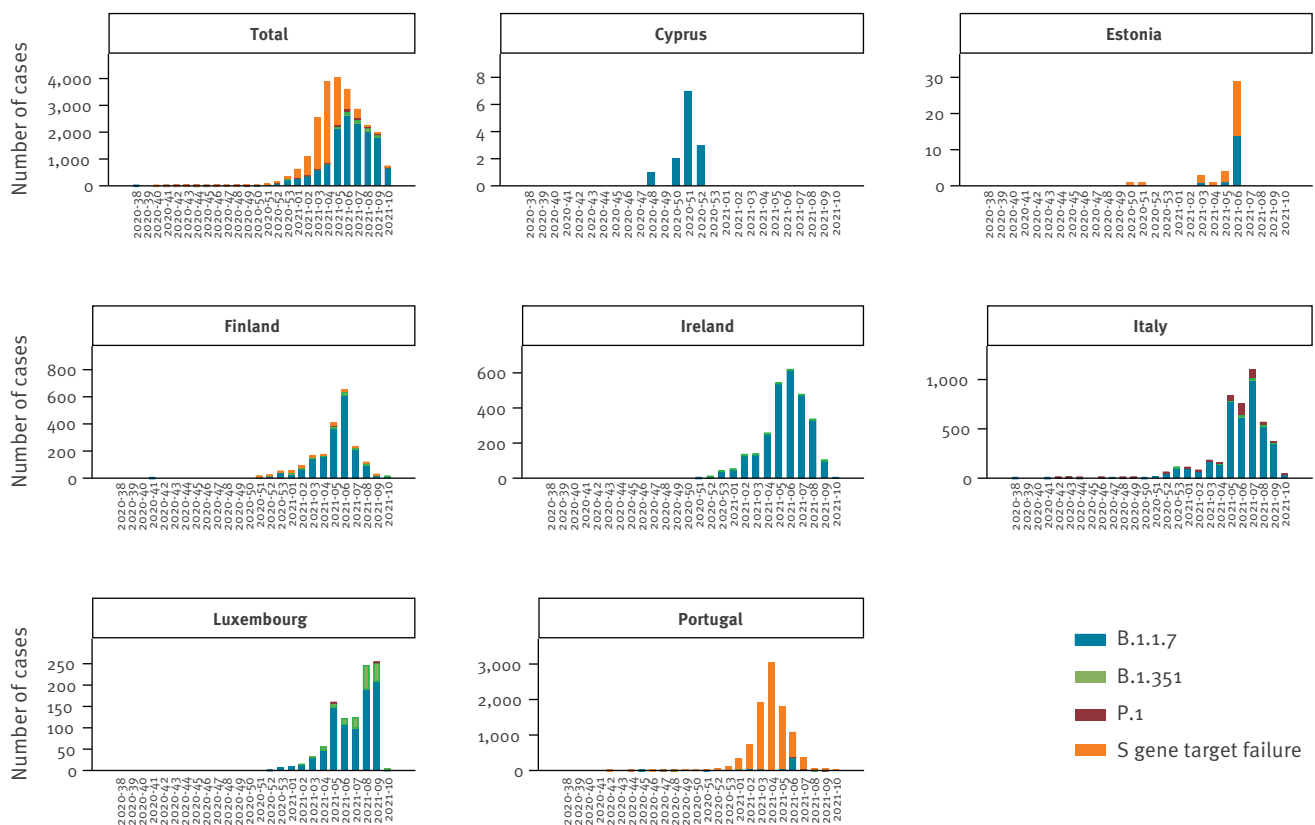
Denmark, B.1.1.7 infections increased rapidly. In parallel to the identification of B.1.1.7, increased whole-genome sequencing (WGS) efforts globally led to the identification of further SARS-CoV-2 VOC, including B.1.351 (described in South Africa) or P.1 (originating in Brazil) [2–6]. While viral evolution is expected and has occurred since the discovery of SARS-CoV-2, these VOC were associated with higher transmissibility and severity as well as altered antigenicity with potential implications for acquired immunity or effectiveness of current vaccines compared with other circulating lineages lacking particular defining mutations such as E484K, N501Y or del69–70 [7–12].

## Reporting of SARS-CoV-2 variants in the EU/EEA

On a weekly basis, countries in the European Union and European Economic Area (EU/EEA) report data on COVID-19 cases to The European Surveillance System (TESSy) hosted at the European Centre for Disease Prevention and Control (ECDC). In response to the emerging VOC, ECDC implemented new reporting variables for variants on 24 December 2020 allowing retrospective data upload (Supplement A). COVID-19 cases

**FIGURE**

Reported SARS-CoV-2 VOC cases, by reporting country and week of reporting, EU/EEA, weeks 38/2020–10/2021 (n = 23,343)



EEA: European Economic Area; EU: European Union; SARS-CoV-2: severe acute respiratory syndrome coronavirus 2; VOC: Variant of concern.

that do not have the VOC-defining mutations should be reported as non-VOC because of the complexity of the taxonomy of SARS-CoV-2. However, countries sequence only a minor proportion of all SARS-CoV-2 positive specimens (Supplement A, Figures S1 and S2 [6]).

We analysed data on COVID-19 cases infected with SARS-CoV-2 VOC (below referred to as B.1.1.7/SGTF, B.1.351 and P.1 cases) reported to TESSy for weeks 38/2020 to 10/2021 by seven countries (Cyprus, Estonia, Finland, Ireland, Italy, Luxembourg and Portugal) (Figure). Data included information on sex, age, clinical symptoms, pre-existing conditions, hospital and intensive care unit (ICU) admission and outcome (i.e. survived or died). The spike (S) gene deletion (del 69–70) is present in multiple lineages including B.1.1.7 and has been used for rapid screening using qRT-PCR (SGTF) because of a strong correlation between B.1.1.7 cases and SGTF [13,14]. Portugal showed a > 90% correlation between SGTF and B.1.1.7 cases and almost all (98%) of the SGTF cases included in this analysis came from Portugal (Figure). We therefore considered all SGTF cases as B.1.1.7 in our analysis [15].

