



## Summary of COVID-19 virus variants in Ireland

Report prepared by HPSC and NVRL on 22/03/2021

All medical practitioners, including clinical directors of diagnostic laboratories, are required to notify the Medical Officer of Health (MOH)/Director of Public Health (DPH) of any confirmed, probable or possible cases of COVID-19 that they identify. Laboratory, clinical and epidemiological data, on notified COVID-19 cases, are recorded on Health Protection Surveillance Centre's (HPSC) Computerised Infectious Disease Reporting System (CIDR).

Whole genome sequencing (WGS) is carried out by the National Virus Reference Laboratory (NVRL) on a proportion of confirmed COVID-19 cases. NVRL use a sampling frame, developed by Prof. Phillip Nolan (chair of the NPHEP Epidemiological Modelling Advisory Group), for selecting cases to sequence from community sources. Hospitals will be asked to refer a proportion of their samples, as decided by the National WGS Steering Group, from confirmed cases for sequencing so that variants that may cause more severe disease can be identified. Specimens from the sentinel GP Surveillance programme will also be sequenced. If sentinel GPs send less than 50 samples for testing in a given week, NVRL will sequence all of them. If more than 50 sentinel samples are referred, they will sequence a random selection based on a random selection tool. In addition, capacity will be built into the National WGS Programme to sequence specific groups of cases (i.e. reactive sequencing) including, suspected vaccine failure cases, reinfections, unusual outbreaks etc.

This report summarises whole genome sequencing and epidemiological data for COVID-19 cases that have been sequenced in Ireland between week 41 2020 (4<sup>th</sup> October 2020) and week 10 2021 (13<sup>th</sup> March 2021). WGS sequencing data were provided by NVRL. Epidemiological data on these cases were extracted from CIDR on 22/03/2021. CIDR is a dynamic system and case details may be updated at any time. Therefore, the data described here may differ from previously reported data and data reported for the same time period in the future.

Table 1 shows whole genome sequencing results since week 51 2020 (week starting December 13<sup>th</sup>) by most likely mode of transmission. No variants of concern were identified in Ireland prior to week 51 2020. Cases of three variants of concern (VOC) have been identified in Ireland since then; UK VOC (B.1.1.7), South African VOC (B.1.351) and Brazilian VOC (P.1). Four variants of interest have also been identified; P.2 (a different variant from Brazil), B.1.525 (variant from Nigeria) B.1.526 (variant from New York) and A.27.