We compared VOC cases caused by variants B.1.1.7/SGTF, B.1.351 or P.1 to non-VOC cases which derived from the same surveillance system (Supplement A).

Cases reported with missing or unknown information on the virus variant were excluded because an increasing number of VOC cases with missing confirmation would be included in this group and introduce a bias when used as a reference category (Supplement A, Table S1 and Figure S3).

Proportions, medians and means were calculated and compared using chi-squared, rank sum and t-tests with a significance of  $p = 0.05$  using STATA v16.1. Different logistic regression models, 1:1 matched (on 10-year age groups, sex and week of reporting, using conditional logistic regression) and unmatched (adjusted for age, sex, week and country, including having a pre-existing condition and healthcare worker status, using logistic regression), were applied to assess differences in severity (hospitalisation, ICU and death) between VOC (B.1.1.7/SGTF, B.1.351 and P.1) and non-VOC cases.

**Characteristics of SARS-CoV-2 variants of concern**

Of 3.2 million COVID-19 cases reported from the included countries during the study period (Supplements A and B), 23,343 had information on SARS-CoV-2 variants, of which 19,995 were VOC and 3,348 non-VOC cases included in this analysis. Among all cases with information on the variant, B.1.1.7/SGTF was the most

frequently reported VOC (19,207; 82.3%), followed by B.1.351 (436; 1.9%) and P.1 (352; 1.5%) (Table 1). Cases from Portugal accounted for almost half (9,740) of the reported VOC. VOC cases have been increasing since week 51/2020, with lower numbers in weeks 6 to 10 probably caused by reporting delay (Figure). The male to female ratio differed slightly between the variants, ranging from 49% to 54% of male cases ( $p < 0.001$ ) (Table 1).

The proportion of B.1.1.7/SGTF cases in the oldest age group decreased slightly over the reporting weeks (Supplement A, Figure S4). Our analysis showed that the proportion of cases in younger age groups ( $< 60$  years) was similar for VOC and non-VOC cases, with similar mean ages for B.1.1.7/SGTF, B.1.351 and non-VOC but significantly older mean age for P.1 cases (Table 1).

Among the VOC cases with available information, the majority were domestic cases, with 1.5% of B.1.1.7/SGTF and P.1 cases and 8.5% of B.1.351 cases reported as importations, compared with 0.4% of non-VOC cases (Table 1). Healthcare workers were slightly less represented among VOC cases than among non-VOC cases. The exception was P.1 with 19.8% of cases being a healthcare worker (Table 1). No COVID-19 case infected with a VOC was reported as pregnant.

Among the B.1.1.7/SGTF cases, 72.6% (5,365/7,390) were reported symptomatic, fewer than among the non-VOC cases (81.4%; 547/672;  $p < 0.001$ ), which in turn was lower than the proportion of symptomatic B.1.351 cases (90.3%; 28/31;  $p = 0.2$ ; Table 1, Supplement A, Figure S5). Cases of infection with P.1 with available information on this variable were too rare to allow a comparison with the other groups. The proportion of cases who reported any pre-existing condition was significantly lower among B.1.1.7/SGTF, B.1.351 and P.1 than among non-VOC cases ( $p < 0.001$ ; Table 1). The lower likelihood of having pre-existing conditions was confirmed in the matched analysis for all VOC cases, with an adjusted odds ratio (aOR) of 0.08 (95% confidence interval (CI): 0.07–0.1) for B.1.1.7/SGTF, an aOR of 0.57 (95% CI: 0.38–0.86) for B.1.351 and an aOR of 0.02 (95% CI: 0.01–0.06) for P.1 compared with non-VOC cases.

### Differences in severity between VOC and non-VOC cases

A larger proportion of VOC cases were admitted to hospital (B.1.1.7/SGTF 11.0%; B.1.351 19.3%, and P.1 20.0%;  $p < 0.001$  for all VOC) and ICU (B.1.1.7/SGTF 1.4%,  $p = 0.002$ ; B.1.351 2.3%,  $p = 0.001$  and P.1 2.1%,  $p = 0.005$ ) compared with non-VOC cases (7.5%, hospitalised and 0.6% requiring ICU; Table 1, Supplement A, Figure S6). Of all hospitalisations with any VOC, 58.3% were male (646/1,108), which was comparable to non-VOC cases (55.4% male;  $p = 0.4$ ). Hospitalised B.1.1.7/SGTF cases were significantly younger (mean age: 63 years, median age: 65 years;  $p < 0.001$ ) than non-VOC

(mean: 69 years, median: 75 years) in contrast to B.1.351 (mean and median age: 67 years;  $p = 0.1$ ) and P.1 cases (mean: 71 years, median: 76 years;  $p = 0.7$ ) which were of a similar age as the non-VOC cases.

Both the matched and unmatched multivariable analysis found that B.1.1.7/SGTF, B.1.351 and P.1 cases had significantly higher odds of hospitalisation than non-VOC cases (aOR: 1.6–4.2 (matched) vs 1.7–3.6 (unmatched)) (Table 2). In the unmatched analysis, B.1.1.7/SGTF, B.1.351 or P.1 cases were, respectively, 2.3, 3.3 and 2.2 times more likely to be admitted to ICU than non-VOC cases.

In the age-stratified models, B.1.1.7/SGTF cases in the age groups 20–39 and 40–59 years had, respectively, 3.0 and 2.3 times higher odds of hospitalisation when compared with non-VOC cases, while ICU admission or death did not differ significantly in any age group (Table 3). For B.1.351 cases, we observed 3.5–3.6 times higher odds of hospitalisation for age groups 40–59 and 60–79 years compared with non-VOC cases of the same age. Admission to ICU was significantly more likely for B.1.351 cases (aOR: 8; 95% CI: 3.7–17.3) aged 40–59 years. For P.1 cases, we observed between 3.0 and 13.1 times higher odds of hospitalisation in the age groups 20–39, 40–59 and 60–79 as well as a 2.9–13.9 times higher odds of ICU admission (40–59, 60–79 and  $\geq 80$  age groups).

A total of 184 (2.2%) deaths were reported among VOC cases; B.1.1.7/SGTF ( $n = 155$ ), B.1.351 ( $n = 17$ ), and P.1 cases ( $n = 12$ ; Table 1), ranging in age between 41–99 years. The matched and multivariable analysis did not show increased risk of death.

### Ethical statement

Ethical approval was not required for this study, data are collected through national surveillance.

### Discussion

This analysis outlines the characteristics of SARS-CoV-2 VOC infections in seven EU/EEA countries and suggests a higher risk for hospitalisation, and also for ICU admission in age groups  $< 60$  years for B.1.1.7/SGTF, B.1.351 and P.1. Similarly, Germany reported increased hospitalisation in age groups  $< 60$  years following B.1.1.7 dominance [16]. Earlier, higher infection rates in younger, school-age age groups with subsequent infections across all age groups have been observed in the UK [7,9]. Higher odds of hospitalisation for B.1.1.7 cases have also been reported by Denmark [8], but there is currently a lack of published data on severity for B.1.351 and P.1.

Overall, only a minor proportion of all SARS-CoV-2-positive specimens are sequenced, however, both VOC and non-VOC cases presented in this analysis are derived from the same sampling frame. It is possible that sampling and sequencing were biased towards hospitalised cases, which could lead to an overestimation

TABLE 1

Characteristics of reported SARS-CoV-2 VOC and non-VOC cases, EU/EEA, weeks 38/2020–10/2021 (n = 23,343)

Characteristics	B.1.1.7/SGTF	%	B.1.351	%	P.1	%	non-VOC	%
Total <sup>a</sup>	19,207		436		352		3,348	
<b>Sex</b>								
Female	9,700	50.5	211	48.4	179	50.9	1,541	46
Male	9,506	49.5*	225	51.6	173	49.1	1,807	54
Total <sup>b</sup>	19,206		436		352		3,348	
<b>Age (years)</b>								
Range	0–103		0–109		2–101		0–105	
Median	39		42		46		38	
Mean	39		43		46*		40	
Standard deviation	21		22		25		21	
<b>Age group (years)</b>								
0–19	3,730	19.4	60	13.8	79	22.4	569	17.0
20–39	6,005	31.3	147	33.7	66	18.8	1,195	35.7
40–59	6,151	32.0	139	31.9	107	30.4	986	29.5
60–79	2,538	13.2	62	14.2	58	16.5	390	11.6
≥ 80	783	4.1	28	6.4	42	11.9	208	6.2
Total <sup>b</sup>	19,207		436		352		3,348	
<b>Symptoms</b>								
No	2,025	27.4	3	9.7	2	33.3	125	18.6
Yes	5,365	72.6*	28	90.3	4	66.7	547	81.4
Total <sup>b</sup>	7,390		31		6		672	
<b>Pre-existing condition</b>								
No	10,608	55.2	89	20.4	254	72.2	369	11.0
Yes	8,599	44.8*	347	79.6*	98	27.8*	2,979	89.0
Total <sup>b</sup>	19,207		436		352		3,348	
<b>Hospitalisation</b>								
No	7,855	89.0	309	80.7	272	80.0	2,399	92.5
Yes	966	11.0*	74	19.3*	68	20.0*	195	7.5
Total <sup>b</sup>	8,821		383		340		2,594	
<b>ICU admission</b>								
No	8,593	98.6	380	97.7	332	97.9	2,553	99.4
Yes	121	1.4*	9	2.3*	7	2.1*	16	0.6
Total <sup>b</sup>	8,714		389		339		2,569	
<b>Mortality/outcome</b>								
Alive/ on treatment	7,490	98.0	309	94.8	295	96.1	1,773	96.0
Died	155	2.0*	17	5.2	12	3.9	73	4.0
Total <sup>b</sup>	7,645		326		307		1,846	
<b>Cases imported</b>								
No	6,143	98.5	107	91.5	263	98.5	694	99.6
Yes	93	1.5*	10	8.5*	4	1.5	3	0.4
Total <sup>b</sup>	6,236		117		267		697	
<b>Healthcare worker</b>								
No	11,985	94.3	358	92.7	85	80.2	2,425	92.0
Yes	730	5.7*	28	7.3	21	19.8*	211	8.0
Total <sup>b</sup>	12,715		386		106		2,636	

EEA: European Economic Area; EU: European Union; ICU: intensive care unit; SARS-CoV-2: severe acute respiratory syndrome coronavirus 2; SGTF: S gene target failure; VOC: variant of concern.

<sup>a</sup> Total number of cases included in the analysis.

<sup>b</sup> Total number of cases for whom information was reported.

Totals for all included cases are given on top; totals for the individual characteristics refer to the cases for whom this information was reported.

\*  $p < 0.05$  compared with non-VOC cases (chi-squared or t-test).

**TABLE 2**

Logistic regression for outcome admission to hospital or intensive care unit for cases with SARS-CoV-2 VOC B.1.1.7/SGTF, B.1.351 and P.1 compared with non-VOC cases, EU/EEA, weeks 38/2020–10/2021 (n = 23,342)

VOC	Hospitalisation						Intensive care unit admission						Death					
	Matched			Multivariable			Matched			Multivariable			Matched			Multivariable		
	Cases	aOR <sup>a</sup>	95% CI	Cases	aOR <sup>b</sup>	95% CI	Cases	aOR <sup>a</sup>	95% CI	Cases	aOR <sup>a</sup>	95% CI	Cases	aOR <sup>a</sup>	95% CI	Cases	aOR <sup>b</sup>	95% CI
B.1.1.7/SGTF <sup>c</sup>	300	1.6	1.2–2.3	11,414	1.7	1.0–2.9	48	1.2	0.5–2.6	11,282	2.3	1.4–3.5	64	0.5	0.3–1.1	9,490	0.5	0.3–0.9
B.1.351	112	3.7	1.9–6.9	2,977	3.6	2.1–6.2	12	2.0	0.4–10.9	2,958	3.3	1.9–5.7	30	1.1	0.4–3.2	2,172	1.1	0.4–3.4
P.1	104	4.2	2.1–8.4	2,934	2.6	1.4–4.8	14	6.0	0.7–49.8	2,908	2.2	1.8–2.9		NR		2,153	0.6	0.3–1.0

aOR: adjusted odds ratio; CI: confidence interval; EEA: European Economic Area; EU: European Union; NR: no result; SARS-CoV-2: severe acute respiratory syndrome coronavirus 2; SGTF: S gene target failure; VOC: variant of concern.