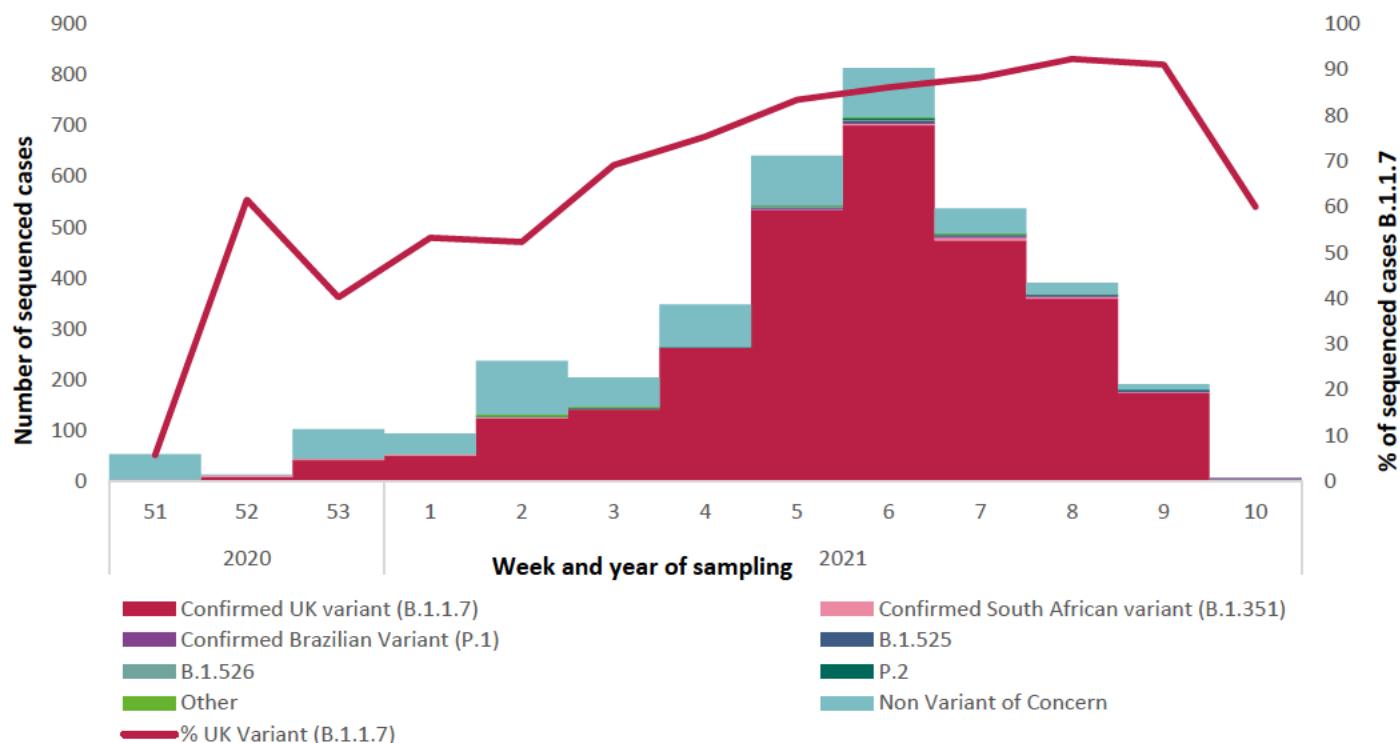
The first case of the UK VOC (B.1.1.7) was identified in Ireland in week 51 2020 (figures 1 & 2). Transmission of this variant is now widespread in Ireland. Of cases sequenced in week 9 2021, 91% were found to be infected with the B.1.1.7 variant. Sequencing results are not yet available for most of the cases sampled and selected for sequencing during week 10 2021. The South African VOC (B.1.351) was first identified in Ireland in a case with a specimen date in week 52 2020 (week starting December 19<sup>th</sup>). A total of 26 COVID-19 cases have been confirmed to have been infected with this variant in Ireland to date. To date the Brazilian VOC (P.1) has been confirmed in nine cases of COVID-19. See table 1, figures 1 & 2, table 2-4 for more details.

**Table 1.** Whole genome sequencing results for COVID-19 cases sampled from week 51 (December 13<sup>th</sup> 2020) to Week 10 (March 13<sup>th</sup> 2021)

Virus variant	Number of cases	Most likely mode of transmission*					
		Close contact with a confirmed case	Travel related*	Community transmission	Healthcare setting acquired: staff	Healthcare setting acquired: patient	Under investigation
<b>Confirmed B.1.351 (South African variant)</b>	<b>26</b>	<b>8</b>	<b>13</b>	<b>4</b>	<b>1</b>		
Probable B.1.351	6	1	5				
Possible B.1.351**	1		1				
<b>Confirmed P.1 (Brazilian variant)</b>	<b>9</b>	<b>2</b>	<b>7</b>				
Probable P.1	2	1	1				
Possible P.1	2		1	1			
<b>Confirmed B.1.1.7 (UK Variant)</b>	<b>2873</b>	<b>1596</b>	<b>23</b>	<b>644</b>	<b>158</b>	<b>146</b>	<b>306</b>
<b>Other variants of interest</b>							
P.2 (Brazil)	12	4	5	2			1
B.1.525 (Nigeria)	14	8	5	1			
B.1.526 (New York)	5	5					
A.27	2		2				
Other - not variants of concern or interest	677	259	11	126	72	94	115
<b>Total</b>	<b>3629</b>	<b>1884</b>	<b>74</b>	<b>778</b>	<b>231</b>	<b>240</b>	<b>422</b>

\*travel related includes imported cases and those cases who acquired their infection from imported cases.