<sup>a</sup> Conditional logistic regression of 1:1 matched (age groups at 10-year increments, sex and week of reporting).

<sup>b</sup> Adjusted for age, sex, week of reporting and country.

<sup>c</sup> Excluding one case with missing information on sex.

The columns 'Cases' represent all respective VOC and non-VOC cases included in the analysis.

**TABLE 3A**

Logistic regression for hospital and intensive care unit admission or death for cases with SARS-CoV-2 VOC B.1.1.7/SGTF B.1.351 and P.1 compared with non-VOC cases, EU/EEA, weeks 38/2020–10/2021 (n = 23,343)

VOC and age group	Hospitalisation		ICU admission		Death	
	aOR <sup>a</sup>	95% CI	aOR <sup>a</sup>	95% CI	aOR <sup>a</sup>	95% CI
<b>B.1.1.7/SGTF</b>						
<b>0–19 years</b>	<b>n = 1,860</b>		<b>n = 121</b>		<b>NR</b>	
B.1.1.7/SGTF	1.0	0.4–2.7	1	Omitted		
Pre-existing condition	1.0	0.2–4.3	1	Omitted		
Healthcare worker	1.0	Omitted	1	Omitted		
<b>20–39 years</b>	<b>n = 3,167</b>		<b>n = 2,642</b>		<b>NR</b>	
B.1.1.7/SGTF	3.0*	1.4–6.8	1.0	Omitted		
Pre-existing condition	0.5	0.2–1.6	0.5	0.3–0.8		
Healthcare worker	1.1	0.5–2.7	Not included			
<b>40–59 years</b>	<b>n = 3,017</b>		<b>n = 3,511</b>		<b>n = 2,546</b>	
B.1.1.7/SGTF	2.3*	1.0–5.4	2.1*	1.0–4.7	0.3	0.1–0.8
Pre-existing condition	0.7	0.1–3.1	5.4*	1.0–29.9	1.0	Omitted
Healthcare worker	0.4	0.2–0.8	Not included		Not included	
<b>60–79 years</b>	<b>n = 1,263</b>		<b>n = 1,490</b>		<b>n = 1,338</b>	
B.1.1.7/SGTF	1.7	0.9–3.4	1.7	0.8–3.8	0.7	0.4–1.2
Pre-existing condition	0.4	0.1–1.5	0.8	0.4–1.5	2.4	0.9–6.4
Healthcare worker	0.3	0.1–0.9	Not included		Not included	
<b>≥ 80 years</b>	<b>n = 565</b>		<b>n = 612</b>		<b>n = 526</b>	
B.1.1.7/SGTF	1.2	0.6–2.3	1.1	0.3–4.2	0.4	0.2–1.0
Pre-existing condition	0.2	0.0–3.3	0.4	0.0–16.3	1.4	0.9–2.0
Healthcare worker	1.0	Omitted	Not included		Not included	
<b>B.1.351</b>						
<b>0–19 years</b>	<b>n = 504</b>		<b>NR</b>		<b>NR</b>	
B.1.351	2.5	0.7–9.1				
Pre-existing condition	0.4	0.1–1.2				
Healthcare worker	1.0	Omitted				
<b>20–39 years</b>	<b>n = 894</b>		<b>NR</b>		<b>NR</b>	
B.1.351	3.0	0.7–12.4				
Pre-existing condition	2.8	0.7–11.6				
Healthcare worker	1.0	Omitted				
<b>40–59 years</b>	<b>n = 869</b>		<b>n = 398</b>		<b>n = 442</b>	
B.1.351	3.5*	2.5–5.1	8.0*	3.7–17.3	1.0	Omitted
Pre-existing condition	0.7	0.3–1.6	1.0	Omitted	1.0	Omitted
Healthcare worker	0.2	0.0–2.0	Not included		Not included	
<b>60–79 years</b>	<b>n = 337</b>		<b>n = 313</b>		<b>n = 236</b>	
B.1.351	3.6*	1.1–11.9	2.0	0.7–6.0	1.8	0.7–4.8
Pre-existing condition	0.7	0.4–1.5	1.0	Omitted	1.0	Omitted
Healthcare worker	0.2	0.0–1.1	Not included		Not included	
<b>≥ 80 years</b>	<b>n = 215</b>		<b>n = 198</b>		<b>n = 168</b>	
B.1.351	4.1	0.8–20.4	4.3	0.6–33.1	1.0	0.3–2.9
Pre-existing condition	1.0	Omitted	1.0	Omitted	1.0	Omitted
Healthcare worker	1.0	Omitted	Not included		Not included	

aOR: adjusted odds ratio; CI: confidence interval; EEA: European Economic Area; EU: European Union; ICU: intensive care unit; NR: no result; SARS-CoV-2: severe acute respiratory syndrome coronavirus 2; SGTF: S gene target failure; VOC: variant of concern.

<sup>a</sup> Adjusted for reporting country (seven clusters), sex and week of reporting.

\* indicates significance (p < 0.05).

Analysis stratified by age group and adjusted for sex, country and week of reporting. n indicates the number of total cases included in the analysis for each age group (B.1.1.7/SGTF, B.1.351 or P.1 as well as non-VOC cases); Omitted variable, no 95% CI calculated.