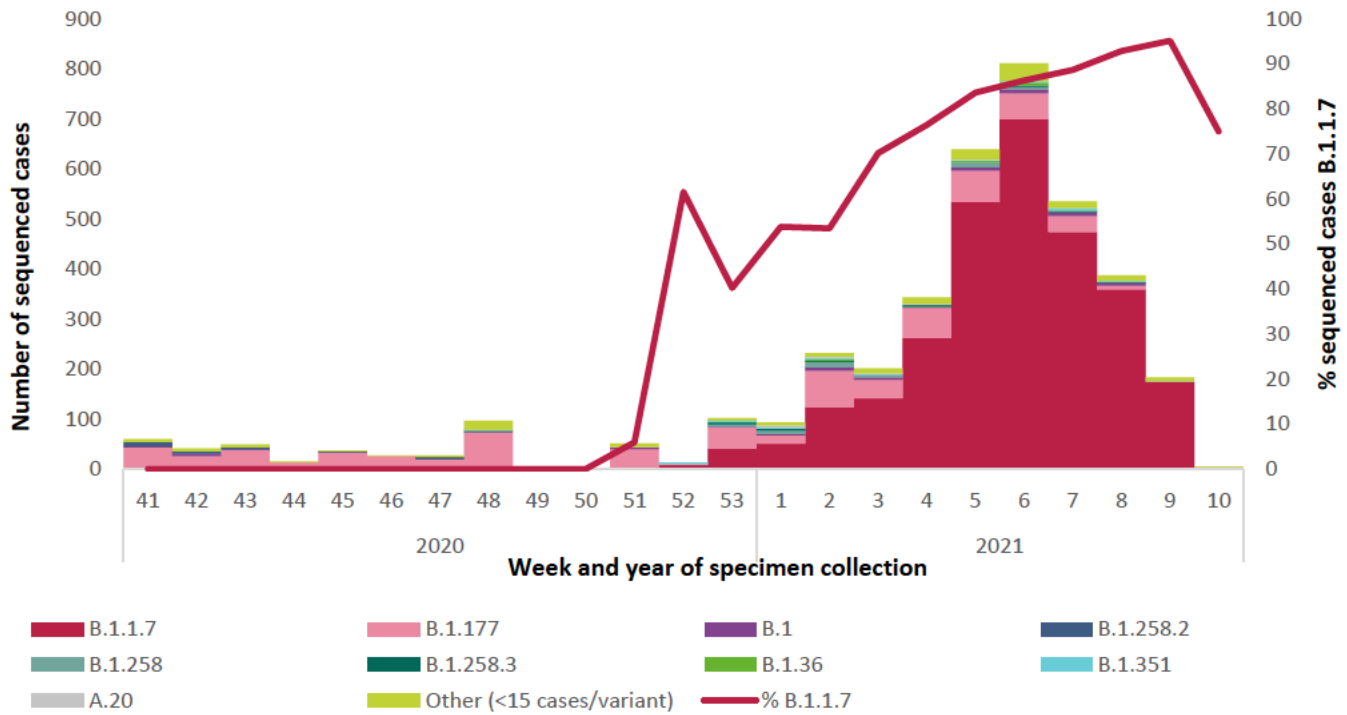
\*\*Prior to the current case definition some cases were considered possible variants of concern, this category is no longer applicable



**Figure 1.** Whole genome sequencing results and percentage of sequenced specimens\* that were found to be the UK variant (B.1.1.7), specimen collection dates from week 51 (13<sup>th</sup> December 2020) to week 10 (13<sup>th</sup> March 2021)

\*The proportion of cases attributed to lineage B.1.1.7 is based on S gene target failure (SGTF) data from the Thermo Fisher TaqPath assay. To date, all those SGTF samples that have undergone WGS have been identified as lineage B.1.1.7.

\*\*Other includes probable or possible variants of concern and other variants of interest.



**Figure 2.** Whole genome sequencing results and percentage of sequenced specimens\* that were found to be the UK variant (B.1.1.7), specimen collection dates from week 41 (Oct 4<sup>th</sup> 2020) to week 10 (13<sup>th</sup> March 2021)

\*Variants with less than 15 cases in total during this time period are included in the 'Other' category. This includes P.1.

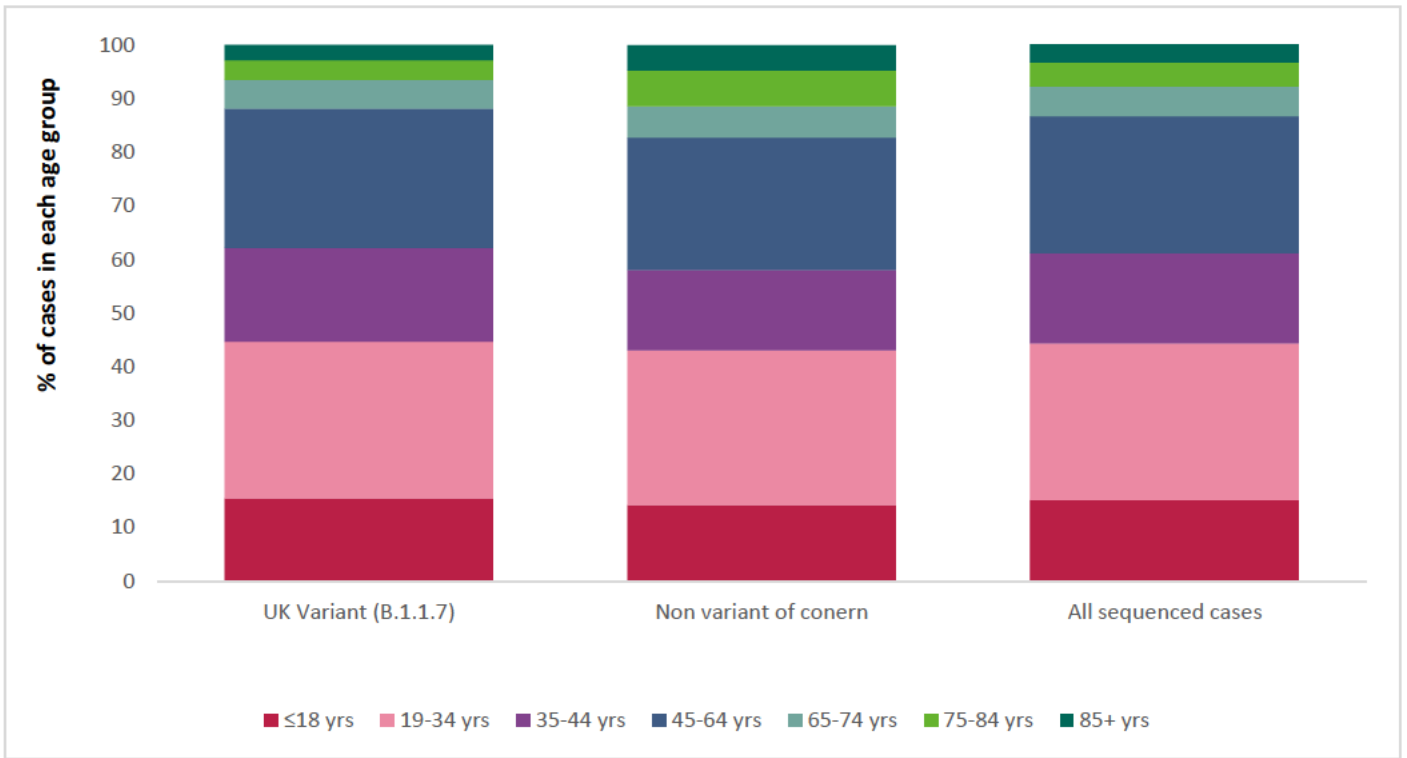
### Comparison of B.1.1.7 (the UK variant) and Non variants of concern

The age profile of cases sequenced from week 51 to date and found to be the UK variant (B.1.1.7) was slightly younger (median: 38 years, mean: 39 years) than those found not to be infected with variants of concern in the same time period (median: 40 years, mean: 42 years), but the overall age distributions were quite similar (table 2 & figure 3).