**TABLE 3B**

Logistic regression for hospital and intensive care unit admission or death for cases with SARS-CoV-2 VOC B.1.1.7/SGTF B.1.351 and P.1 compared with non-VOC cases, EU/EEA, weeks 38/2020–10/2021 (n = 23,343)

VOC and age group	Hospitalisation		ICU admission		Death	
	aOR <sup>a</sup>	95% CI	aOR <sup>a</sup>	95% CI	aOR <sup>a</sup>	95% CI
<b>P.1</b>						
<b>0–19 years</b>	<b>n = 453</b>					
P.1	1.0	Omitted	<b>NR</b>		<b>NR</b>	
Pre-existing condition	0.6	0.2–2.2				
Healthcare worker	1.0	Omitted				
<b>20–39 years</b>	<b>n = 811</b>					
P.1	13.1*	6.5–26.5	<b>NR</b>		<b>NR</b>	
Pre-existing condition	2.7	1.2–6.1				
Healthcare worker	1.0	Omitted				
<b>40–59 years</b>	<b>n = 787</b>		<b>n = 363</b>		<b>n = 442</b>	
P.1	3.0*	1.5–5.8	6.8*	2.4–19.6	1.0	Omitted
Pre-existing condition	0.5	0.2–1.0	1.0	Omitted	1.0	Omitted
Healthcare worker	0.1	0.0–1.7	Not included		Not included	
<b>60–79 years</b>	<b>n = 294</b>		<b>n = 340</b>		<b>n = 267</b>	
P.1	3.7*	1.9–7.0	2.9*	1.6–5.4	1.6	0.8–3.2
Pre-existing condition	0.9	0.5–1.6	1.5	0.6–4.0	7.7	3.0–19.6
Healthcare worker	0.2	0.0–1.1	Not included		Not included	
<b>≥ 80 years</b>	<b>n = 191</b>		<b>n = 183</b>		<b>n = 176</b>	
P.1	1.5	0.8–2.6	13.9*	2.1–89.4	1.3	0.6–3.0
Pre-existing condition	1.0	Omitted	1.0	Omitted	3.7	3.4–4.0
Healthcare worker	1.0	Omitted	Not included		Not included	

aOR: adjusted odds ratio; CI: confidence interval; EEA: European Economic Area; EU: European Union; ICU: intensive care unit; NR: no result; SARS-CoV-2: severe acute respiratory syndrome coronavirus 2; SGTF: S gene target failure; VOC: variant of concern.

<sup>a</sup> Adjusted for reporting country (seven clusters), sex and week of reporting.

\* indicates significance (p < 0.05).

Analysis stratified by age group and adjusted for sex, country and week of reporting. n indicates the number of total cases included in the analysis for each age group (B.1.1.7/SGTF, B.1.351 or P.1 as well as non-VOC cases); Omitted variable, no 95% CI calculated.

of the risk; however, this would be the same for non-VOC cases included in the analysis. Reporting of variant cases is likely to be affected by both under-reporting and reporting delay, as WGS efforts take time (≥ 3 weeks), but countries are setting up systematic sampling for WGS monitoring of the circulation of emerging VOC (Supplement A) [17,18]. Supplement B presents a summary of B.1.1.7 and SGTF cases and of all COVID-19 cases including those with unknown or missing variant information as well as the logistic regression models comparing all non-VOC cases and those with missing/unknown information (possibly including unconfirmed B.1.1.7 cases), indicating also potential higher mortality associated with B.1.351 and P.1. Data were included until week 10/2021 and this may have been too soon after the introduction of these VOC into EU/EEA countries to detect higher mortality as observed in countries not included in this analysis for B.1.1.7 [8–10]. Also, information about hospitalisation, ICU admission and outcome may not have been available for the most recently infected cases. Although testing for variant viruses in December 2020 mainly targeted travellers from affected countries and their contacts, only a minority of cases in our analysis for whom data was available for the study period were reported

as importations. Testing of contacts of travellers or targeted testing in schools or workplaces generally or in response to outbreaks could also explain higher detection rates in younger age groups. Finally, the pooling of SGTF cases with B.1.1.7 cases could have led to some misclassification, despite evidence of high correlation between these cases. However, a small minority of 130 such cases had information on hospitalisation, which makes it unlikely that they had substantially impacted the severity outcomes.

## Conclusion

We show an increased risk for hospitalisations and ICU admission associated with the SARS-CoV-2 variants B.1.1.7/SGTF, B.1.351 and P.1, also in middle-aged individuals, which underlines the necessity to rapidly reach high levels of vaccine coverage and adhere to public health measures to reduce SARS-CoV-2 incidence and prevent severe cases. Enhanced testing and contact tracing implemented with a special focus on cases with VOC are also measures to reduce spread.

## Acknowledgements

We thank all public health experts working on SARS-CoV-2 for their tireless commitment in collecting and providing high-quality European surveillance data. We thank all the laboratories at local level involved in the RNA sequencing on COVID-19-positive confirmed cases. The authors want to acknowledge the data provision by the experts in Cyprus. We are also grateful to the TESSy data managers for their support and ECDC staff for their critical review. We would like to thank all people involved in the ECDC PHE response.

**Funding:** ECDC internal funds. The ICSC and the AIID Cohort are supported by Science Foundation Ireland under the Science Foundation Ireland, Enterprise Ireland, IDA Ireland COVID-19 Rapid Response Funding Call (Grant number: COVID-RRC 20/COV/0103 and COVID-RRC 20/COV/0305).

### COVID study groups:

#### IRELAND:

NVRL: Michael Carr, Gabriel Gonzalez, Guerrino Macori, Lauren Russell, Zoe Yandle, Charlene Bennett, Emer O'Byrne, Aoife Murphy, Grainne Tuite, Ann Conroy, Margaret Duffy, Ursula Morley, Brian Keoghan, Irene Ford, Maeve Kennedy, Sandra McDonnell, Aileen Flynn, Aoife Clarke, Andrea Crowley, Caoimhe Martin, Ellen Kelly, Joan Foxton, Daniel Hare, Linda Dunford, Jeff Connell, Joanne Moran, Jonathan Dean, Séamus Fanning, Lillian Rajan, Cillian De Gascun.

ICSC: Teagasc and APC Microbiome Ireland: Fiona Crispie, John Kenny, Paul Cotter, Calum Walsh, Elaine Lawton, Amy Fitzpatrick; Teagasc: Ewen Mullins, Michele Della Bartola, Matt McCabe; Limerick University Hospital: Patrick Stapleton, Carolyn Meaney; University College Cork, Cork University Hospital and APC Microbiome Ireland: Liam Fanning, Michael Prentice; University College Cork and APC Microbiome Ireland: John MacSharry; University College Cork and Cork University Hospital: Catherine Dempsey; University College Dublin: Dr Patrick Mallon, Alejandro Leon; National Virus Reference Laboratory, University College Dublin: Gabriel Gonzalez, Michael Carr, Aditi Chaturvedi, Jonathan Dean, Cillian De Gascun; NUI Galway: Simone Coughlan, Grainne McAndrew, Kate Reddington; NUI Maynooth: Fiona Walsh, David Fitzpatrick, Cian Smyth; Genuity Science Ireland: Tom O'Dwyer, Tim Chambers, Lara Clarke, David Jebb, Jessica Klopp, David Kavanagh, Karl Haslam, Patrick Buckley, Kate Lemass; The Royal College of Surgeons in Ireland, Dublin and Department of Clinical Microbiology, Beaumont Hospital, Dublin: Fidelma Fitzpatrick; Health Protection Surveillance Centre, Dublin and Department of Clinical Microbiology, Beaumont Hospital, Dublin: Karen Burns; Department of Clinical Microbiology, Beaumont Hospital: Jacqueline Cafferkey, Aisling Richmond, Margaret Foley; Trinity College Dublin: Jose Sanchez-Morgado; Helixworks Technologies, Ltd., Cork: Sachin Chalapati, Nimesh Pinnamaneni, Conor Crosbie, Dixita Limbachiya.

AIID: All Ireland Infectious Diseases Cohort investigators: UCD Centre for Experimental Pathogen Host Research: Patrick W. G. Mallon, Willard Tinago, Alejandro Abner Garcia Leon, Sarah Miles, Dana Alalwan, Riya Negi, Alan Macken. St Vincent's University Hospital; Eoin Feeney, Grace Kenny, Kathleen McCann, Neil Kelly, Matthew Blair, Rachel McCann, Claire Kenny, Cathal O'Brion, Sarmad Waqas, Stefano Savinelli. University College Dublin (UCD): Peter Doran, Tommy Bracken, Pooja Varghese. Mater Misericordiae University Hospital: John S Lambert, Aoife Cotter, Eavan Muldoon, Gerard Sheehan, Tara McGinty, Jack Lambert, Sandra Green, Kelly Leamy. Beaumont University Hospital: Eoghan de Barra, Sam McConkey, Christine Kelly. University

College Cork: Mary Horgan, Corinna Sadlier. Wexford General Hospital: Obada Yousif.

HPSC: Joan O'Donnell, Margaret Fitzgerald, Naomi Petty-Saphon and John Cuddihy.

#### FINLAND:

We would like to thank all clinical microbiology laboratories for their contribution in providing specimens for sequencing and sequencing results to the National Infectious Disease Register (NIDR).

#### PORTUGAL:

Portuguese Laboratory Network for the Diagnosis of COVID-19 and Public Health Department of the Health Administrative Regions, Physicians that provided data and samples from suspected cases and SARS-CoV-2 genetic characterization. INSA laboratory team for the diagnosis of SARS-CoV-2. Algarve Biomedical Center and Unilabs

#### ITALY:

COVID-19 Italian Microbiology Surveillance Study Group: Stefano Fiore, Concetta Fabiani, Eleonora Benedetti, Giuseppina Di Mario, Marzia Facchini, Simona Puzelli, Laura Calzoletti, Stefano Fontana, Giulietta Venturi, Claudia Fortuna, Giulia Marsili, Antonello Amendola, Dept Infectious Diseases, Istituto Superiore di Sanità; Liborio Stuppia, Laboratorio di Genetica Molecolare del Centro di Tecnologie Avanzate (CAST) "Università G. d'Annunzio di Chieti", Chieti; Giovanni Savini, Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "Giuseppe Caporale", Teramo; Antonio Picerno, Teresa Lopizzo, A.O.R. San Carlo – Potenza U.O.C di Analisi Chimico Cliniche e Microbiologiche; Domenico Dell'Edera, P.O. Madonna delle Grazie - Matera - U.O.S.D. Laboratorio di Genetica Medica; Pasquale Minchella, Laboratorio di Virologia e Microbiologia Azienda Ospedaliera Pugliese-Ciaccio; Francesca Greco, M.V. Mauro, UOC di Microbiologia e Virologia AO Annunziata, Cosenza; Giuseppe Viglietto, Laboratorio di genomica e patologia molecolare, Dipartimento di medicina sperimentale e clinica, Università Magna Graecia di Catanzaro, AOU Mater domini, Catanzaro; Luigi Atripaldi, AORN Azienda Sanitaria dei Colli, Naple; Antonio Limone, Istituto Zooprofilattico Sperimentale del Mezzogiorno, Naple; Laboratorio di Virologia – UCO Igiene e Sanità pubblica; Pierlanfranco D'Agaro, Azienda Sanitaria Universitaria Giuliano-Isontina (ASUGI), Trieste; Danilo Licastro, Laboratorio di Genomica e Epigenomica, Area Science Park, Basovizza, Trieste; Alessandro Marcello, Laboratory of Molecular Virology, International Centre for Genetic Engineering and Biotechnology (ICGEB), Padriciano, Trieste; Maria Rosaria Capobianchi, Laboratorio di Virologia, Istituto Nazionale Malattie Infettive IRCCS "L. Spallanzani", Rome; Giancarlo Icardi, Bianca Bruzzone, Flavia Lillo, Laboratorio di Patologia Clinica – ASL 2 Liguria; Adrea Orsi Laboratorio di Riferimento Regionale per le Emergenze di Sanità Pubblica (LaRESP); Elena Pariani, Dipartimento di Scienze Biomediche per la Salute, Università di Milano; Fausto Baldanti, Molecular Virology Unit, Fondazione IRCCS Policlinico San Matteo, Pavia, Italy; Maria Rita Gismondo, U.O.C Microbiologia Clinica, Virologia e diagnostica delle Bioemergenze, ASST FBF-Sacco, Milan; Fabrizio Maggi, ASST Sette Laghi; Arnaldo Caruso, ASST Spedali Civili di Brescia; Ferruccio Ceriotti, Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico di Milano; Beatrice Boniotti, Istituto Zooprofilattico Sperimentale Brescia; Patrizia Bagnarelli, Laboratorio di Virologia, Azienda Ospedaliero Universitaria - Ospedali Riuniti Ancona; Silvio Garofalo, Massimiliano Scutellà, UOC Laboratorio Analisi P.O. "A. Cardarelli" Campobasso; Elisabetta Pagani, Laboratorio Aziendale di Microbiologia e Virologia, Azienda Sanitaria dell'Alto Adige; Lucia Collini, Microbiologia e Virologia