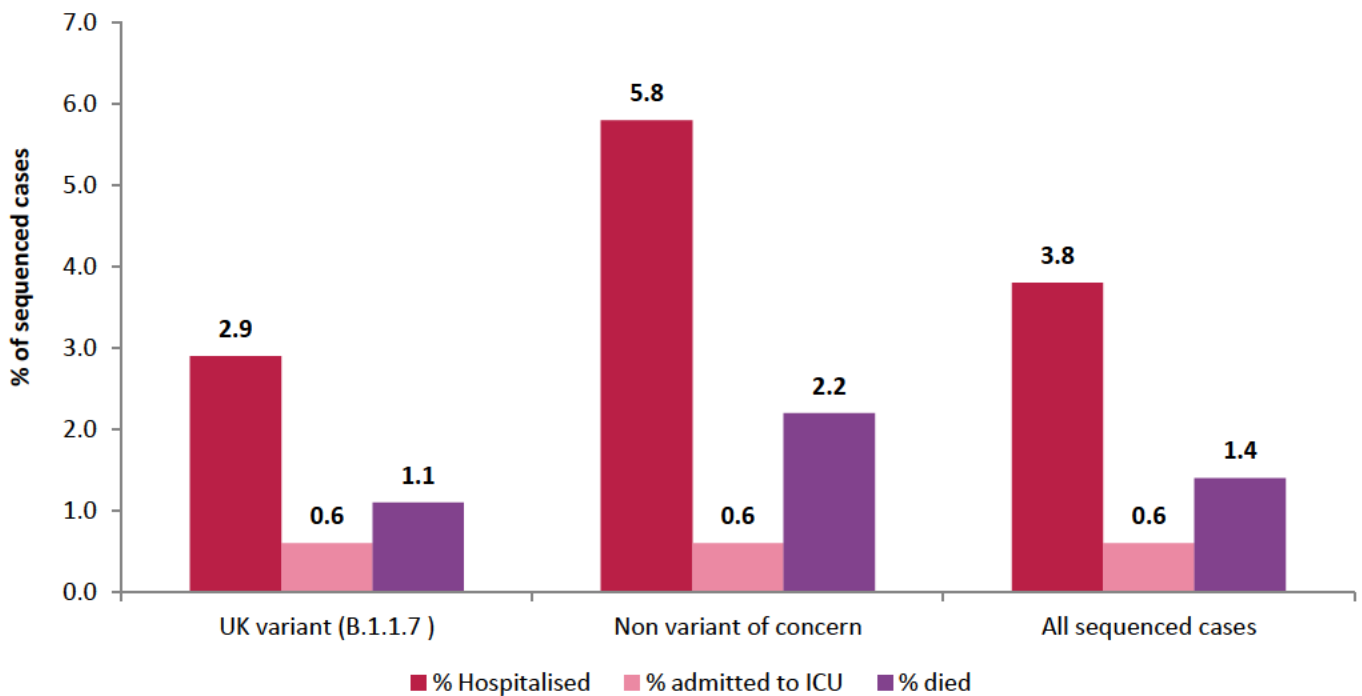
After adjusting for age, there was no statistically significant difference in hospital admissions, ICU admissions or deaths in cases with the B.1.1.7 variant compared to cases not infected with variants of concern (table 2 & figure 4).