- Presidio Ospedaliero Santa Chiara, Trento; Valeria Ghisetti, Laboratorio di Microbiologia e Virologia - ASL Città di Torino, Torino; Giuseppe Ru, Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Torino; Maria Chironna, Laboratorio di Epidemiologia Molecolare e Sanità Pubblica - AOU Policlinico di Bari; Antonio Parisi, Istituto Zooprofilattico Sperimentale di Puglia e Basilicata per la Puglia; Salvatore Rubino, Caterina Serra, Dipartimento di Scienze Biomediche, Università di Sassari, S.C. Microbiologia e Virologia Laboratorio Virologia - AOU di Sassari; Giovanna Piras, Laboratorio Specialistico U.O. Ematologia Ospedale "San Francesco" ASSL, Nuoro; Ferdinando Coghe, Laboratorio Generale (HUB) di analisi chimico cliniche e microbiologia - P.O. Duilio Casula - AOU di Cagliari; Francesco Vitale, Fabio Tramuto, Laboratorio di Riferimento Regionale per la Sorveglianza Epidemiologica e Virologica del P.R.O.M.I.S.E. - AOU "Giaccone" di Palermo; Guido Scalia, Concetta Ilenia Palermo, BIOMETEC UNICT e AOU "G. Rodolico-S. Marco, Catania; Giuseppe Mancuso, UOC Microbiologia, Azienda Ospedaliera Universitaria "G. Martino, Messina; Francesca Di Gaudio, Scuola di Medicina, Università di Palermo, CRQ, Sicilia; Stefano Vullo, Stefano Reale, Istituto Zooprofilattico Sperimentale della Sicilia; Maria Grazia Cusi UOC Microbiologia e Virologia, Azienda Ospedaliera Universitaria Senese Dipartimento Biotecnologie Mediche, Università degli Studi di Siena; Gian Maria Rossolini SOD Microbiologia e Virologia Azienda Ospedaliera Universitaria Careggi; Mauro Pistello, UOC Virologia Azienda Ospedaliera-Universitaria Pisana, Pisa; Antonella Mencacci, Barbara Camilloni, Microbiology and Clinical Microbiology, Department of Medicine and Surgery, University of Perugia, Perugia, Italy; Silvano Severini, Istituto Zooprofilattico Sperimentale delle Regioni Umbria e Marche; Massimo Di Benedetto Laboratorio Analisi Cliniche dell'Ospedale Parini di Aosta; Terregino Calogero, Isabella Monne, SCS5 - Ricerca e innovazione. Istituto Zooprofilattico Sperimentale delle Venezie; Valeria Biscaro, U.O.C. Microbiologia-Virologia- AULSS2 La Marca - P.O. Treviso.

## Conflict of interest

None declared.

## Authors' contributions

CA and TF: conceptualisation (lead); writing – original draft (lead); formal analysis (lead); writing – review and editing (equal); JGD: data analysis (equal) – review and editing (equal); AP, AM, GS, and NB: writing – review and editing (equal). All other co-authors coordinated collection of specimens and epidemiological data, analysed the specimens and provided data to TESSy, reviewed the analysis and approved the final manuscript. All authors contributed to the work, reviewed and approved the manuscript before submission.

## References

- Public Health England (PHE). Investigation of novel SARS-CoV-2 variant - variant of concern 202012/01. London: PHE; 2020. Available from: [https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment\\_data/file/959438/Technical\\_Briefing\\_VOC\\_SH\\_NJL2\\_SH2.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/959438/Technical_Briefing_VOC_SH_NJL2_SH2.pdf)
- European Centre for Disease Prevention and Control (ECDC). Risk assessment: Risk related to spread of new SARS-CoV-2 variants of concern in the EU/EEA - first update. Stockholm: ECDC; 2021. Available from: <https://www.ecdc.europa.eu/en/publications-data/covid-19-risk-assessment-spread-new-variants-concern-eueea-first-update>
- Japanese National Institute of Infectious Diseases (NIID). Brief report: new variant strain of SARS-CoV-2 identified in travelers from Brazil: Tokyo: NIID; 2021. Available from: <https://www.niid.go.jp/niid/en/2019-ncov-e/10108-covid19-33-en.html>
- Faria NR, Claro IM, Candido D, Franco LAM, Andrade PS, Coletti TM, et al. Genomic characterisation of an emergent SARS-CoV-2 lineage in Manaus: preliminary findings. *Virological.org*. 2021. Available from: <https://virological.org/t/genomic-characterisation-of-an-emergent-sars-cov-2-lineage-in-manauas-preliminary-findings/586>
- Tegally H, Wilkinson E, Giovanetti M, Iranzadeh A, Fonseca V, Giandhari J, et al. Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa. *medRxiv*. 2020:2020.12.21.20248640. <https://doi.org/10.1101/2020.12.21.20248640>
- European Centre for Disease Prevention and Control (ECDC). COVID-19 country overviews, week 12/2021, 1 April 2021. Stockholm: ECDC; 2021. Available from: [https://covid19-surveillance-report.ecdc.europa.eu/archive-COVID19-reports/archive/2021W12\\_country\\_overview\\_report\\_20210331.zip](https://covid19-surveillance-report.ecdc.europa.eu/archive-COVID19-reports/archive/2021W12_country_overview_report_20210331.zip)
- Horby P, Huntley C, Davies N, Edmunds J, Ferguson N, Medley G, et al. NERVTAG note on B.1.1.7 severity. London: Government Digital Service; 2021. Available from: [https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment\\_data/file/955239/NERVTAG\\_paper\\_on\\_variant\\_of\\_concern\\_\\_VOC\\_\\_B.1.1.7.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/955239/NERVTAG_paper_on_variant_of_concern__VOC__B.1.1.7.pdf)
- Bager P, Wohlfahrt J, Fonager J, Rasmussen M, Albertsen M, Yssing Michaelsen T, et al. Increased risk of hospitalisation associated with infection with SARS-CoV-2 lineage B.1.1.7 in Denmark. *Preprints with the Lancet*. 2021. Available from: <https://ssrn.com/abstract=3792894> or <http://dx.doi.org/https://doi.org/10.2139/ssrn.3792894>
- Davies NG, Jarvis CI, Edmunds WJ, Jewell NP, CMMID COVID-19 Working Group, Diaz-Ordaz K, et al. Increased mortality in community-tested cases of SARS-CoV-2 lineage B.1.1.7. *Nature*. 2021. <https://doi.org/10.1038/s41586-021-03426-1> PMID: 33723411
- Challen R, Brooks-Pollock E, Read JM, Dyson L, Tsaneva-Atanasova K, Danon L. Risk of mortality in patients infected with SARS-CoV-2 variant of concern 202012/1: matched cohort study. *BMJ*. 2021;372(579):n579. <https://doi.org/10.1136/bmj.n579> PMID: 33687922
- Madhi SA, Baillie V, Cutland CL, Voysey M, Koen AL, Fairlie L, et al. Efficacy of the ChAdOx1 nCoV-19 Covid-19 Vaccine against the B.1.351 Variant. *N Engl J Med*. 2021;NEJMoa2102214. <https://doi.org/10.1056/NEJMoa2102214> PMID: 33725432
- Wang P, Liu L, Iketani S, Luo Y, Guo Y, Wang M, et al. Increased resistance of SARS-CoV-2 variants B.1.351 and B.1.1.7 to antibody neutralization. *bioRxiv*. 2021:2021.01.25.428137. <https://doi.org/10.1101/2021.01.25.428137>
- Novel variant incident management team, Public Health England with Imperial College, the University of Edinburgh, the University of Birmingham and the Wellcome Sanger Institute. New evidence on VUI-202012/01 and review of the public health risk assessment. London: Public Health England; 2020. Available from: <https://khub.net/documents/135939561/338928724/New+SARS-COV-2+variant+-+information+and+risk+assessment.pdf/b56d4591-0466-1a18-28dc-010e0fdeef53?t=1608569319930>
- Public Health England (PHE). Investigation of SARS-CoV-2 variants of concern in England. London: PHE; 2021. Available from: [https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment\\_data/file/961299/Variants\\_of\\_Concern\\_VOC\\_Technical\\_Briefing\\_6\\_England-1.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/961299/Variants_of_Concern_VOC_Technical_Briefing_6_England-1.pdf)
- Borges V, Sousa C, Menezes L, Gonçalves AM, Picão M, Almeida JP, et al. Tracking SARS-CoV-2 lineage B.1.1.7 dissemination: insights from nationwide spike gene target failure (SGTF) and spike gene late detection (SGTL) data, Portugal, week 49 2020 to week 3 2021. *Euro Surveill*. 2021;26(10):2100131. <https://doi.org/10.2807/1560-7917.ES.2021.26.10.2100130> PMID: 33706862
- Robert Koch-Institut (RKI). Risikobewertung zu COVID-19. [Risk assessment of COVID-19]. Berlin: RKI; 2021. German. Available from: [https://www.rki.de/DE/Content/InfAZ/N/Neuartiges\\_Coronavirus/Risikobewertung.html](https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/Risikobewertung.html)
- European Centre for Disease Prevention and Control (ECDC), World Health Organization Regional Office for Europe (WHO/Europe). Methods for the detection and identification of SARS-CoV-2 variants. Stockholm and Copenhagen: ECDC and WHO/Europe; 2021. Available from: <https://www.ecdc.europa.eu/sites/default/files/documents/Methods-for-the-detection-and-identification-of-SARS-CoV-2-variants-WHO-ECDC.pdf>
- European Centre for Disease Prevention and Control (ECDC). Risk related to spread of new SARS-CoV-2 variants of concern in the EU/EEA - 29 December 2020. Stockholm: ECDC; 2020. Available from: <https://www.ecdc.europa.eu/sites/default/files/documents/COVID-19-risk-related-to-spread-of-new-SARS-CoV-2-variants-EU-EEA.pdf>

## License, supplementary material and copyright

This is an open-access article distributed under the terms of the Creative Commons Attribution (CC BY 4.0) Licence. You may share and adapt the material, but must give appropriate credit to the source, provide a link to the licence and indicate if changes were made.

Any supplementary material referenced in the article can be found in the online version.

This article is copyright of the authors or their affiliated institutions, 2021.