**Table 2.** Summary of sequenced cases infected with B.1.1.7 (UK variant) compared to non-variants of concern, specimen collection dates from week 51 (13<sup>th</sup> December 2020) to week 10 (13<sup>th</sup> March 2021)

Characteristic	B.1.1.7 (UK Variant)		Non variants of concern	
	Num	%	Num	%
<b>Age group</b>				
≤18 yrs	442	15.4	89	13.1
19-34 yrs	836	29.1	155	22.9
35-44 yrs	500	17.4	102	15.1
45-64 yrs	743	25.9	188	27.8
65-74 yrs	154	5.4	39	5.8
75-84 yrs	103	3.6	57	8
85+ yrs	83	2.9	35	5
Unknown	12	0.4	12	2
<b>Sex</b>				
Male	1379	48.0	306	45.2
Female	1482	51.6	359	53.0
Unknown	1	0	0	0
<b>Clinical</b>				
<b>Hospitalised</b>	<b>84</b>	<b>2.9</b>	<b>32</b>	<b>4.7</b>
<19 yrs	1	0.2	0	0.0
19-44 yrs	20	1.5	3	1.2
45-64 yrs	22	3.0	6	3.2
65+ yrs	41	12.1	23	17.6
Admitted to ICU	18	0.6	4	0.6
Died	31	1.1	18	2.7
<b>CHO area</b>				
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██████████	████	██	██	████
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██████████	██	1.9	25	3.7
<b>Total</b>	<b>2873</b>		<b>677</b>	



**Figure 3.** Age profile of sequenced specimens that were found to be the UK variant (B.1.1.7) compared to cases found not to be infected with variants of concern, specimen collection dates from week 51 (13<sup>th</sup> December 2020) to week 10 (13<sup>th</sup> March 2021)



**Figure 4.** Percentage of sequenced cases hospitalised, admitted to ICU and who died, UK variant (B.1.1.7) compared to cases found not to be infected with variants of concern and all sequenced cases, specimens from week 51 (13<sup>th</sup> December 2020) to week 10 (13<sup>th</sup> March 2021)

## Focus on the emerging variants of concern and variants of interest (excluding variant B.1.1.7)

The South African VOC (B.1.351) was first identified in Ireland in a case with a specimen date in week 52 2020 (week starting December 19<sup>th</sup>). A total of 26 COVID-19 cases have been confirmed to have been infected with this variant in Ireland to date (table 3). Of these, nine had a history of international travel, four were infected through contact with a case who had travelled outside Ireland, eight were reported to be contacts of known cases, one was reported to be a healthcare worker who acquired the infection in a work setting and four cases are currently classified as community transmission. Twenty three of these cases are associated with fourteen outbreaks, most of which were family clusters. Four of the outbreaks had no further linked cases. No links have been identified between the remaining three cases, one of which was linked to travel (table 4).

To date the Brazilian VOC (P.1) has been confirmed in nine cases of COVID-19 (table 3). Five were part of two separate outbreaks involving families who had travelled from Brazil. Two further cases are reported to be contacts of confirmed cases, but are not currently linked to an outbreak on CIDR and the remaining two cases were associated with travel (table 4).

**Table 3.** Summary of sequenced cases infected with the B.1.351, P.1, B.1.525 and B.1.526 variants, specimen collection dates from week 51 (13<sup>th</sup> December 2020) to week 10 (13<sup>th</sup> March 2021)

Characteristic	B.1.351 (South African variant)		P.1 (Brazilian variant)		B.1.525		B.1.526	
	Num	%	Num	%	Num	%	Num	%
<b>Age group</b>								
≤18 yrs	3	12	1	11	2	14	5	100.0
19-34 yrs	6	23.1	6	66.7	7	50.0	0	0.0
35-44 yrs	4	15.4	0	0.0	3	21.4	0	0.0
45-64 yrs	10	38.5	2	22.2	2	14.3	0	0.0
65-74 yrs	1	3.8	0	0.0	0	0.0	0	0.0
75-84 yrs	2	8	0	0	0	0	0	0.0
85+ yrs	0	0	0	0	0	0	0	0.0
Unknown	0	0	0	0	0	0	0	0.0
<b>Sex</b>								
Male	11	42.3	4	44.4	7	50.0	3	60.0
Female	15	57.7	5	55.6	7	50.0	2	40.0
Unknown	0	0	0	0	0	0	0	0
<b>Clinical</b>								
Hospitalised	3	11.5	0	0	1	0.7	0	0
Admitted to ICU	0	0	0	0	0	0	0	0
Died	0	0	0	0	0	0	0	0
<b>CHO area</b>								
█	█	█	█	█	█	█	█	█
█	█	█	█	█	█	█	█	█
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Unknown	0	0	0	0	0	0	0	0
<b>Total</b>	<b>26</b>		<b>9</b>	<b>100</b>	<b>14</b>		<b>5</b>	

**Table 4.** Description of cases infected with the P.1 (Brazilian variant) and B.1.351 (South African variant), and summary of associated cases, from week 51 (13<sup>th</sup> December 2020) to week 10 (13<sup>th</sup> March 2021)

Outbreak Identifier	Outbreak location or mode of transmission	Total number of cases linked to outbreak on CIDR	Whole genome sequencing results							
			Total number of cases with WGS results	B.1.351	Probable B.1.351	B.1.1.7	Non variant of concern	B.1.525	B.1.526	P.1
B.1.351 outbreak 1	HCW Residential institution, disability setting, no travel	26	1	1						
B.1.351 outbreak 2	Travel related	1	1	1						
B.1.351 outbreak 3	Travel related	3	1	1						
B.1.351 outbreak 4	Travel related - South Africa	3	3	3						
B.1.351 outbreak 5	Indirect travel link to Zambia	1	1	1						
B.1.351 outbreak 6	Private house	1	1	1						
B.1.351 outbreak 7	Travel related - South Africa	3	3	1	2					
B.1.351 outbreak 8	Travel related - Tanzania	2	2	2						
B.1.351 outbreak 9	Travel related	3	2	2						
B.1.351 outbreak 10	Travel related	1	1	1						
B.1.351 outbreak 11	Private house, no travel	4	4	2	1		1			
B.1.351 outbreak 12	Private house, no travel	4	2	1		1				
B.1.351 outbreak 13	Private house, no travel	3	3	3						
B.1.351 outbreak 14	Two families - link to outbreak 13	7	3	3						
B.1.351. No outbreak. Case 1	Healthcare acquired: staff, no travel	0	1	1						
B.1.351. No outbreak. Case 2	Travel related	0	1	1						
B.1.351. No outbreak. Case 3	Contact with confirmed case	0	1	1						
P.1 Outbreak 1	Travel related - Brazil	3	3							3
P.1 Outbreak 2	Travel related - Brazil	2	2							2
P.1 No outbreak. Case 1	Travel related	0	1							1
P.1 No outbreak. Case 2	Close contact with confirmed case	0	1							1
P.1 No outbreak. Case 3	Close contact with confirmed case	0	1							1
P.1 No outbreak. Case 4	Travel related	0	1							1

**Table 5.** Description of cases infected with the P.1.526 and P.1.525 variants, and summary of associated cases, from week 51 (13<sup>th</sup> December 2020) to week 10 (13<sup>th</sup> March 2021)

Outbreak Identifier	Outbreak location or mode of transmission	Total number of cases linked to outbreak on CIDR	Whole genome sequencing results							
			Total number of cases with WGS results	B.1.351	Probable B.1.351	B.1.1.7	Non variant of concern	B.1.525	B.1.526	P.1
B.1.525. Outbreak 1	Travel related - Nigeria	5	4					4		
B.1.525. Outbreak 2	Travel related - UAE	2	2					2		
B.1.525. Household cluster, OB not yet created on CIDR	Travel related - Brazil	0	3					3		
B.1.525. No outbreak. Case 1	Travel related - Nigeria	0	1					1		
B.1.525. No outbreak. Case 2	Community transmission	0	1					1		
B.1.525. No outbreak. Case 3	Contact with confirmed case	0	1					1		
B.1.525. No outbreak. Case 4	Contact with confirmed case	0	1					1		
B.1.525. No outbreak. Case 5	Contact with confirmed case	0	1					1		
B.1.526. Outbreak 1	Contact with confirmed cases who had travelled from US	8	7				2		5	